

GenCore version 5.1.7

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OM protein - nucleic search, (using ~~same~~ plms\_p2n model)

Run on: April 1, 2006, 04:29:01 ; Search time 10735.5 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525A-21

Perfect score: 2893

Sequence: 1 CVALSRDLGLPEPIAG.....LLGRANEARHVKRLHVGPCR 539

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.cm.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.sts.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2893	100.0	1620	6	AR106498 Sequence
2	2861	98.9	1749	6	BD071187 Plant lik
3	2861	98.9	1752	6	AR106494 Sequence

4	2832	97.9	2008	6	BD249566
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7	2832	97.9	2491	6	BD249559
8	2832	97.9	2491	6	AR340007
9	2818	97.4	2383	6	A93359
10	2818	97.4	2383	6	AR174874
11	2818	97.4	2383	6	AR411327
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13	2757	95.3	2990	6	AR049919
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30	2466.5	85.3	2239	6	AR535116
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32	2466.5	85.3	2771	6	BD209997
33	2466.5	85.3	2771	6	BD54865
34	2466.5	85.3	2771	6	AX010492
35	2324	80.3	2055	15	TAU48227
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38	2043	70.6	1415	6	AR340013
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81	1103	38.1	2418	6	AR220363	AR220363 Sequence							
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83	1101	38.1	2394	15	AF395537	AF395537 Oryza sat							
84	1099.5	38.0	2988	15	PSSTASYNT	X88790 P. sativum m							
85	1097	37.9	3049	15	AF026421	AF026421 Chlamydom							
86	1095	37.8	2010	6	BD071186	BD071186 Plant lik							
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100	1080	37.3	2645	15	AK066446	AK066446 Oryza sat							
101	1077.5	37.2	2793	15	TAE269504	AJ269504 Triticum							
102	1075	37.2	2433	15	AB115917	AB115917 Oryza sat							
103	1075	37.2	2433	15	AB115918	AB115918 Oryza sat							
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106	1070.5	36.3	2842	15	AF155217	AF155217 Triticum							
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123	978.5	33.8	2085	6	AR049920	AR049920 Sequence							
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127	909	31.4	2221	15	AR029546	AR029546 Phaseolus							
128	906	31.3	1609	15	AK061803	AK061803 Oryza sat							
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139	871	30.1	2274	6	AR220357	AR220357 Sequence							
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ALIGNMENTS

RESULT 1	AR106498	1620 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR106498				
DEFINITION	Sequence 20 from patent US 6107060.				
ACCESSION	AR106498				
VERSION	AR106498.1	GI:12821028			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1620)				
AUTHORS	Keeling, P. and Guan, H.				
TITLE	Starch encapsulation				
JOURNAL	Patent: US 6107060-A 20 22-AUG-2000;				
FEATURES	Location/Qualifiers				
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Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	100.0%	Indels:	0		
DB:	6	Gaps:	0		
US-10-628-525A-21 (1-539) x AR106498 (1-1620)					
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QY	21	SerIleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLys	40		
Db	61	TCCATCGATAACACAGTAGTGTGTGGCAAGTACAGGATTTCTGAGATTGTGGTGGAAAG	120		
QY	41	GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerPro	60		
Db	121	GAGCAAGCTCGAGCTAAAGTAAACAAAGCATGTGTTGTAAACCGCGAAGCTTCTCT	180		
QY	61	TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaLa	80		
Db	181	TATGCANAAGTCTGGGGGCTAGGAGATGTTGTGGTTCATTGCCAGTTGCTTCTGCTCT	240		
QY	81	ArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsn	100		
Db	241	CGTGTGTCACCGTGTGATGGTGTGTAATGCCAGATATTTAAATGGTACCTCCGATAAGAT	300		
QY	101	TyrAlaAsnAlaPheThrGluLysHisIleArgIleProCysPheGlyGlyGluHis	120		
Db	301	TATGCAATGCAATTTACAGAAAAACATTCGATTCGATTCCTTTGGCGGTGAACAT	360		
QY	121	GluValThrPhePheHisGluTyrArgAspSerValAspTrrpValPheValAspHisPro	140		
Db	361	GAAGTTACTCTTCCATGAGTATAGATTCAGTTGACTGGGTGTTGTTGATCATCC	420		
QY	141	SerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGln	160		
Db	421	TCATATCACAGACCTGGAAATTTATATGAGAGATAAGTTGGTGTGTTGGTGTATATCAG	480		
QY	161	PheArgTyrThrLeuLeuCystYrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly	180		
Db	481	TTGAGTACACACTCCTTGTGTCATGTCATGAGGCTCCTTTGATCCTTGAATTGGGA	540		
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Db      601  CCAGTCTCTTCTGTCGCAAAATATAGACCATATGTTGTTTATAAGACTCCCGCAGCATT 660
Qy      221  LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyProAspLeu 240
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Qy      241  GlyLeuProGluTyrGlyValAlaLeuGluTyrValPheProGluTyrAlaArgArg 260
Db      721  GGGTTGCCACTGAATGGTATGAGACTCTGAGTGGGTATTCCTGATGGCCAGAGG 780
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Qy      281  ArgIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGln 300
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Qy      301  GlyLeuAsnGluLeuLeuSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320
Db      901  GGCTCAATGAGCTCTTAAGCTCCGAAAGAGTGTATTAAACGGAATTTGTAATGGAATT 960
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Db      1021  GACCTCTCTGGAAGGCCAATGTAAAGGTGCATTGCGAAGGAGCTGGGTTTACCTATA 1080
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Qy      441  IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460
Db      1321  ATATTGTTAATGTCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTATATGCTATGCG 1380
Qy      461  TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe 480
Db      1381  TATGGACAGATTCCTGTTGTTCATGCAACTCGGGGGCTTAGAGATACCGTGAGAACTTC 1440
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Qy      521  LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
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RESULT 2

BD071187

LOCUS

BD071187

1749 bp

DNA

linear

PAT 27-AUG-2002

DEFINITION Plant like starches and the method of making them in hosts.  
ACCESSION BD071187  
VERSION BD071187.1 GI:22616790  
KEYWORDS JP 2001519664-A/26.  
SOURCE Zea mays  
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 1749)

Guan,H. and Keeling,P.L.

Plant like starches and the method of making them in hosts

Patent: JP 2001519664-A 26 23-OCT-2001;

EXSEED GENETICS LLC

OS Zea mays

PN JP 2001519664-A/26

PD 23-OCT-2001

PF 03-APR-1998 JP 1998542940

PR 04-APR-1997 US 60/042939

PI HANPING GUAN,PETER L KEELING

PC A01H5/00,C12N15/29,C12N15/31,C12N15/54,C12N15/70,C12N15/74, PC C12N15/80

PC C12N15/81,C12N15/82,C12P19/04

CC Plant like starches and the method of making them in hosts PH

Key Location/Qualifiers

FT CDS Location/Qualifiers

1..1749

/organism="Zea mays"

/mol\_type="genomic DNA"

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## ORIGIN

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Pred. No.: 5,52e-233 Length: 1749  
Score: 2861.00 Matches: 539  
Percent Similarity: 92.5% Conservative: 0  
Best Local Similarity: 92.5% Mismatches: 0  
Query Match: 98.9% Indels: 44  
DB: 6 Gaps: 1

US-10-628-525A-21 (1-539) x BD071187 (1-1749)

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Qy 8 ----- 8

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Qy 9 -----AppleGlyLeuGluProGluGly 16

Db 121 TGAACCCCGCGCGCGCTGTCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 180

Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36

Db 181 ATTGCTGAAGGTTCCATCGATAACAGTAGTTGTGGCAAGTGAGCAAGATCTGAGATT 240

Qy 37 ValValGlyGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56

Db 241 GTGGTTGGAAAGGAGCAAGCTCGAGCTAAAGTAACACAAAGCATTTGCTTTGTAAACCGGC 300

Qy 57 GluAlaSerProTyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProVal 76

Db 301 GAAGCTTCTCCTTATGCAAAAGCTCGGGGTCTAGGAGATGTTTGTGTTTCATTGCCAGTT 360

Qy 77 AlaLeuAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96

Db 361 GCTCTTGTCTGCTCGTGTGTCACCGTGTGATGTTGTAATGCCAGATATTTAATGATACC 420

Qy 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116

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QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
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QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
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DEFINITION Sequence 12 from patent US 6107060.  
ACCESSION AR106494  
VERSION AR106494.1 GI:12821024  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1752)  
AUTHORS Keeling, P. and Guan, H.  
TITLE Starch encapsulation  
JOURNAL Patent: US 6107060-A 12 22-AUG-2000;  
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US-10-628-525A-21 (1-539) x AR106494 (1-1752)  
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QY 8 ----- 8  
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QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
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QY	8	-----8		Db	1259	TATTCCTGTTGAGACTCTCTCGAAAGGCCAAATGTAAAGGTGCATTGCAGAAAGGAGCTG	1318
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QY	9	-----AspLeuGlyLeuGluProGluGly	16	Db	1319	GGTTTACCTATTAAGCCCTGATGTTCTCTGATTTGGCTTTATTTGAAGGTGGATATACAG	1378
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QY	17	IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle	36	Db	1379	AAAGGCATTGATCTCATCTCACTTATCATPACCAGATCTCATCGCGAAGATGTTCAATTT	1438
Db	299	ATTGCTGAAGTTCCATCGATAACACAGTAGTTGTGCAAGTGAGCAAGATTCTGAGATT	358	QY	397	ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle	416
QY	37	ValValGlyIleGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly	56	Db	1439	GTCACTGCTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC	1498
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QY	57	GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal	76	Db	1499	TTCAAGGATAAATTTCTGGATGGGTGGATTTAGTTTCCAGTTTCCACCGAATAACT	1558
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QY	137	ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe	156	Db	1739	CCCTTAACACACAGAAAAACATGTT-GTGGACATTCGCAATTCGCAATATCTACATACAGGA	1797
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QY	157	GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle	176	Db	1798	ACACAAGTCTCTCGGGAAGGGCTAATGAAGCAGCATGTCAAAGACTTCACGTGGGA	1857
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Db	899	TCCCGCAGCATTTCTTGTAATAGATATTTAGCACATCAGGGTGTAGAGCCTCGAAGCAC	958	VERSION	Unknown.		
QY	237	TyrProAspLeuGlyLeuProGluTyrPyrGlyValAlaLeuGluTyrValPheProGlu	256	KEYWORDS	Unknown.		
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Db	1019	TGGCGGAGGAGCATGCCCTTGACAAGGGTGGAGGAGTAAATTTTTTGAAGGTGCAGTT	1078	AUTHORS	Broglie, K.E. and Lightner, J.E.		
QY	277	ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrPyrGluValThrAla	296	TITLE	Modification of starch biosynthetic enzyme gene expression to produce starches in grain crops		
Db	1079	GTGACAGCAGATCGAATCGTGTGCTAGTAAGGGTATTCGTGGGAGGTCAACTGCT	1138	JOURNAL	Patent: US 6570008-A 12 27-MAY-2003;		
QY	297	GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle	316	FEATURES	E. I. du Pont de Nemours and Company; Wilmington, DE		
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US-10-628-525A-21 (1-539) x AR340014 (1-2008)

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Qy 8 -----8

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RESULT 6

AP036891 2357 bp mRNA linear PLN 01-SBP-2004

LOCUS Zea mays plastid starch synthase I precursor (Ssl) mRNA, complete cds; nuclear gene for plastid product.

DEFINITION AP036891

ACCESSION AP036891

VERSION AP036891.2 GI:51832612

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 2357)

AUTHORS Knight,M.E., Harn,C., Lilley,C.E., Guan,H., Singletary,G.W., MuForster,C., Wasserman,B.P. and Keeling,P.L.

TITLE Molecular cloning of starch synthase I from maize (W64) endosperm and expression in Escherichia coli

JOURNAL Plant J. 14 (5), 613-622 (1998)

PUBMED 9675904

REFERENCE 2 (bases 1 to 2357)

AUTHORS Knight,M.E., Harn,C., Lilley,C.E.R., Guan,H.P., Singletary,G.W.,

```

Mu-Forester, C., Wasserman, B. P. and Keeling, P. L.
Direct Submission
Submitted (03-DEC-1997) ExSeed Genetics, 1568 Food Science
Building, ISU, Ames, IA 50011, USA
REFERENCE
3 (bases 1 to 2357)
Knight, M. E., Harn, C., Lilley, C. E. R., Guan, H. P., Singletary, G. W.,
Mu-Forester, C., Wasserman, B. P. and Keeling, P. L.
Direct Submission
Submitted (01-SEP-2004) ExSeed Genetics, 1568 Food Science
Building, ISU, Ames, IA 50011, USA
REMARK
Sequence update by submitter
COMMENT
On Sep 1, 2004 this sequence version replaced gi:2828011.
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Score: 2832.00 Matches: 538
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Query Match: 97.9% Indels: 45
DB: 15 Gaps: 1
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QY 8 -----8
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Db 832 CTGTAATTTGGGAGGATATATTTATGGACAGAATTCGATGTTTGTCTCAATGATGGCAT 891
QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 892 GCCAGTCTAGTGCCAGTCTCTTCTGCTCAAAATATAGACCATATGGTGTGTATAAAGAC 951
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
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QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
Db 1072 TGGGCGAGGAGCATGCCCTTGACAAGGTGAGGCAGTTAATTTTGAAGGTGCAGTT 1131
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
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QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316
Db 1192 GAAAGTGGACAGGGCTCAATGAGCTCTTAAGCTCAAGAAAGGTGATTAACCGAAT 1251
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 1252 GTAAATGGAATTGACATTAATGATTTGGAACCTGCCACAGACAAATGTATCCCTGTCAT 1311
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 1312 TATTCCTGTGATGACCTCTCGAAAGGCCAAATGTAAGGTGTCATTGAGAAAGGAGCTG 1371
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1372 GGTTTACTATAGAGCTGTGATGTTCTCTGATGGCTTTATTTGGAAGGTGGATATATCAG 1431
QY 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396
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QY 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
Db 1552 TTCAGGATTAATTTCTGGATGGGTTGGATTTAGTTTCAGTTTCCACCGCAATAACT 1611
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1612 GCCGGCTCGCATATATGTTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 1671
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1672 TATCTATGCAATGATGACAGATGTTCTCTGTTGTCATGCAACTGGGGGCTTTAGAGATACC 1731
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496
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QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
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QY 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 1851 ACACAACTCTCTGGGAAGGCTTAATGAACGAGGATGTCAAAGACTTTCACGTGGGA 1910
QY 537 ProCysArg 539
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RESULT 7
BD249559
LOCUS
DEFINITION
  BD249559 2491 bp DNA linear PAT 17-JUL-2003
  Modification of starch biosynthesis enzyme gene expression for
  production of starch in grain crops.
ACCESSION
  BD249559
VERSION
  BD249559.1 GI:33059329
KEYWORDS
  JP 2002525029-A/5.
SOURCE
  Zea mays
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
    clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 2491)
  Broglie, K.E. and Lightner, J.R.
  Modification of starch biosynthesis enzyme gene expression for
  production of starch in grain crops
  Patent: JP 2002525029-A 5 13-AUG-2002;
  E1 DU PONT DE NEMOURS AND CO
  OS Zea mays (maize)
  PN JP 2002525029-A/5
  PD 13-AUG-2002
  PF 26-JUL-1999 JP 2000562537
  PR 28-JUL-1998 US 60/094436
  PI KAREN E BROGLIE, JONATHAN EDWARD LIGHTNER
  PC A01H5/00, A01H1/00, C08B33/00, C12N15/09, C12N15/00 CC
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  CC production
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Percent Similarity: 92.3% Conservative: 0
Best Local Similarity: 92.3% Mismatches: 1
Query Match: 97.9% Indels: 45
DB: 6 Gaps: 1

US-10-628-525A-21 (1-539) x BD249559 (1-2491)

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QY 8 -----8
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QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
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QY 57 GluAlaSerProTyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 562 GAAGCTTCTCTTATGCAAAGTCTGGGGGTCTAGGAGATGTTGTGTGCTTCAATGCCAGTT 621
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96
Db 622 GCTCTTGTGCTCGTGGTCAACCGTGTGATGTTGTAAATGCCAGATATTTAAATGGTACC 681
QY 97 SerAspLysAsnTyrAlaAlaAlaPheTyrThrGluLysHisIleArgGlyLeuProCysPhe 116
Db 682 TCCGATAAGATTTATGCNAATGATTTTACACAGAAAACACATTCGATTCGATGCTTT 741
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Db 742 GCGCGTGAACATCAAGTTACTCTTCCATGATATAGAGATTCAAGTTGAGTGGTGT 801
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QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 862 GGTGATAATCAGTTTCAGATACACACTCTTTTGTGTATGCTGCATGTAGGGCTTCTTTGATC 921
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196
Db 922 CTTGAATTGGCAGGATATATTTATGCACAGAAATTCGATGTTGTTGTCAATGATGGCAT 981
QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
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QY	297	GluGlyGlyGlnGlyLeuAenGluLeuLeuSerSerArgLysSerValLeuAenGlyIle	316
Db	1282	GAAGGTGGACAGGCCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAATT	1341
QY	317	ValAenGlyIleAspIleAenAspTrpAenProAlaThrAspLysCysIleProCysHis	336
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QY	357	GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln	376
Db	1462	GGTTTACCTATAAGGCTCATGATTCCTCTGATTGGCTTTATTGGAAGGTTGGATTATCAG	1521
QY	377	LysGlyIleAspIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe	396
Db	1522	AAAGGCATTGATCTCATTCACCTTATCATACAGATCTCATGCGGAAGATGTTCAATTT	1581
QY	397	ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle	416
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QY	417	PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr	436
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QY	497	ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAenIleTyrIleGlnGly	516
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QY	517	ThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHisValLysArgLeuHisValGly	536
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DEFINITION	Sequence 5 from patent US 6570008.		
ACCESSION	AR340007		
VERSION	AR340007.1	GI:33731301	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2491)		
AUTHORS	Broglie, K.E. and Lightner, J.E.		
TITLE	Modification of starch biosynthetic enzyme gene expression to		
JOURNAL	produce starches in grain crops		
	Patent: US 6570008-A 5 27-MAY-2003;		
	E. I. du Pont de Nemours and Company; Wilmington, DE		

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Query Match:	97.9%	Indels:	45
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QY	17	IleAlaGluGlySerIleAspAenThrValValAlaSerGluGlnAspSerGluIle	36
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QY	37	ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly	56
Db	502	GTGGTGGAAAGGAGCAAGCTCGAGCTAAAGTAAACACAAAGCATTTGTCTTTGTAACCGC	561
QY	57	GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal	76
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QY	77	AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAenGlyThr	96
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QY	137	ValAspHisProSerTyrHisArgProGlyAenLeuTyrGlyAspLysPheGlyAlaPhe	156
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QY	157	GlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle	176
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ACCESSION      A93359
VERSION        A93359.1      GI:6741623
KEYWORDS       .
SOURCE        Zea mays
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2383)
Kossmann, J. and Froberg, C.
NUCLEIC ACID MOLECULES CODING SOLUBLE MAIZE STARCH SYNTHASES
Patent: WO 9744472-A 1 27-NOV-1997;
KOSSMANN JENS (DE); FROBERG CLAUS (DE)
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VERSION ARI174874.1 GI:17915194  
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ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2383)  
AUTHORS Kosemann, J. and Prohberg, C.  
TITLE Nucleic acid molecules encoding soluble starch synthases from maize  
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VERSION AR411327.1 GI:40163429  
KEYWORDS Unknown.  
SOURCE Unknown.  
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AUTHORS Kossmann,J. and Prohberg, C.  
TITLE Nucleic acid molecules encoding soluble starch synthases from maize  
JOURNAL Patent: US 6635804-A 1 21-OCT-2003;  
PlantTec Biotechnologie, GmbH;;  
DEX;  
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Hsieh,J.S., Chen,M.R. and Hsing,Y.I.C.  
Molecular cloning of a Sorghum cDNA encoding the soluble starch  
synthase SBSSS  
Unpublished  
2 (bases 1 to 2592)  
Hsieh,J.S., Chen,M.R. and Hsing,Y.I.C.  
Direct Submission  
Submitted (14-JUL-1999) Agronomy, National Taiwan University, No.  
1, Sec. 4, Roosevelt Rd., Taipei 10617, Taiwan  
3 (bases 1 to 2592)  
Hsieh,J.S., Chen,M.R. and Hsing,Y.I.C.  
Direct Submission  
Submitted (03-JAN-2001) Agronomy, National Taiwan University, No.  
1, Sec. 4, Roosevelt Rd., Taipei 10617, Taiwan  
Sequence update by submitter  
On Jan 3, 2001 this sequence version replaced gi:5616514.  
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QY	255	ProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274
DB	1091	CCTGAATGGGCAAGGAGGCATGCCCTTGACAGGGTGAGCAGTAAATTTTTTGAAGGT 1150
QY	275	AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThr 294
DB	1151	GCAGTTGTGACACAGATCGAATGTGACTGTGAGTAAGGGTTATTCATGGAGGTGACA 1210
QY	295	ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314
DB	1211	ACTGCTGAAGTGCACAGGGTCTCAATGAGCTCTTAAGCTCCCGAAGAGTGTATTAAAC 1270
QY	315	GlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro 334
DB	1271	GGAAATTGTAATGGAATTGACATTAATGATTGGAACCTCGACCGGACAAATGTATCCCT 1330
QY	335	CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354
DB	1331	TGTCATTATTCGTGTGATGACCTCTCTGGAAAGCCAAATGTAAAGTGCATTGCAGAG 1390
QY	355	GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374
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QY	375	TyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspVal 394
DB	1451	TATCAGAAAGGCATTCATCTCACTCACTTATCATACCATCTCATCGGAGCAGCGTT 1510
QY	395	GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGlu 414
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QY	415	SerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArg 434
DB	1571	TGGACTTCAAGGATATAATTTGCTGCTGGTGGTGGATTTAGTCTTCCAGTTTCCACCGA 1630
QY	435	IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454
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Alignment Scores:		QY	316 eValAenGlyIleAspIleAenAspTrpAenProAlaThrAspLysCysIleProCysHi 336
Pred. No.:	7,34e-224	Db	1798 TGTAAATGGAAATTGACATTAATGATTGGAACCTCGCCACAGACAAATGTATCCCTGTCA 1857
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	1	Db	1978 GAAAGCATTTGATCTCAATCAACTTATCATACAGATCTCATCGCGAAGAAATGTTCAATT 2037
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		QY	416 ePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHieArgIleTh 436
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VERSION        A63308.1  GI:3717138
KEYWORDS
SOURCE        unidentified
ORGANISM      unclassified sequences.
REFERENCE      1
AUTHORS       Keeling, P.L. and Knight, M.E.
TITLE         MODIFICATION OF STARCH SYNTHESIS IN PLANTS
JOURNAL       Patent: WO 9720936-A 1 12-JUN-1997;
              ZENECA LTD (GB)
COMMENT       Other publication AU 1037197 19970627.
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US-10-628-525A-21 (1-539) x A63308 (1-2992)
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QY      57 GluAlaSerPro-TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVa 76
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QY      156 eGlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuI 176
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1 (bases 1 to 1528)  
AUTHORS  
TITLE  
Brogie,K.E. and Lightner,J.E.  
Modification of starch biosynthetic enzyme gene expression to  
produce starches in grain crops  
JOURNAL  
Patent: US 6570008-A 6 27-MAY-2003;  
E. I. du Pont de Nemours and Company; Wilmington, DE  
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US-10-628-525A-21 (1-539) x AR340008 (1-1528)

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Sequence 9 from Patent WO2004065537.  
CQ879887  
PAT 11-OCT-2004  
CQ879887.1 GI:54033803

KEYWORDS

SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
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 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Heim, U., Herbers, K., Sonnewald, U. and Glickmann, E.  
 TITLE Expression cassette for nucleic acids in plant tissue containing  
 starch

JOURNAL

Patent: WO 2004065537-A 9 05-AUG-2004;

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 US-10-628-525A-21 (1-539) x CQ879887 (1-1881)

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 QY 9 -----AspLeuGly----- 11  
 DB 220 ACGCAGTCGCGCGCGCGCGCGCCCGCGCGCTTCGCGACTCCGCGCTGGGGAG 279  
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 QY 110 HieIleArgIleProCysPheGlyGlyGluHieGluValThrPhePheHieGluTyrArg 129  
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 DB 1300 GCTGAATTCGAGAAGGAGCTGGTGTACCTATAAGCCCGATGTCCTCTGATTGCTTT 1359  
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QY 510 CysAenIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHis 529
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RESULT 18
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LOCUS E06904 2533 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding soluble starch synthase.
ACCESSION E06904
VERSION E06904.1 GI:2175060
KEYWORDS JP 1994070779-A/1.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE
AUTHORS Baba,T. and Shimada,H.
TITLE SOLUBLE RICE STARCH SYNTHETASE GENE AND ITS USE
JOURNAL Patent: JP 1994070779-A 1 15-MAR-1994:
COMMENT MITSUI GIYOUSAI SHOKUBUTSU BIO KENKUSHO:KK
OS Oryza sativa
PN JP 1994070779-A/1
PD 15-MAR-1994
PF 07-JUL-1992 JP 1992179947
PI BABA TADASHI, SHIMADA HIROAKI
PC C12N15/52,A01H5/00;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue_type=ripening seed;
FH Key Location/Qualifiers
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FT CDS 114..1994
FT /product='Soluble starch synthase' FT
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FT 3'UTR 1992..2533.

FEATURES
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/mol_type='genomic RNA'
/db_xref='taxon:4530'

ORIGIN
Alignment Scores:
Pred. No.: 2,63e-204 Length: 2533
Score: 2525.50 Matches: 475
Percent Similarity: 85.8% Conservative: 31
Best Local Similarity: 80.5% Mismatches: 33
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US-10-628-525A-21 (1-539) x E06904 (1-2533)
QY 1 CysValAlaGluLeuSerArgGlu-----8
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Db 213 TGCCTGCGAGCTGAGCAGGAGCGGTGGGTCCGCGCAGCGCCCGCTGCGCAGCGCGCCG 272
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QY 9 -----11
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Db 573 GTTGTGGTTCATGCGCAATGCTCTTGTCTTTCGTGGTTCATCGTGTGATGTTGTAATG 632
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Db 633 CCGAGATACATGACGGGCGCTTGAACAAAATTTTGCAACGCCATTTTACACTGAGAAG 692
QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
Db 693 CACATTAAGATTCCATGCTTTGGCGGAGAACATGAAGTTACTTTTTTTCACGAGTAGG 752
QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAenLeuTyr 149
Db 753 GATTCGTGTGATTGGGTGTTGTGATCATCCTCATATCATAGACCTCGAAATTTGTAT 812
QY 150 GlyAspLyPheGlyValaPheGlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAla 169
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QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAenCysMet 189
Db 873 GCGTGTGAAGCCCCATTAAATCTTGAACCTGGGAGGATATATCTATGACAGAAATGCATG 932
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QY 250 LeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLyVsGlyGluAlaVal 269
Db 1113 TTAGAATGGGTGTTTCCAGAGTGGGCAAGCGCGCATGCCCTTTGACAAAGGTGAGGCAGTC 1172
QY 270 AenPheLeuLyVsGlyValValValThrAlaAspArgIleValThrValSerLyVsGlyTyr 289
Db 1173 AATTTTTTAAAGGCGCAGTTGTGACAGCATCGAATCGAATTTGTGACTGTGACGCGGGGTAT 1232
QY 290 SerTrpGluValThrThrAlaGluGlyGlnGlyLeuAenGluLeuLeuSerSerArg 309
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QY 310 LysSerValLeuAenGlyIleValAenGlyIleAspIleAenAspTrpAenProAlaThr 329
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DB: 6 Gaps: 3

US-10-628-525A-21 (1-539) x AX653976 (1-1926)

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QY 9 -----AspLeuGly-----11

DB 220 ACGCAGTGGCGGCG 279

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QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69

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QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129

DB 580 CACATTAAGATTCATGCTTTGGCGGAGAACATGAAGTTACTTTTTTTCACGAGTATAGG 639

QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149

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QY 170 AlaCysGluAlaProLeuIleLeuGluGlyGlyTyrIleTyrGlyGlnAsnCysMet 189

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DB 1300 GCTGAATTTGCAAGGAGCTGGGTTTACCTATAAGCCCGATGTGCTCTGATTGGCTTT 1359

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## RESULT 22

AKI09458

LOCUS

DEFINITION

Oryza sativa (japonica cultivar-group) cDNA clone:001-125-C03, full

insert sequence.

AKI09458

VERSION

AKI09458.1 GI:32994667

KEYWORDS

FLI\_CDNA; oligo capping.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

REFERENCE

1

AUTHORS

The Rice Full-Length cDNA Consortium, National Institute of

Agrobiological Sciences Rice Full-Length cDNA Project Team;

Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,

Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,

Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,

Ohtsuka, K., Shishiki, T., Foundation of Advancement of International

Science Genome Sequencing &amp; Analysis Group; Ohtsuka, Y., Murakami, K.,

Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,



Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,  
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,  
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,  
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,  
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,  
Hara, A., Hashizume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,  
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,  
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,  
Yoshino, M., and Hayashizaki, Y.  
Collection, mapping, and annotation of over 28,000 cDNA clones from  
Japanese rice  
Science 301 (5631), 376-379 (2003)  
12869764

# JOURNAL PUBMED REFERENCE AUTHORS

2 (bases 1 to 2623)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,  
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,  
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,  
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,  
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,  
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,  
Kodama, F., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Kurotsaki, T., Kusumegi, T., Li, C., Lu, M.,  
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,  
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,  
Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K.,  
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,  
Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,  
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,  
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,  
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,  
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,  
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., and  
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and  
Yoshimura, A.

# TITLE JOURNAL

Direct Submission  
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of  
Agrobiological Sciences, Department of Molecular Genetics, Head of  
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki  
305-8602, Japan (E-mail:skkikuchi@nias.affrc.go.jp,  
Tel:81-29-838-7007, Fax:81-29-838-7007)  
This clone is one of the 28K full-length cDNA clones from japonica  
rice.

# COMMENT

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>  
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,  
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,  
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,  
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and  
Yamamoto, M.  
PAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,  
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,  
Kodama, T., Kurotsaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,  
Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,  
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,  
Yoshimura, A., Matsubara, K. and Murakami, K.  
Genome Exploration Research Group in Riken Genomic Sciences Center  
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,  
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,  
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,  
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,  
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,  
Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,  
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,  
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,  
Yasunishi, A. and Hayashizaki, Y.  
Location/Qualifiers  
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# FEATURES source

/cultivar="Nipponbare"  
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/clone="001-125-C03"

# ORIGIN

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Score: 2511.50 Matches: 476  
Percent Similarity: 85.9% Conservative: 31  
Best Local Similarity: 80.7% Mismatches: 32  
Query Match: 86.8% Indels: 52  
DB: 15 Gaps: 3

US-10-628-525A-21 (1-539) x AK109458 (1-2623)

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RESULT 23
LOCUS AY299404
DEFINITION Oryza sativa (indica cultivar-group) soluble starch synthase I precursor, mRNA, complete cds.
ACCESSION AY299404
VERSION AY299404.1 GI:31745887
KEYWORDS Oryza sativa (indica cultivar-group)
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 2547)  
Jiang, H.W., Dian, W.M. and Wu, P.  
Oryza sativa (indica cultivar-group) putative soluble starch synthase I gene  
Unpublished  
2 (bases 1 to 2547)  
Jiang, H.W., Dian, W.M. and Wu, P.  
Direct Submission  
Submitted (15-MAY-2003) State Key Laboratory of Plant Physiology and Biochemistry, College of Life Sciences, Kaixuan Road 268#, Hangzhou, Zhejiang Province 310029, P R China

## FEATURES

Location/Qualifiers

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## ORIGIN

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US-10-628-525A-21 (1-539) x AY299404 (1-2547)

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Qy 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69

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V	E	R	AJ292522.1 GI:9369335	
K	E	Y	starch synthase I-2; wssI-2 gene.	
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S	O	R	Triticum aestivum	
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R	E	F	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
E	N	C	Pooideae; Triticeae; Triticum.	
R	E	F	1	
A	U	T	Peng,M., Hucl,P. and Chibbar,R.N.	
I	T	I	Isolation, characterization and expression analysis of starch	
J	O	U	synthase I from wheat (Triticum aestivum L.)	
R	E	F	Plant Sci. 161, 1055-1062 (2001)	
A	U	T	2 (bases 1 to 2421)	
I	T	I	Chibbar,R.N.	
J	O	U	Direct Submision	
R	E	F	Submitted (18-JUL-2000) Chibbar R.N., Cereal Biotechnology, Plant	
A	U	T	Biotechnology Instn., Natl. Research Council Canada, 110 Gymnasium	
J	O	U	Place, Saskatoon, Saskatchewan, S7N 0W9, CANADA	
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AUTHORS	Peng, M., Hucl, P. and Chibbar, R.N.			Db	616	CAACCTCAAGCTAAAGTTACACGTAGCATCGTGTGTGTGACCTGGTGAAGCTGCTCCTTAT	675
TITLE	Isolation, characterization and expression analysis of starch synthase I from wheat (Triticum aestivum L.)			QY	62	AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAaArg	81
JOURNAL REFERENCE	Plant Sci. 161, 1055-1062 (2001)			Db	676	GCAAAAGTCAGGGGGCTGGAGATGTTTGTGGTTCGTTACCAATTCCTCTTGTGCTCGT	735
AUTHORS	Chibbar, R.N.			QY	82	GlyHisArgValMetValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr	101
TITLE	Direct Submission			Db	736	GGTCCACCGGTGATGGTGTGTAATGCCAAGTACTTGAATGGGTCTCTGATAAAAACTAT	795
JOURNAL	Submitted (18-JUL-2000) Chibbar R.N., Cereal Biotechnology, Plant Biotechnology Inst., Natl. Research Council Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan, S7N 0W9, CANADA			QY	102	AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu	121
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## ORIGIN

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 AF091803  
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 SOURCE  
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 1 (base 1 to 2591)  
 Li, Z.; Rahman, S., Kosar-Hashemi, B., Mouille, G., Appels, R. and  
 Morell, M. K.  
 Cloning and characterization of a gene encoding wheat starch  
 synthase I  
 Theor. Appl. Genet. 98, 1208-1216 (1999)  
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 Li, Z.; Rahman, S., Kosar-Hashemi, B., Mouille, G., Appels, R. and  
 Morell, M. K.  
 Direct Submission  
 Submitted (10-SEP-1998) CSIRO Division of Plant Industry, GPO Box  
 1600, Canberra, ACT 2601, Australia  
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## ORIGIN

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 Best Local Similarity: 86.2% Mismatches: 41  
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REFERENCE
Li, Z., Morell, M. and Rahman, S.
AUTHORS Regulation of gene expression in plants
TITLE Patent: WO 99/4314-A 11 25-MAR-1999;
JOURNAL GOODMAN FIELDER LTD (AU) ; LI ZHONGYI (AU) ; MORELL MATTHEW (AU) ;
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AUTHORS 1 (bases 1 to 2239)  
Block, M., Lorz, H., Lutticke, S., Walter, L., Frohberg, C. and  
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Best Local Similarity: 86.4% Mismatches: 41  
Query Match: 85.3% Indels: 4  
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ACCESSION AR535116  
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SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2239)  
AUTHORS Block,M., Lorz,H., Lutticke,S., Walter,L., Frohberg,C. and Kosemann,J.

TITLE Nucleic acid molecules encoding enzymes from wheat which are involved in starch synthesis  
JOURNAL Patent: US 6734339-A 1 11-MAY-2004;  
Hoechst Schering AgrEvo, GmbH;;  
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QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
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QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg 81  
Db GCNAAGTCAGGGGGTGGAGATGTTTGGTTCGTACCAATTCCTTCTGCTGCTCGT 260  
QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
Db GGTCCCGAGTGTATGTTGTAATGCCAAGATCTTAATAAGGCTCTCTGATTAATAACTAT 320  
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
Db GCAAAGGCATTTATACACTCGAAGCACATTAAGATTCATGCTTTGGGGGATCATCATGAA 380  
QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer 141  
Db GTGACCTTTTTCATGATGATAGACAAACGTCGATTTGGGTGTTTGTGATCATCCGTCA 440  
QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyValaPheGlyAspAsnGlnPhe 161  
Db TATCACAGACACGAGGATTTATATGAGATATAATTTGGTCTTTTGGTGTATATCATGTC 500  
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly 181  
Db AGATACACACTCTCTTTGCTATGCTGATCGAGGCCCCACATAATCTTGAATTTGGGAGGA 560  
QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValPro 201  
Db TATATTATGGACAGAAATTCATGTTTGTGTGAACGATTTGGCATGCCAGCTTTGGCCA 620  
QY 202 ValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221  
Db GTCTCTTCTGTCGAAAATATAGACCATACGGTGTTTACAGAGATTCCTCCGACGACCCCT 680  
QY 222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
Db GTTATACATAATTTAGCACATCAGGGTGTGGAGCCCTGCAAGTACATATCTCATCTGGGA 740  
QY 242 LeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHis 261  
Db TTGCTCTCTGAAATGGTATGGAGCTTTTAGAATGGGTATTTTCCAGAAATGGGAGGAGCAT 800

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QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281
DB |||||||
DB 801 GCCCTTGACACAGGGTGAGCAGTTAACTTTTGAAGGAGCAGTTGTGACAGCATCGG 860
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGly 301
DB |||||||
DB 861 ATTGTGACCGTCAGTCAGGGTTATTATGCGAGGTCAAACTGCTGAAGGTGGACAGGCG 920
QY 302 LeuAsnGluLeuLeuSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321
DB |||||||
DB 921 CTCATGAGCTCTTAAGCTCCCGAAAAGTGATTGAATGGAATTGTAATGGAATTGAC 980
QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341
DB |||||||
DB 981 ATTAATGATTGGNACCCACACAGCAAGTGTCCTCATCATTTATTCTGTCGATGAC 1040
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361
DB |||||||
DB 1041 CTCCTCGAAAGGCCAAATGTAAGCTGAATTCAGAGAGAGTTGGGTTTACCTGTAAGG 1100
QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381
DB |||||||
DB 1101 GAGGATGTTCTCTGATTGGCTTTATTGAAGACTGGATTACAGAAAGGCATTGATCTC 1160
QY 382 IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401
DB |||||||
DB 1161 ATTAAATGGCCATCCAGAGCTCATGAGGAGGAGTGCAATTTGTGCTTGGATCT 1220
QY 402 GlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPhe 421
DB |||||||
DB 1221 GGGGATCCCAATTTTGAAGGCTGGATGAGATCTACCGAGTCGAGTTTACAAGGATAAATTC 1280
QY 422 ArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441
DB |||||||
DB 1281 CGTGGATGGGTTGGATTTTAGTGTTCAGTTTCCCACAGAATAACTGCAGGTTGCGATATA 1340
QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461
DB |||||||
DB 1341 TTGTTAATGCCATCGAGATTGNACCTTGGGTCTTAATCAGCTATATGCTATGCATAT 1400
QY 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn 481
DB |||||||
DB 1401 GGTACAGTTCTGTAGTTTCATGGAACTGGGGGCTCCGAGACACAGTCGAGACCTTCAAC 1460
QY 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGlu 501
DB |||||||
DB 1461 CCTTTTGGTGCAAAAGGAGGAGGGGTACAGGGTGGCGCTTCTCACCGCTAACCGTGGAC 1520
QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521
DB |||||||
DB 1521 AAGATGTT-GTGGCATTCGNAACCGCATGTCGACATTCAGGGAGCACAGCCGCTCTG 1579
QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538
DB |||||||
DB 1580 GGAGGGGCTCATGAAGCGGAGGATACGAAAGACCATACGTGGGACCATGC 1630
```

Search completed: April 1, 2006, 15:17:35  
Job time : 10831.5 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 00:15:06 ; Search time 1269 Seconds  
(without alignments)  
2830.777 Million cell updates/sec

Title: US-10-628-525A-21

Perfect score: 2893

Sequence: 1 CVALSREDLGLEPEGIAGS.....LLGRANEARHVKRLHVGPCR 539

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-O=/abes/ABSWEB/spool/US10628525/runat\_31032006\_095109\_16557/app\_query.fasta\_1  
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-LOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes06h  
-USER=US10628525 @CGN 1.1 1404 @runat\_31032006\_095109\_16557 -NCPU=6 -ICPU=3  
-NO\_WMAP -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N\_Geneseq 21:\*

1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2893	100.0	1620	2	Aav29759 Zea mays
2	2861	98.9	2991	8	Abx09932 DNA encod
3	2858	98.8	1752	2	Aav29756 Zea mays
4	2856	98.7	1749	2	Aav70960 DNA encod

5	2832	97.9	2008	3	AAZ50643	Aaz50643 Corn solu
6	2832	97.9	2491	3	AAZ50636	Aaz50636 Corn solu
7	2818	97.4	2383	2	AAT95785	Aat95785 Maize eta
8	2757	95.3	2990	2	AAV66832	Aav66832 Zea mays
9	2757	95.3	2992	2	AAT67285	Aat67285 Soluble s
10	2655	91.8	1528	3	AAZ50637	Aaz50637 Corn solu
11	2538	87.7	1855	13	ADX36677	Adx36677 Plant ful
12	2525.5	87.3	1881	12	ADQ37148	Adq37148 Cell prol
13	2525.5	87.3	1881	12	ADQ15732	Adq15732 Rice stre
14	2525.5	87.3	1881	13	ADQ40094	Adq40094 Rice star
15	2525.5	87.3	2533	2	AAQ45183	Aaq45183 Soluble r
16	2511.5	86.8	1926	8	ADA70523	Ada70523 Rice gene
17	2470.5	85.4	2747	13	ADT20132	Adt20132 Plant cDN
18	2467.5	85.3	2662	2	AAZ34651	Aaz34651 cDNA sequ
19	2466.5	85.3	2239	2	AAV01527	Aav01527 Wheat sol
20	2466.5	85.3	2805	3	AAZ24487	Aaz24487 Wheat sol
21	2043	70.6	1415	3	AAZ50642	Aaz50642 Corn solu
22	1742	59.5	1984	3	AAC46797	Aac46797 Arabidops
23	1645.5	56.9	1758	2	AAT32325	Aat32325 Soluble s
24	1496	51.7	1294	13	ADX59939	Adx59939 Plant ful
25	1459	50.4	1300	13	ADX08949	Adx08949 Plant ful
26	1280	44.2	10336	2	AAZ34652	Aaz34652 Wheat sta
27	1193	40.9	1860	13	ADX13652	Adx13652 Plant ful
28	1130.5	39.1	2097	2	AAV29755	Aav29755 Zea mays
29	1130.5	39.1	2480	8	ABX09934	Abx09934 DNA encod
30	1125.5	38.9	2423	2	AAV70958	Aav70958 DNA encod
31	1103	38.1	2418	6	ABS52841	Abes2841 Typha lat
32	1103	38.1	2418	10	AD62716	Ad62716 Typha lat
33	1095	37.8	2865	8	ABX09933	Abx09933 DNA encod
34	1093	37.8	1798	3	AAZ50647	Aaz50647 Corn star
35	1093	37.8	2019	3	AAZ50646	Aaz50646 Corn star
36	1093	37.8	2248	3	AAZ50651	Aaz50651 Corn star
37	1084	37.5	1824	14	ABE48376	Aeb48376 Maize Bri
38	1084	37.5	2073	14	ABE48372	Aeb48372 Curcuma z
39	1084	37.5	2348	6	ABS52826	Abes2826 Curcuma z
40	1084	37.5	2348	10	AD62701	Ad62701 Curcuma z
41	1077.5	37.2	2939	3	AAC86433	Aac86433 Wheat sta
42	1077.5	37.2	2939	3	AAC86410	Aac86410 Wheat sta
43	1075	37.2	2607	8	ACC70869	Acc70869 Rice star
44	1071	37.0	1888	13	ADX63440	Adx63440 Plant ful
45	1070.5	37.0	2807	3	AAC86435	Aac86435 Wheat sta
46	1070.5	37.0	2842	3	AAC86411	Aac86411 Wheat sta
47	1069.5	36.9	2520	6	ABX88112	Abx88112 cDNA enco
48	1068.5	36.9	2951	6	ABX88114	Abx88114 cDNA enco
49	1067.5	36.9	2950	6	ABX88113	Abx88113 cDNA enco
50	1066	36.8	2607	8	ACC70868	Acc70868 Rice star
51	1053.5	36.4	2946	6	ABX88115	Abx88115 cDNA enco
52	1050.5	36.3	2826	3	AAV01528	Aav01528 Wheat gra
53	1038.5	35.9	2107	3	AAC86412	Aac86412 Wheat sta
54	1038.5	35.9	2107	3	AAC86434	Aac86434 Wheat sta
55	1029	35.6	2412	10	ADC07863	Adc07863 Rice DNA
56	1029	35.6	2412	12	ADJ40034	Adj40034 Plant cDN
57	980.5	33.9	1828	13	ADO82332	Ado82332 Plant ful
58	978.5	33.8	2007	2	AAV29754	Aav29754 Zea mays
59	978.5	33.8	2007	2	AAV70959	Aav70959 DNA encod
60	978.5	33.8	2085	2	AAT67286	Aat67286 Soluble s
61	978.5	33.8	2085	2	AAV66833	Aav66833 Zea mays
62	972	33.6	1724	6	ABA01821	Aba01821 Rice star
63	893	30.9	2161	6	ABK53210	Abk53210 Potato gr
64	891.5	30.8	1502	13	ADX60901	Adx60901 Plant ful
65	880.5	30.4	2380	2	AAV66834	Aav66834 Zea mays
66	880.5	30.4	2478	2	AAT67287	Aat67287 Soluble s
67	878.5	30.4	2176	6	ABS52832	Abes2832 Canna edu
68	878.5	30.4	2176	10	AD62707	Ad62707 Canna edu
69	871	30.1	2274	6	ABS52835	Abes2835 Typha lat
70	871	30.1	2274	10	AD62710	Ad62710 Typha lat
71	867.5	30.0	2183	6	ABK53215	Abk53215 Canna edu
72	863	29.8	1833	12	ADN73902	Adn73902 Thale cre
73	863	29.8	2115	3	AAC32824	Aac32824 Arabidops
74	851	29.4	2179	8	ABQ80055	Abq80055 Soybean g
75	849.5	29.4	1937	10	ADC53778	Adc53778 Low amylo
76	849.5	29.4	2542	2	AAV29753	Aav29753 Oryza sat
77	846.5	29.3	1937	10	ADC53776	Adc53776 Low amylo

78	842.5	29.1	2067	6	ABS52838	AbS52838 Typha fos
79	842.5	29.1	2067	10	AD62713	Ad62713 Tulipa fo
80	839	29.0	1818	14	ADW87816	Adw87816 Maize gra
81	838	29.0	1818	10	AD63600	Ad63600 Maize UDP
82	838	29.0	1818	14	ADW87799	Adw87799 Maize gra
83	838	29.0	2263	11	ADM77902	Adm77902 Maize wax
84	837.5	28.9	1818	8	ACC44559	Acc44559 Maize gra
85	833	28.8	1915	2	AXX60319	Axx60319 DNA seque
86	832.5	28.8	2267	2	AXX63355	Axx63355 Granule b
87	832	28.8	2267	11	ADM77903	Adm77903 Maize wax
88	831.5	28.7	1863	11	ADW87808	Adw87808 Corn line
89	824	28.5	2098	13	ADX09509	Adx09509 Plant ful
90	823	28.4	2399	8	ABQ80054	Abq80054 Corn gran
91	822	28.4	2297	13	ADT19869	Adt19869 Plant cdN
92	819	28.3	2028	10	ADP92505	Adp92505 Bread whe
93	812.5	28.1	2202	6	ABS52823	AbS52823 Curcuma z
94	812.5	28.1	2202	10	AD62698	Ad62698 Curcuma z
95	802.5	27.7	598	13	ACN46188	Acn46188 Cotton pr
96	777.5	26.9	11384	2	AAV52178	Aav52178 Streptoco
97	777.5	26.9	110000	10	ABS56454_09	Continuation (10 o
98	777	26.9	1431	10	ABX06832	Abx06832 S. pneumo
99	776	26.9	1431	13	ADT49969	Adt49969 Streptoco
100	776	26.8	1434	13	ADK44636	Adk44636 Streptoco
101	776	26.8	1455	13	ADR93230	Adr93230 Novel S.
102	776	26.8	1455	14	AEAS7100	Aea57100 Streptoco
103	768.5	26.6	1645	13	ADX61230	Adx61230 Plant ful
104	768	26.5	1623	13	ADO84116	Ado84116 Plant ful
105	753	26.0	2595	13	ADT19099	Adt19099 Plant cdN
106	749.5	25.9	110000	6	ABA90521_06	Continuation (7 of
107	749	25.9	1377	13	ADT44429	Adt44429 Bacterial
108	749	25.9	1440	14	ACL70982	AcL70982 M. xanthu
109	749	25.9	4991	14	ACL64256	AcL64256 M. xanthu
110	745	25.8	1452	13	ADT43607	Adt43607 Bacterial
111	742.5	25.7	5928	8	ACC70867	Acc70867 Rice star
112	741	25.6	71979	13	ADV87736	Adv87736 Streptoco
113	741	25.6	71979	13	ADV78989	Adv78989 Streptoco
114	741	25.6	110000	13	ADV81204_08	Continuation (9 of
115	741	25.6	110000	13	ADV81204_09	Continuation (10 o
116	740	25.6	1479	6	ABO90258	Abg90258 M. capsul
117	740	25.6	1479	6	ABQ90406	Abq90406 M. capsul
118	739.5	25.6	110000	6	ABN71527_08	Continuation (9 of
119	736	25.4	1431	13	ADW83394	Adw83394 Streptoco
120	736	25.4	2571	2	AAZ96227	Aaz96227 S. pneumo
121	733	25.3	1428	6	ABN68223	Abn68223 Streptoco
122	726	25.1	5935	8	ACC70866	Acc70866 Rice star
123	719.5	24.9	1455	13	ADT48515	Adt48515 Bacterial
124	718.5	24.8	1427	6	ABK73466	Abk73466 Bacillus
125	715.5	24.7	2597	10	ADC07867	Adc07867 Rice DNA
126	689.5	23.8	1449	13	ADS50014	AdS50014 Bacterial
127	689.5	23.8	1449	13	ADS55529	AdS55529 Bacterial
128	680	23.5	1110	10	ADC08761	Adc08761 Wheat DNA
129	680	23.5	1110	12	ADJ43323	Adj43323 Plant cdN
130	680	23.5	1428	13	ADT41925	Adt41925 Bacterial
131	666	23.0	9024	3	ACA86431	Aac86431 Wheat SSI
132	663	22.9	1419	13	ADS58001	AdS58001 Bacterial
133	662.5	22.9	1428	13	ADT45680	Adt45680 Bacterial
134	654.5	22.6	1437	13	ADT44967	Adt44967 Bacterial
135	648.5	22.4	1461	13	ADS48236	AdS48236 Bacterial
136	646.5	22.3	1431	13	ADT46964	Adt46964 Bacterial
137	646	22.3	418	13	ADX29492	Adx29492 Plant ful
138	640	22.1	1431	13	ADT44248	Adt44248 Bacterial
139	636.5	22.0	1440	13	ADS62946	AdS62946 Bacterial
140	636.5	22.0	1440	13	ADS59388	AdS59388 Bacterial
141	636.5	22.0	1440	13	ADS62792	AdS62792 Bacterial
142	636.5	22.0	1440	13	ADS63283	AdS63283 Bacterial
143	635.5	22.0	1383	13	ADT46165	Adt46165 Bacterial
144	633	21.9	1434	13	ADT48834	Adt48834 Bacterial
145	631.5	21.8	1536	11	ACH98067	Ach98067 Klebsiell
146	630	21.8	2818	10	ADF92501	Adf92501 Bread whe
147	630	21.8	2818	14	ABA79534	Aba79534 waxy gene
148	626	21.6	1464	2	AAQ25978	Aaq25978 glgA.. 3/2
149	626	21.6	1464	2	AAV23649	Aav23649 E. coli g
150	626	21.6	1464	9	ACD28044	AcD28044 DNA encod

ALIGNMENTS

RESULT 1

AAV29759  
ID AAV29759 standard; DNA; 1620 BP.

XX AC AAV29759;  
XX DT 11-SEP-1998 (first entry)  
XX DE Zea mays pEXS52 starch synthase gene.  
XX KW SER; starch-encapsulating region; fusion vector; starch synthase;  
glucosyl transferase; pEXS52; ss.  
XX OS Zea mays.  
XX FH Key Location/Qualifiers  
FT CDS 1..2007  
FT /\*tag= a  
FT /product= "starch synthase"

XX WO9814601-A1.  
XX PD 09-APR-1998.  
XX PF 30-SEP-1997; 97WO-US017555.  
XX PR 30-SEP-1996; 96US-0026855P.  
XX PA (EXSE-) EXSEED GENETICS LLC.  
XX PI Keeling P, Guan H;  
XX DR WPI; 1998-240100/21.  
XX DR P-PSDB; AAW56491.

XX Hybrid polypeptide comprising starch-encapsulating region and protein -  
useful for, e.g. producing protein(s) resistant to degradation by stomach  
acids.

XX Example 5; Page 51-53; 156pp; English.

XX The sequence is that of the starch synthase coiding region from pEXS52. It  
can be used in the production of a hybrid polypeptide comprising a starch  
-encapsulating region (SER) fused to a payload protein. The hybrid  
polypeptide can be used to make modified starches comprising the payload  
protein, selected from, e.g. hormones, growth factors, antibodies,  
enzymes, dyes, immunoglobulins, etc. The modified starch can also be used  
to provide grain feeds enriched in amino acids. By encapsulating the  
payload protein in starch, it is more resistant to degradation by stomach  
acids

XX Sequence 1620 BP; 426 A; 313 C; 422 G; 459 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,298-296 Length: 1620  
Score: 2893.00 Matches: 539  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-21 (1-539) x AAV29759 (1-1620)

QY 1 CysValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyLeuAlaGluGly 20  
Db 1 TCGTTCGGAGCTCAGCAGGAGGACCTCGTCTCGACCTGAGGGATTCTGAAGGT 60  
QY 21 SerIleAspAsnThrValValAlaSerGluGlnAspSerGluIleValGlyLys 40

Db 61 TCCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCCTGAGATTGTGGTGGAAAG 120  
Qy 41 GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerPro 60  
Db 121 GAGCAAGCTCGAGCTAAAGTAACACAAAGCAATTCCTTTGTGAACCGCGAAGCTTCCT 180  
Qy 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAla 80  
Db 181 TATGCAAAAGCTGGGGGTGTAGGAGATGTTGTGGTTCATTTGCCAGTGTCTCTGTGCT 240  
Qy 81 ArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsn 100  
Db 241 CGTGGTCACCGTGATGTTGTAATGCCAGATATTTAAATGTGTACTCCGATAGAAAT 300  
Qy 101 TyrAlaAsnAlaPheThrGluLysHisIleArgIleProCysPheGlyGlyGluHis 120  
Db 301 TATGCAAAATGCATTTTACACAGAAAAACACATTCGGATTCATGCTTTGGCGGTGAACAT 360  
Qy 121 GluValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisPro 140  
Db 361 GAAGTTAACCTTCTTCCATGAGTATAGAGATTTCACTGGGTGTTTGTGTATCATCCC 420  
Qy 141 SerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGln 160  
Db 421 TCATATCACAGACTGGAAATTTATATGGAGATAAGTTTGGTCTTTTGGTGAATATCAG 480  
Qy 161 PheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 180  
Db 481 TTCAGATACACACTCTCTTGTCTATGCTGCTGATGTGAGGCTCTTTGATCTTTGAATTGGA 540  
Qy 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200  
Db 541 GGATATATTTATGGACAGAAATTCGATGTTGTGTTGTCAATGATTTGGCATGCCAGTCTAGTG 600  
Qy 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
Db 601 CCAGTCTCTTCTGCGCAAAATATAGACCATATGTTGTGTTTATAAGACTCCCGGAGCAT 660  
Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
Db 661 CTGTGTAATACATAATTTAGCACATCAGGTTGAGAGCTGCAAGCACATATCTCGACCTT 720  
Qy 241 GlyLeuProGluTyrTrpTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260  
Db 721 GGTTTGCACCTGAATGGTATGAGCTCTGGATGGGTATTCCTGAAATGGCGGAGAGG 780  
Qy 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280  
Db 781 CATGCCCTTGACAAAGGGTGAGGCAGTTAATTTTTGAAAGTGCAGTTGTGACAGCAGAT 840  
Qy 281 ArgIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGln 300  
Db 841 CGAATCGTGACTGTAGTAAGGGTTATTCGTGGAGGTCACTCACTGCTGAAGGTGGACAG 900  
Qy 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
Db 901 GGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACGGAATTTGAATGGAAT 960  
Qy 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
Db 961 GACATTTAATGATTTGGAAACCTCGCACAGCAAAATGATCCCTGTCAATATCTGTGTAT 1020  
Qy 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360  
Db 1021 GACCTCTCTGAAAGGCCAAATGTAAAGGTGCATTCAGAAAGGAGCTGGGTTTACCTATA 1080  
Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
Db 1081 AGCCCTGATGTTCTCTGATGCTTTATTTGGAAGGTGGAATATCAGAAAGGCATTTGAT 1140  
Qy 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
Db 1141 CTCATTTCAATATATACAGATCTCATCGCGGAAGATGTTCAATTTGTCTATGCTTGA 1200

Qy 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420  
Db 1201 TCTGGTGACCCACAGAGCTTGAAGATTGGATGAGATCTACAGATCGATCTTCAAGGATATA 1260  
Qy 421 PheArgGlyTyrTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
Db 1261 TTTTCGTGGATGGGTGGATTTAGTGTTCAGATTTCCACCGAAATAACTGGCGGCTGGCAT 1320  
Qy 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
Db 1321 ATATTTGTTAATGTCATCCAGATTCGAACCTTGTGTCTCAATCAGCTATATGCTATGAG 1380  
Qy 461 TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe 480  
Db 1381 TATGGCACAGTCTCTGTGTTCATGCACTGGGGCTTAGAGATACCGTGGAGAACTTC 1440  
Qy 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThr 500  
Db 1441 AACCTTTCGTGTGAGAAATGGAGAGCAGGGTACAGGGTGGGCATTCGCACCCCTAACCA 1500  
Qy 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520  
Db 1501 GAAAAATGTTTGTGACATTCGAATTCGAATATCTACATACAGGGAACACAAGTCTCTC 1560  
Qy 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
Db 1561 CTGGGAAGGGCTAATGAAGCGAGGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 1617  
RESULT 2  
ABX09932  
ID ABX09932 standard; DNA; 2991 BP.  
XX  
AC ABX09932;  
XX  
DT 17-FEB-2003 (first entry)  
XX  
DE DNA encoding maize Starch synthase I.  
XX  
DE Starch; starch synthase; glucan association domain; GLASS; linker domain;  
KW LINKR; glucosyl transferase domain; GLYTR; C-terminal end; CTEND;  
KW granule bound starch synthase; GBSS; morphology; retrogradation;  
KW waterbinding; swelling potential; gene; ds.  
XX  
OS Zea mays.  
XX  
PN WO200279410-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 29-MAR-2002; 2002WO-US0009574.  
XX  
PR 30-MAR-2001; 2001US-0279720P.  
XX  
PA (BADI ) BASF PLANT SCI GMBH.  
XX  
PI Commuri P, Keeling PL, Ramirez N, McKean A, Gao Z, Guan H;  
XX WPI; 2003-040678/03.  
XX  
PT New DNA encoding fusion protein consisting of 4 different functional  
PT domains selected from glucan association domain, linker domain, glucosyl  
PT transferase domain, and C-terminal end, useful for producing modified  
XX starches.  
XX  
PS Claim 33; Page 222-223; 265pp; English.  
XX  
CC The invention describes an isolated DNA molecule encoding a fusion  
CC protein consisting of 4 different functional domains selected from glucan  
CC association domain (GLASS), linker domain (LINKR), glucosyl transferase  
CC domain (GLYTR), and C-terminal end (CTEND) which are operably linked to  
CC one another. The DNA molecule is useful for expressing in plants  
CC polypeptides including starch synthase enzymes as fusion proteins with

CC improved affinity to starch and modified catalytic capabilities and to  
CC the in vivo and in vitro synthesis of glucan chains of modified lengths  
CC as compared to plants producing native starch or starch produced with  
CC native starch synthases. Expression of the starch synthase fusion  
CC proteins along with granule bound starch synthase (GBSS) will lead to a  
CC modified starch having an altered or improved morphology, retrogradation,  
CC waterbinding, or swelling potential of the granules, gel strength,  
CC adhesiveness, cohesiveness, hardness, elasticity, increased or decreased  
CC granule size, degree of branching, crystallinity, degree of cross-  
CC linking, and increased or decreased glucan chain lengths. This sequence  
CC encodes a starch synthase used in the invention  
XX  
SQ Sequence 2991 BP; 750 A; 660 C; 804 G; 776 T; 0 U; 1 Other;  
Alignment Scores:  
Pred. No.: 1,39e-292 Length: 2991  
Score: 2861.00 Matches: 539  
Percent Similarity: 92.5% Conservative: 0  
Best Local Similarity: 92.5% Mismatches: 0  
Query Match: 98.9% Indels: 44  
DB: 8 Gaps: 1  
US-10-628-525A-21 (1-539) x ABX09932 (1-2991)  
QY 1 CysValAlaGluLeuSerArgGlu-----8  
DB 719 TCGTTCGGAGCTGAGCAGGGGGGGCCGCGCGCGCGCTGCCACCCCGCTGCTG 778  
QY 8 -----8  
DB 779 GCGCCCCCGCTCGTGGCCGGCTTCGCGCGCGCGCGCGAGCCACGGTGAGCGCGCA 838  
QY 9 -----AspLeuGlyLeuGluProGluGly 16  
DB 839 TCGACGCCCGCCCGCTGCCAGCGCGCGCTGGGGGACCTCGGTCTCGAACCCTGAAGGG 898  
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
DB 899 ATTGCTGAAGGTTCCATCATCAACACAGTAGTTGTGGCAAGTGAGCAAGATTTCTGAGATT 958  
QY 37 ValValGlyLeuGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
DB 959 GTGGTTGGAAGAGGAGCAGCTCGAGCTAAAGTAAACACAAAGCATTTGCTTTGTAACCGGC 1018  
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
DB 1019 GAAGCTTCTCCTTATGCAAGTCTGGGGTCTAGGAGATGTTGTGGTTTCATTCGCAGTT 1078  
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
DB 1079 GCTCTGTCTGCTCGTGTCCCGTCACTGATGGTTGTAATGCCAGATATTTAATGGTACC 1138  
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
DB 1139 TCCGATAAGAAATTATGCAATGCAATTTTACACAGAAAAACACATTCGGATTCCATGCTTT 1198  
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspThrValPhe 136  
DB 1199 GCGGTGAAATGAAGTTACCTTCTTCATGATAGTAGATTCAGTTGACTGGGGTGT 1258  
QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
DB 1259 GTTGATCATCCTCATATCACAGACCTGGAAATTTATATGGAGATAAGTTTGGTCTTTT 1318  
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
DB 1319 GGTGATAATCAGTTAGATACACACTCCTTTGCTATGCTGCTGCTGTGAGGCTCCTTTGATC 1378  
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspThrHis 196  
DB 1379 CTGTGAATTTGGGAGGATATATTTATGACAGAAATTCATGTTGTGTCATGATTTGGCAT 1438  
QY 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216

DB 1439 GCCAGTCTAGTGCCAGTCTCTTCTGCTCAAAATATAGACCATATGGTGTATTATAAGAC 1498  
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
DB 1499 TCCCGCAGCATTTCTTGTATAATACATAATTTAGCACATCAGGGTGTAGAGCTTCAAGCACA 1558  
QY 237 TyrProAspLeuGlyLeuProProGluTyrGlyAlaLeuGluTyrValPheProGlu 256  
DB 1559 TATCTCTGACCTTGGGTGGCCACTGAATGGTATGAGGCTCTGGAGTGGGTATTTCCCTGAA 1618  
QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
DB 1619 TGGCGGAGGAGCATGCCCTTGACAAGGGTGAGGAGTTAATTTTGAAGGTGCAGTT 1678  
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
DB 1679 GTGACAGCAGATCGAATCGTGAATCGTGAATAGGGTTATTCGTGGGAGTCAACATGCT 1738  
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
DB 1739 GAAGGTGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGAAT 1798  
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
DB 1799 GTAAATGGAATTTGACATTAATGATTGGAACCTGCCACAGACAAATGATATCCCTGTCAT 1858  
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
DB 1859 TATTCTGTGTAGTACCTCTCTGGAAGGCCAAATGTAAGGTGCAATTGCAGAAGGAGCTG 1918  
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
DB 1919 GGTTTACCTATTAAGCCCTGATGTTCTCTGATTGGCTTTATTGGAAGGTTGGATTATACG 1978  
QY 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
DB 1979 AAAGCATTGATCTCATTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2038  
QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
DB 2039 GTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 2098  
QY 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
DB 2099 TTCAGGATAAATTTCTGTGGATGGGTGGATTGATTGTTCCAGTTTCCACCAGATTAAT 2158  
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
DB 2159 GCGGCTCGGATATATTGTTAATGCCATCCAGATTGGAACCTTGTGGTCTCAATCAGCTA 2218  
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
DB 2219 TATGCTATGCAATATGGCAGCATGCTCTGTGTGTCATGCAACTGGGGGCTTAGAGATACC 2278  
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496  
DB 2279 GTGGAGAACTTCAACCCCTTGGTGAGATGGAGAGCAGGGTACAGGGTGGGCATTCGCA 2338  
QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
DB 2339 CCCCTAACACAGAAAAACATGTTTGTGGACATTCGAACTGCAATATCTACATACAGGCA 2398  
QY 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
DB 2399 ACACAAGTCTCTCTGGGAAGGGCTAATGAGCGAGGCTATGTAAGAGCTTCACCGTGGGA 2458  
QY 537 ProCysArg 539  
DB 2459 CCATGCCGC 2467  
RESULT 3  
AAV29756

AAV29756 standard; DNA; 1752 BP.  
 AAV29756;  
 11-SEP-1998 (first entry)  
 Zea mays soluble starch synthase I gene.  
 SER; starch-encapsulating region; fusion vector;  
 soluble starch synthase I; glucosyl transferase; ss.  
 Zea mays.  
 Key Location/Qualifiers  
 CDS 1..2007  
 /\*tag= a  
 /product= "soluble starch synthase I"  
 WO9814601-A1.  
 09-APR-1998.  
 30-SEP-1997; 97WO-US017555.  
 30-SEP-1996; 96US-0026855P.  
 (EXSE-) EXSEED GENETICS LLC.  
 Keeling P, Guan H;  
 WPI; 1998-240100/21.  
 P-PSDB; AAW56488.  
 Hybrid polypeptide comprising starch-encapsulating region and protein -  
 useful for, e.g. producing protein(s) resistant to degradation by stomach  
 acids.  
 Example 2; Page 39-41; 156pp; English.  
 The sequence is that of the soluble starch synthase I gene. It can be  
 used in the production of a hybrid polypeptide comprising a starch-  
 encapsulating region (SER) fused to a payload protein. The hybrid  
 polypeptide can be used to make modified starches comprising the payload  
 protein, selected from, e.g. hormones, growth factors, antibodies,  
 enzymes, dyes, immunoglobulins, etc. The modified starch can also be used  
 to provide grain feeds enriched in amino acids. By encapsulating the  
 payload protein in starch, it is more resistant to degradation by stomach  
 acids  
 SQ Sequence 1752 BP; 433 A; 379 C; 469 G; 471 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.33e-292 Length: 1752  
 Score: 2858.00 Matches: 538  
 Percent Similarity: 92.5% Conservative: 1  
 Best Local Similarity: 92.3% Mismatches: 0  
 Query Match: 98.8% Indels: 44  
 DB: 2 Gaps: 1  
 US-10-628-525A-21 (1-539) x AAV29756 (1-1752)  
 QY 1 CysValAlaGluLeuSerArgGlu----- 8  
 DB 1 TGCCTGCGGAGCTGAGCAGGAGGGGCCGCGCGCGCTGCCACCCGCGCTGCTG 60  
 QY 8 ----- 8  
 DB 61 GCSCCCCCGCTGTCGCCGCTTCCTCGCGCGCGCGCGCGAGCCACGGGTGAGCGGCA 120  
 QY 9 -----AspLeuGlyLeuGluProGluGly 16  
 DB 121 TCGACGCGCGCGCGCTGTCGCCGAGCGCGCGCTGGGGGACCTCGGTCTCGACCTGAGGG 180

17 IleAlaGluGlySerIleAspAsnThrValValValAlaSerGluGlnAspSerGluIle 36  
 181 ATTGCTGAAGGTTCCATCGATAACACAGTAGTTGTGGCAAGTGACGAAGATTCAGATT 240  
 QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
 241 GTGGTTGGAAAGGAGCAAGCTCGAGCTAAAGTAGAACAAAGCATTTGCTTTGTAAACCGGC 300  
 QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
 301 GAAGCTTCTCTTATGCAAGCTCTGGGGGCTAGGAGATGTTTGTGGTTCATTGCCAGTT 360  
 QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
 361 GCTCTTGCTGCTCGTGGTCCACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACC 420  
 QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
 421 TCCGATAAGAAATTATGCAATGCATTTTACAGAGAAAAACACATTCGGATTCCCATGCTTT 480  
 QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
 481 GCGGTGAACATGAAGTTACTTCTTCATGAGTATAGAGATTCAGTTGCTGGTGTGTTT 540  
 QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
 541 GTTGATCATCCCTCATATCACAGACCTGGAAATTTATATGAGAGATAAGTTTGGTGTCTTT 600  
 QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
 601 GGTGATAATCAGTTTCAGATACACACTCTTTCGTATGCTGATGATGAGGCTCTCTTTGATC 660  
 QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
 661 CTTGAATTGGGAGGATATATTTATGGACAGAAATTCATGCTGTTGTTGTCATGATGGCAT 720  
 QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
 721 GCCAGTCTAGTGGCAGTCTCTTCTGTGCAAAATATAGACCATATGCTGTTTATAAAGAC 780  
 QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
 781 TCCCGCAGCAGTCTTGTATACATAATTTAGACATCAGGGGTGAGAGCTTCGAAGCACA 840  
 QY 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
 841 TATCCTGACCTTGGTGGCCCTGATGGTATGGAGCTCTGGAGTGGGTATTCCTCCGAA 900  
 QY 257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
 901 TGGCGGAGGAGGATGCCCTTGACAAGGGGTGAGGAGTAAATTTTGAAGGGTGCAGTT 960  
 QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
 961 GTGACAGCAGATCGAATCGTGACTGTGAGTAAAGGGTATTTTCGGGGAGGTCACAACTGCT 1020  
 QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
 1021 GAAGGTGGACAGGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACGGNAAT 1080  
 QY 317 ValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHis 336  
 1081 GTAAATGGAAATTGACATTAATGATTGGAACCCCTGCCACAGACAAATGTATCCCTGTGCAT 1140  
 QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
 1141 TATTCCTGTGATGACCTCTCTGAAAGGGCCAAATGTAAGGGTGCATTTGCAAGAGGAGCTG 1200  
 QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
 1201 GGTTCATCTATAAGGCTGATGTTCTCTGATTGGCTTTATTTGGAAGGTGGATTATCAG 1260  
 QY 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396



Db	1261	AAAGGCATTGATCTCATTTCAACTTATCATACCAAGATCTCATGCGGGAAGATGTTCAATTT	1320
Qy	397	ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle	416
Db	1321	GTCAATGTTGGATCTGTTGACCCAGACCTTGAAGATTGGATGAGATCTACAGAGTCGATC	1380
Qy	417	PhelysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr	436
Db	1381	TTCAAGGATAAATTTCTGCGATGGTTGGATTTAGTGTTCAGTTTCCCACCGAATAACT	1440
Qy	437	AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu	456
Db	1441	GCCGGCTGCGATATATTGTTTAATGCCATCCAGATTCCGAACCTTGTGGTCTCAATCAGCTA	1500
Qy	457	TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr	476
Db	1501	TATGCTATGAGTATGACACAGTTCCTGTTGTCCATGCAACTGGGGCCCTTAGAGATACC	1560
Qy	477	ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla	496
Db	1561	GTGAGAACTTCAACCCCTTTCGGTGAAGATGGAGAGCAGGATACAGGTTGGCATTCGCA	1620
Qy	497	ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly	516
Db	1621	CCCTTAACCAACAGAAACATGTTTCTGGACATTCGGAACATGCAATATCTACATACAGGA	1680
Qy	517	ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValIysArgLeuHisValGly	536
Db	1681	ACCAAGTCTCTCTGGGAGGGCTAATGAAGCAGGCGATGTCAAAAGACTTCACGTGGGA	1740
Qy	537	ProCysArg 539	
Db	1741	CCATGCCGC 1749	
RESULT 4			
AAV70960			
XX	ID	AAV70960 standard; DNA; 1749 BP.	
XX	AC	AAV70960;	
XX	XX		
XX	DT	23-AUG-1999 (first entry)	
XX	DE	DNA encoding maize starch soluble synthase I-2.	
XX	XX		
KW	XX	Non-glycogen-like polysaccharide production; fermentation;	
KW	XX	starch synthetase enzyme; glycogen-synthetase enzyme; glycogen synthesis;	
KW	XX	non-starch branching gene; amylopectin; amylose; plant-like starch;	
KW	XX	maize starch soluble synthase I-2; ss.	
OS	XX	Zea mays.	
XX	XX		
PN	XX	WO9844780-A1.	
XX	XX		
PD	XX	15-OCT-1998.	
XX	XX		
PF	XX	03-APR-1998; 98WO-US006660.	
XX	XX		
PR	XX	04-APR-1997; 97US-0042939P.	
XX	XX		
XX	XX	(EXSE-) EXSEED GENETICS LLC.	
XX	XX		
PI	XX	Guan H, Keeling PL;	
XX	XX		
DR	XX	WPI; 1998-568285/48.	
DR	XX	P-PSDB; AAV70894.	
XX	XX		
PT	XX	Producing non-glycogen-like polysaccharides in bacteria, fungi or plants	
PT	XX	transformed with genes for enzymes involved in starch or glycogen	
PT	XX	synthesis allows fermentative production of starches with engineered	
XX	XX	properties.	
XX	XX		
PS	XX	Disclosure; Fig 52; 150pp; English.	

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Db 721 GCCAGTCTAGTGCAGTCTCTTCTGCTGCAAAATATAGACCATATGCTGTTTAAAGAC 780
Qy 217 SerArgSerLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 781 TCCCGCAGCATCTCTGTAATACATAATTTAGCACATCAGGGTGTAGAGCCTGCAAGACA 840
Qy 237 TyrProAspLeuGlyLeuProGluTyrProGluTyrGlyAlaLeuGluTyrValPheProGlu 256
Db 841 TATCCTGACCTTGGTGTGCACCTGAAATGATGAGCTCTGGAGTGGGTATTCCTCGAA 900
Qy 257 TrpAlaArgArgHisAlaLeuAspLeuGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
Db 901 TGGCGAGGAGGATGCCCTTGACAGGGTGAGCGATTAATTTTTGAAAGGTGCAGTT 960
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
Db 961 GTGACAGCAGATCGAATCGTGACTGTCTCAGTAAGGGTTATTCGTGGAGGTCACAACTGCT 1020
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316
Db 1021 GAAGGTGGACAGGCGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGGAAT 1080
Qy 317 ValAsnGlyIleAspIleAsnAspTTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 1081 GTAAATGGAAATTCACATTAATGATTGGAACCTCGCCACACAAATGTATCCCTGTGCAT 1140
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 1141 TATTCCTGATGACCTCTCTGGAAGGCCAAATGTAAGGTGCATTCAGAGGAGCTG 1200
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1201 GGTTCACCTATTAAGGCTGATGTCTCTGATTTGCTTTATTCGAAAGGTTGATATCAG 1260
Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1261 AAAGGCATTAATCTCAATTCATCAACAGATCTCATCCAGATCTCATCGGAGAGTTCATTT 1320
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
Db 1321 GTCATGCTTGGATCTGTCACCCAGAGCTTGAAGATTGGATGAGATCTACAGATCGATC 1380
Qy 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
Db 1381 TTCAGGATAAAATTTCTGATGGGTGGATTTAGTGTTCAGTTTCCACCCGAAATAACT 1440
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerAtqPheGluProCysGlyLeuAsnGlnLeu 456
Db 1441 GCCGGCTGCATATATTGTTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 1500
Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1501 TATGCTATGAGTATGTCACAGTCTCTGTTGTCATGCAACTGGGGGCTTAGAGATACC 1560
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496
Db 1561 GTGGAGAACTTCAACCTTTTCGGTGAGAAATGGAGACAGGGTACAGGGTGGGCATTCGCA 1620
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
Db 1621 CCCCTAACACACAGAAACATGTTTGGACATTTGCCAATTCGAATATCTACATACAGGA 1680
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 1681 ACACAGTCTCTCTGGGAGGGCTATTAAGCGAGGCATGTCAAAAGACTTCACGTGGGA 1740
Qy 537 ProCysArg 539
Db 1741 CCATGCCGC 1749
```

RESULT 5  
AAZ50643

```
ID AAZ50643 standard; cDNA; 2008 BP.
AC AAZ50643;
DT 23-MAY-2000 (first entry)
DE Corn soluble starch synthase gene fragment inserted in pSS65-C11.
XX Soluble starch synthase; starch fine structure; corn; transgenic plant;
KW amylose; amylopectin; amylose polymerisation;
KW non-granule bound starch synthase; non-GBSSI; altered starch; food;
XX paper; plastic; adhesive; ss.
OS Zea mays.
XX MO200006755-A2.
PN 10-FEB-2000.
PD 26-JUL-1999; 99WO-US016296.
XX 28-JUL-1998; 98US-0094436P.
PR (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Broglie KB, Lightner JE;
XX WPI; 2000-195311/17.
XX Producing transgenic cereal crops with altered starch structure useful
PT for preparing foodstuff, paper, plastic or adhesives, comprises
PT transforming crops with chimeric sense or antisense gene construct
PT encoding starch synthase.
XX Claim 5; Page 53; 56pp; English.
XX The present sequence is the corn soluble starch synthase (SSI) DNA
CC sequence comprising the entire SSI coding region and a 3' UTR fragment
CC inserted into plasmid pSS65-C11. The chimeric gene containing the zein
CC promoter followed by the 3'UTR is used as a sense construct for
CC preparation of transgenic corn expressing altered starch structure. The
CC starch fine structure derived from a grain of the cereal crop can be
CC altered in the transformed cereal crop by changes in amylose to
CC amylopectin ratio, amylopectin fine structure, increased abundance of
CC very short amylopectin chains and in the degree of polymerisation of
CC amylose. These modifications can be created by controlling the expression
CC of non-GBSSI (non-granule bound starch synthase) in transgenic plants.
CC Altered starches are useful in foods, paper, plastics or adhesives
XX Sequence 2008 BP; 486 A; 463 C; 543 G; 516 T; 0 U; 0 Other;
```

Alignment Scores:  
Pred. No.: 9 3e-290 Length: 2008  
Score: 2832.00 Matches: 538  
Percent Similarity: 92.3% Conservative: 0  
Best Local Similarity: 92.3% Mismatches: 1  
Query Match: 97.9% Indels: 45  
DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x AAZ50643 (1-2008)  
Qy 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 119 TCGTTCGGAGACTGAGCAGGAGGGGGCCCGCGCGCGCGCGCGCGCTGCTGCTGCTG 178  
Qy 8 ----- 8  
Db 179 GCGCCCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 238  
Qy 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 239 TCGACGCCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 298



The present sequence is the corn soluble starch synthase (SSI) composite-gene. This was used in the construction of plasmid pSS31 for the generation of an antisense construct for suppression of SSI expression in corn. The starch fine structure derived from a grain of the cereal crop can be altered in the transformed cereal crop by changes in amylose to amylopectin ratio, amylopectin fine structure, increased abundance of very short amylopectin chains and in the degree of polymerisation of amylose. These modifications can be created by controlling the expression of non-GBSSI (non-granule bound starch synthase) in transgenic plants. Altered starches are useful in foods, paper, plastics or adhesives

Sequence 2491 BP; 597 A; 610 C; 657 G; 627 T; 0 U; 0 Other;

**Alignment Scores:**

Pred. No.:	1.27e-289	Length:	2491
Score:	2832.00	Matches:	538
Percent Similarity:	92.3%	Conservative:	0
Best Local Similarity:	92.3%	Mismatches:	1
Query Match:	97.9%	Indels:	45
DB:	3	Gaps:	1

US-10-628-525A-21 (1-539) x AAZ50636 (1-2491)

Qy	1	CysValAlaGluLeuSerArgGlu	381
Db	262	TGCGTCGCGAGCTGAGCAGGAGGGCCGCGCGCGCGCTGCCACCGCGCTGCTG	321
Qy	8	-----8	
Db	322	GGGCCCCCGCTCGTCCCGGCTTCTCGCGCGCGCGCGAGCCCGAGGGTGAGCCGGCA	381
Qy	9	-----AspLeuGlyLeuGluProGluGly	16
Db	382	TCGACGCCGCCCGCTGCCCGACGCCCGCGCTGGGGGACCTCGGTCTCGAACTGGAAGG	441
Qy	17	IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle	36
Db	442	ATTGCTGAAGGTTCCATCGATAACACACTAGTTGTGGCAAGTGAGCAAGATTCGAGATT	501
Qy	37	ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly	56
Db	502	GTGGTTGGAAAGGAGCAAGCTCGAGCTAAAGTAAACACAAAGCATTTGTTGTAACCGCG	561
Qy	57	GluAlaSerProTyrAlaLysSerGlyClyLeuGlyAspValCysGlySerLeuProVal	76
Db	562	GAAAGCTTCTCTTATGCAAGTCTGGGGGTCTAGGAGATGTTGTGGTTCAATGCCAGTT	621
Qy	77	AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr	96
Db	622	GCTCTTGCTGCTGCGGTACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTGACC	681
Qy	97	SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe	116
Db	682	TCCGATAGAAATTATGCAATGCATTTTACACAGAAACACATTCGATTCATGCTTT	741
Qy	117	GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrpValPhe	136
Db	742	GGCGGTGAACATGAAGTTTACCTTCTCCATCAGTATAGAGATTCCAGTTGACTGGGTGTT	801
Qy	137	ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe	156
Db	802	GTTTGATCATCCCTCATATCACAGACCTGGAATTTATATGGAGATAAGTTTGGTGCTTT	861
Qy	157	GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle	176
Db	862	GGTGATAATCAGTTCCAGATACACATCTCTTGGCTATGCTGCATGTGAGGCTCTCTTGATC	921
Qy	177	LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis	196
Db	922	CTTGAAATTGGGAGGATATATTATTTGGAACAGAAATTCATGTTGTTGTCAAAGATTGGCAT	981
Qy	197	AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp	216





Db 1558 ATATCTCGACCTTGGGTTGCCACCTGAATGGTATGAGGCTCTGGAGTGGGTATTCCTCGA 1617  
Qy 256 uTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyValaVa 276  
Db 1618 ATGGCGAGGAGCATGCCCTTGACAAAGGGTGAGGCAGTTAAATTTTGAAGGTGCAGT 1677  
Qy 276 lValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAl 296  
Db 1678 TGTGACAGCATCGAATCGTACTGTCTAGTAAGGGTTATTCATGGAGGTCACAACTGC 1737  
Qy 296 adluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyI 316  
Db 1738 TGAAGGTGCACAGGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAT 1797  
Qy 316 eValaenGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIlePrCysHi 336  
Db 1798 TGTAAATGGAAATGCAATTAATGATTGGAACCTGCCACAGACAAATGATCCCTGTCA 1857  
Qy 336 sTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLe 356  
Db 1858 TTATCTGTGTGATGACCTCTCTTGAAGGCTAAATGTAAAGGTGCATTGCCAAGGAGCT 1917  
Qy 356 uGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGl 376  
Db 1918 GGGTTTACCTATAAGGCTGATGTTCTCTGATTGGCTTTATTGGAAGATTGGATTATCA 1977  
Qy 376 nLysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPh 396  
Db 1978 GAAAGCATGTGATTCATTCATCTATCATACAGATCTCATGCCGAGAATGTTCAAT 2037  
Qy 396 eValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIl 416  
Db 2038 TGTCTATGCTTGATCTGTTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGATCGAT 2097  
Qy 416 ePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleTh 436  
Db 2098 CTTCAAGGATAAATTTCTGTGGATGGGTTGCAATTTAGTTTCCAGTTTCCACCGCAATAAC 2157  
Qy 436 rAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLe 456  
Db 2158 TCGCGGTGGCAGATATATTGTTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCT 2217  
Qy 456 uTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspTh 476  
Db 2218 ATATGCTATGATGATGGCACAGTTCCTGTTGTCATGCAACTGGGGGCTTAGAGATAC 2277  
Qy 476 rValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAl 496  
Db 2278 CGTGAGAACTTCAACCCCTTTCGGTGAGAAATGGAGAGCAGGGGTACAGGGTGGGCATTGCG 2337  
Qy 496 aProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGl 516  
Db 2338 ACCCTTAACCAAGAAATCATGTTGTGGACATTCGAACTGCAATATATCATACAGGG 2397  
Qy 516 YThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGl 536  
Db 2398 AACACAGTAATAATGGGAAGGGCTAATGAAGCCAGGCATGTCAAAAGAGTTCACTGGG 2457  
Qy 536 YProCysArg 539  
Db 2458 ACCATGCCGC 2467

RESULT 9  
AAT67285  
ID AAT67285 standard; cDNA; 2992 BP.  
XX  
AC AAT67285;  
XX  
DT 17-OCT-2003 (revised)  
DT 11-SEP-1997 (first entry)  
XX  
DE Soluble starch synthase cDNA clone SSS10.52.  
XX

KW Soluble starch synthase; SSS10.52; transgenic plant; cereal; maize; ss.  
XX  
OS Zea mays; inbred line W64A.  
FN W09720936-A1.  
XX  
PD 12-JUN-1997.  
XX  
PF 04-DEC-1996; 96WO-CB002990.  
XX  
PR 06-DEC-1995; 95GB-00024938.  
XX  
PA (ZONE ) ZENECA LTD.  
XX  
PI Keeling PL, Knight ME;  
XX  
DR WPI; 1997-319782/29.  
XX  
PT cDNA encoding soluble starch synthase - used to produce transgenic plants  
with increased capacity for producing and storing starch.  
XX  
PS Claim 5; Page 17-20; 44pp; English.  
XX  
CC cDNA clones SSS10.52, SSS6.31 and SSS56 (AAT67285-87) code for maize  
soluble starch synthase (SSS). They were isolated from a maize inbred  
line W64A library by screening with a probe (AAT67288) based on pea SSS,  
rice SSS and maize GBSS. The cDNAs can be used to produce plants with an  
increased capacity for producing starch, or a capacity to produce starch  
with an altered fine structure. They can also be used to isolate the  
corresponding genomic sequences from crop plants, to determine the  
contribution of the SSS gene to the net regulation of starch  
biosynthesis, and to modify the levels of starch produced by the plant.  
CC Transgenic plants (esp. maize) can be used to produce hybrid plants which  
have higher rates of starch synthesis at temperatures above the normal  
optimum. (Updated on 17-OCT-2003 to standardise OS field)  
XX  
SQ Sequence 2992 BP; 758 A; 655 C; 801 G; 776 T; 0 U; 2 Other;  
Alignment Scores:  
Pred. No.: 1.51e-281 Length: 2992  
Score: 2757.00 Matches: 523  
Percent Similarity: 90.9% Conservative: 8  
Best Local Similarity: 89.6% Mismatches: 8  
Query Match: 95.3% Indels: 45  
DB: 2 Gaps: 1  
US-10-628-525A-21 (1-539) x AAT67285 (1-2992)  
Qy 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 719 TCGCTCGGAGCTGAGCAGGAGGGCGCGCGCGCGCTGCCACCGCGCTGCTG 778  
Qy 8 ----- 8  
Db 779 GCGCCCGCGCTGTCGCGGCTTCTCTCGCGCGCGCGCGAGCCACGCGGTGAGCGCGCA 838  
Qy 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 839 TCGACCGCGCGCGCTGCCGCGCGCGCTGCGGGGACCTCGGTCTCGAACTCGAAGGG 898  
Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 899 ATTGCTGAAGTTCCATCGATTAACACAGTAGTTGTGGCAAGTACAGATTTCTGAGATT 958  
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 959 GTGGTTGGAAGGACCAAGCTCAGCTAAAGTAAACACAAAGCATTTCTTCTTAACCGGC 1018  
Qy 57 GluAlaSerPro-TyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProVa 76  
Db 1019 GAAGCTTCTCCTTAATCGAAAGTCTGGGGGTCTAGAGATGTTTGTGGTTCATTGCCAGT 1078  
Qy 76 lAlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyTh 96



1079 TGCTCTTGTCTGCTCGCGGTACCGGTGATGTTGTAATGCCAGACATTTAAATGGTAC 1138  
Qy rSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPh 116  
1139 CTCGATAAGAAATATGCAAAATGCAATTTACTCAGAAAAACACATTCGGATTCATCTT 1198  
Qy eGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValph 136  
1199 TGGCGGTGAACATGAAGTCTCTTCCATGATGATAGAGATTCACTGACTGGGTGTT 1258  
Qy eValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaph 156  
1259 TGTGATCATCCCTCATATACAGACCTCGAAATTTATATGGAGATAAGTTTGGTCTTT 1318  
Qy eGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuII 176  
1319 TGGTGATAATCAGTTTCAGATACACACTCTTGTCTATGCTGCTGATGGAGCTCTTTGGT 1378  
Qy eLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHi 196  
1379 CCTTGAATTGGGAGGATATATTTATGACAGAAATTCATGTTGTTGTCATGATGGCA 1438  
Qy sAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAs 216  
1439 TGCAGTCTAGAGCCAGTCTCTTCTGCTGCAAAATATAGACCATATGTTGTTTATAAGA 1498  
Qy pSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerTh 236  
1499 CTCCCGCAGCATCTTGTATATACATAATTTAGCACATCAGGGTGTAGAGCTCGAAGCAC 1558  
Qy rTyrProAspLeuGlyLeuProGluTyrPyrGlyAlaLeuGluTyrPValPheProGl 256  
1559 ATATCTGACCTTGGGTGTCACCTGAATGATGAGAGTCTCGAGTGGGTATTCCTGTA 1618  
Qy uTPrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVa 276  
1619 ATGGGCGAGGAGCAGTCCCTTGACAGGGGTGAGGCAGTTTAATTTTGAAGGTGAGT 1678  
Qy lValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThrAl 296  
1679 TGTGACAGCAGATCGAATCGTACTGTCAAGAGGTATTCATGGAGGTCACAACTGC 1738  
Qy aGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyI 316  
1739 TGAAGGTGACAGGCGCTCAATCAGCTCTTAAGCTCCAGAAAGAGTGTATTAACGGAAT 1798  
Qy eValAsnGlyIleAspIleAsnAspTyrPheProAlaThrAspLysCysIleProCysHi 336  
1799 TGTAAATGGAATTGACATTAATGATTTGGAAACCTGCCACAGACAAATGATCCCTGTCA 1858  
Qy sTyrSerValAspAspLeuSerGlyLysAlaLysCysLysValAlaLeuGlnLysGluLe 356  
1859 TTATTCGTGTGATGACCTCTCTGAAGGCTAAATGTAAAGGTGCATTCGAGNAGAGGT 1918  
Qy uGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGl 376  
1919 GGGTTTACCTATAAGGCGCTGATGCTCTGATTTGGCTTTTATTTGAAGATTGGATTATCA 1978  
Qy nLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnph 396  
1979 GAAAGCATGATGATCTCATTCACCTTATCATACAGATCTCATCGGAAAGAAATGTTCAAT 2038  
Qy eValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerI 416  
2039 TGTGATGCTTGGATCTGGTGACCCAGAGCTTGAGATTGGATGAGATCTACAGATCGAT 2098  
Qy ePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleTh 436  
2099 CTTCAAGGATAAATTTCTGGATGGGTGGATTTAGTGTTCAGTTTCCACCGCAATAAC 2158  
Qy rAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnle 456

Db 2159 TGGCGGTGGCGATATATTTGTAATGCCATCCAGATTCCGAACCTTGTGTCTCAATCAGCT 2218  
Qy uTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspTh 476  
Db 2219 ATATGCTATGCAGTATGGCACAGTCTCTGTTGTCATGCAACTGGGGGCGCTTAGAGATAC 2278  
Qy rValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAl 496  
Db 2279 CGTGGAGAACTTCAACCCCTTCGGTGAGATGGAGAGCAGGGTACAGGGTGGGCATTCGC 2338  
Qy aProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGl 516  
Db 2339 ACCCTTAACACAGAAACATGTTGTGGACATTTGGCACTTGGCAATATCTACATACAGG 2398  
Qy yThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGl 536  
Db 2399 AACACAGTAATTAATGGGAAGGCTAATGAGCCAGGCATGTCAAAGAGTTTACGTGGG 2458  
Qy yProCysArg 539  
Db 2459 ACCATGCCGC 2468  
RESULT 10  
AAZ50637/c  
ID AAZ50637 standard; cDNA; 1528 BP.  
XX  
AC AAZ50637;  
DT  
XX 23-MAY-2000 (first entry)  
DE  
XX Corn soluble starch synthase gene fragment inserted in pSS42.  
XX Soluble starch synthase; starch fine structure; corn; transgenic plant;  
KW amylose; amylopectin; amylose polymerisation;  
KW non-granule bound starch synthase; non-GBSSI; altered starch; food;  
KW paper; plastic; adhesive; ss.  
XX  
OS Zea mays.  
XX  
PN WO200006755-A2.  
XX  
PD 10-FEB-2000.  
XX  
PF 26-JUL-1999; 99WO-US016296.  
XX  
PR 28-JUL-1998; 98US-0094436P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Broglie KE, Lightner JE;  
XX  
XX WPI; 2000-195311/17.  
DR  
XX Producing transgenic cereal crops with altered starch structure useful  
PT for preparing foodstuff, paper, plastic or adhesives, comprises  
PT transforming crops with chimeric sense or antisense gene construct  
PT encoding starch synthase.  
XX  
PS Claim 5; Page 51-52; 56pp; English.  
XX  
CC The present sequence is the corn soluble starch synthase (SSI) DNA  
CC sequence inserted into plasmid pSS42. Chimeric gene of pSS42 was cloned  
CC into the vector pKS17 for the generation of an antisense construct for  
CC suppression of SSI expression in corn. The starch fine structure derived  
CC from a grain of the cereal crop can be altered in the transformed cereal  
CC crop by changes in amylose to amylopectin ratio, amylopectin fine  
CC structure, increased abundance of very short amylopectin chains and in  
CC the degree of polymerisation of amylose. These modifications can be  
CC created by controlling the expression of non-GBSSI (non-granule bound  
CC starch synthase) in transgenic plants. Altered starches are useful in  
CC foods, paper, plastics or adhesives  
XX  
SQ Sequence 1528 BP; 440 A; 383 C; 300 G; 405 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	3,76e-271	Length:	1528
Score:	2855.00	Matches:	495
Percent Similarity:	99.8%	Conservative:	0
Best Local Similarity:	99.8%	Mismatches:	1
Query Match:	91.8%	Indels:	1
DB:	3	Gaps:	0
US-10-628-525A-21 (1-539) x AAZ50637 (1-1528)			
QY	44	ArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLys	63
DB	1527	CGAGCTAAAGTAACACAAAGATTGCTTTGTAACCGCGGAAGCTTCTCTTATGCAAG	1468
QY	64	SerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHis	83
DB	1467	TCGGGGGCTAGGAGATGTTTGTTGTTCAATGGCCAGTTGCTCTTGCTGCTGGTGCAC	1408
QY	84	ArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsn	103
DB	1407	CGTGTGATGGTTGTAATGCCCCAGATATTAAATGGTACTCCGATGAAGTAATTATGCAAT	1348
QY	104	AlaPheTyrThrGlyLysHisIleArgIleProCysPheGlyGlyGluHisGluValThr	123
DB	1347	GCATTTTACACAGAAAAACACATTCGATTCCATGCTTTGGCGTGAACATGAAGTTACC	1288
QY	124	PhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSerTyrHis	143
DB	1287	TTCTTTCCATGAGTATAGAGATTTCAGTTGACTGGGTGTTTGTGGTATCATCCCTCATATCAC	1228
QY	144	ArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr	163
DB	1227	AGACCTGGAATTTATATGAGATAGATTGGTGTCTTTGGTGAATATCAGTTCAGATAC	1168
QY	164	ThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIle	183
DB	1167	ACACTCCCTTTGCTATGCTCATGTGAGGCTCCTTTGATCCTTGAATGGGAGGATATATT	1108
QY	184	TyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValProValLeu	203
DB	1107	TATGGACAGAAATGCAATGTTGTTGTCAATGATTTGGCATGCCAGTCTAGTGGCAGTCTTT	1048
QY	204	LeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIle	223
DB	1047	CTTGCTGCAAAATATAGACCATATGTTGTTTAAAGACTCCCGCAGCAATTTTGTAAATA	988
QY	224	HisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuPro	243
DB	987	CATAATTTAGCACATCAGGGTGTAGAGCTGCAAGCACATATCCTGACCTTGGTGGCCA	928
QY	244	ProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgHisAlaLeu	263
DB	927	CCTGAATGATATGGAGCTCTGGAGTGGGTATTTCCCTGAATGGCGGAGGAGCATGCCCTT	868
QY	264	AspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleVal	283
DB	867	GACAAGGTGAGGCAGTTAAATTTTGAAGGTGCAGTTGTGCACAGCATCGAATCGTG	808
QY	284	ThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlyGlnGlyLeuAsn	303
DB	807	ACTGTCAAGTAAAGGTTATTTCGTGGGAGGTCACAACTGCTGGAAGGTGGACAGGCTCAAT	748
QY	304	GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn	323
DB	747	GAGCTCTTAAGCTCCAGAAAGATGTATTAAACGGAAATTTGTAATGGAATTCACATTAAT	688
QY	324	AspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSer	343
DB	687	GATTGGACCCCTGCCACAGCAAGTATCCCTGTCTATTTCTGTTGATGACCTCTCT	628
QY	344	GlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp	363

Db	627	GGAAAGGCCAAATGTAAAGGTGCATTGTCAGAAAGGAGCTGGGTTTACCTATAAGGCCTGAT	568
QY	364	ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln	383
DB	567	GTTCCTCTGATTGGCTTTATTGGAAGGTTGGATTATCAGAAAGGCATTGATCTCATTTCAA	508
QY	384	LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp	403
DB	507	CTTATCATACCAAGATCTCATGCGGGAAGATGTTCAATTTGTCTGATCTGGTGAC	448
QY	404	ProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPheArgGly	423
DB	447	CCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATCTTCAAGGATAAATTTTCGTGGA	388
QY	424	TyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu	443
DB	387	TGGGTGGATTAGTGTTCAGTTTCCCACCAATAAATGCGCGCTGCGATATATTGTTTA	328
QY	444	MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr	463
DB	327	ATGCCATCCAGATTGGAACCTTGTGGTCTCAATCAGTATATGCTATGCGATATGGCACA	268
QY	464	ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProphe	483
DB	267	GTTCCTGTGTCCATGCAACTGGGGCTTTAGAGATACCGTGGAGAACTTCAACCCCTTC	208
QY	484	GlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet	503
DB	207	GGTGAAATGGAGACAGGGTACAGGGTGGGCAATTCGCCACCCCTAACCCAGAAACATG	148
QY	504	PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg	523
DB	147	TT-GTGACATTCGCACTGCAATATCTACATACAGGGGACACCAAGTCTCTCTGGGAAGG	89
QY	524	AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg	539
DB	88	GCTAATGAAGCGAGCATGTCAAAAGACTTCACGTGGGACCACATGGCGC	41
RESULT 11			
ADX36677			
ID	ADX36677	standard; cDNA; 1855 BP.	
XX	AC	ADX36677;	
XX	XX	21-APR-2005 (first entry)	
DT	XX	Plant full length insert polynucleotide seqid 19497.	
XX	XX	plant protectant; plant growth regulant; gene therapy; plant;	
XX	XX	recombinant DNA construct; physical array; plant breeding marker;	
XX	XX	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;	
XX	XX	extreme osmotic condition; pathogen tolerance; pest tolerance;	
XX	XX	growth rate; cell cycle pathway; disease resistance;	
XX	XX	galactomannan production; lignin production; plant growth regulator;	
XX	XX	yield; plant growth; plant development; seed oil; protein yield;	
XX	XX	protein content; gene; ss.	
OS	XX	Unidentified.	
XX	XX	US2004034888-A1.	
PN	XX	19-FEB-2004.	
XX	XX	28-APR-2003; 2003US-00425114.	
PF	XX	06-MAY-1999; 99US-00304517.	
PR	XX	05-NOV-2001; 2001US-00985678.	
XX	XX	(LIU/) LIU J.	
PA	XX	(ZHOU/) ZHOU Y.	
PA	XX	(KHOV/) KOVALIC D K.	
PA	XX	(SCRE/) SCREEN S E.	
PA	XX	(TABA/) TABASKA J E.	

(CAOY/) CAO Y.

Liu J, Zhou Y, Kovalic DK, Screen SG, Tabaska JE, Cao Y;

WPI; 2004-180133/17.

New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.

Claim 1; SEQ ID NO 19497; 15pp; English.

The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at [ftp://seqdata.uspto.gov/sequence.html?DocID:2004034888](http://seqdata.uspto.gov/sequence.html?DocID:2004034888). The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.

SQ Sequence 1855 BP; 492 A; 371 C; 461 G; 531 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.29e-258 Length: 1855  
Score: 2538.00 Matches: 471  
Percent Similarity: 99.8% Conservative: 0  
Best Local Similarity: 99.8% Mismatches: 1  
Query Match: 87.7% Indels: 1  
DB: 13 Gaps: 0

US-10-628-525A-21 (1-539) x ADX36677 (1-1855)

QY 68 GlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetVal 87  
DB 1 GGAGATGTTTGTGTTCAATGGCCAGTTGCTCTTGCTCGTGTCAACCGTGTGATGTT 60  
QY 88 ValMetProArgTyrLeuAenGlyThrSerAspIysAsnTyrAlaAenAlaPheTyrThr 107  
DB 61 GTAAATGCCAGATATTAAATGGTGTACCTCCGATAAGAAATATGCAATGCAATTTTACACA 120  
QY 108 GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127  
DB 121 GAAACACATTCGGATTCATGCTTTGGCGGTGACATGACATGACCTTCTTCCATGAG 180  
QY 128 TyrArgAspSerValAspTyrValPheValAspHisProSerTyrHisArgProGlyAsn 147  
DB 181 TATAGAGATTCACTGGGTGTTTGTGATCATCTCCATATACACACACCTGGAAAT 240  
QY 148 LeuTyrGlyAspIysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys 167  
DB 241 TTATATGGAGATAAGTTTGGTGTCTTTTGGTGAATAATCAGTTTCAGATACACACTCTTGC 300  
QY 168 TyrAlaAlaCysGluAlaProLeuLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn 187  
DB 301 TATGCTGCATGTGAGGCTCTTTGATCTTGAATGGAGATATATTATGACAGAAAT 360  
QY 188 CysMetPheValValAenAspTyrPheAlaSerLeuValProValLeuLeuAlaAlaLys 207  
DB 361 TGCATGTTTGTGTAATGATGGCATGCCAGTCTAGTCCAGTCTCTTCTTGTGCAAAA 420  
QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAla 227

DB 421 TATAGACCATATGTTTATAAAGACTCCCGCAGCATCTCTGTAAATACATAATTTAGCA 480  
QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247  
DB 481 CATCAGGTTGTAGAGCTTCGCAAGCACAATATCTGACCTTGGGTTGCCACCTGGAATGGTAT 540  
QY 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspLysGlyGlu 267  
DB 541 GGAGCTCTGGAGTGGGTATTCCTGAATGGCGAGGAGGCATGCCCTTGACAGGGTGAG 600  
QY 268 AlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLys 287  
DB 601 GCAGTTAAATTTTGAAGGTGCAATTTGTGACAGCAGATCGAATCGTACTGTTCAGTAAG 660  
QY 288 GlyTyrSerTyrGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307  
DB 661 GGTATTTCTGGGAGGTCAACATGCTGAAAGTGGACAGGCGCTCAATGAGCTCTTAAGC 720  
QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnPro 327  
DB 721 TCCAGAAAGAGTGTATTAACGGAATTTGTAATGGAATTCACATTAATGATTGGAACCT 780  
QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspLeuSerGlyLysAlaLys 347  
DB 781 GCCACAGACAAATGTATCCCTGTCTCATTTATCTGTGATGACCTCTCTGGAAGGCCAAA 840  
QY 348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIle 367  
DB 841 TGTAAAGTGCATTCGCAAGAGGAGTGGGTTTACCTATAAGGCGCTGATGTCTCTGATT 900  
QY 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIlePro 387  
DB 901 GGCTTTATTCGAAAGTTGGATTTATCAGAAAGCATTGATCTCATTCACCTATCATACCA 960  
QY 388 AspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGlu 407  
DB 961 GATCTCATTCGCGAAGATGTTCAATTTGTCTGATCTGCTGACCCAGAGCTTGAA 1020  
QY 408 AspTyrMetArgSerThrGluSerIlePheLysAspIysPheArgGlyTyrValGlyPhe 427  
DB 1021 GATTGATGAGATCTACAGAGTGCATCTTCAAGGATAAATTTCTGTGATGGTGGATTT 1080  
QY 428 SerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArg 447  
DB 1081 AGTGTTCAGTTTCCACCGAATAACTGCCGGCTGCGATATATGTTAATGCCATCCAGA 1140  
QY 448 PheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValVal 467  
DB 1141 TTCGAACCTTGTGTTCTCAATCAGCTATATGCTATGCAAGTATGTCACAGTTCCTGTGTC 1200  
QY 468 HisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGly 487  
DB 1201 CATGCAACTGGGGGCTTTAGAGATACCGTGGAGAACTTCAACCTTTCCGTGAGAAATGGA 1260  
QY 488 GluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIle 507  
DB 1261 GAGCAGGTTACAGGGTGGGCAATTCGCACCCCTTAACCCACAGAAACATGTTTGTGGACATT 1319  
QY 508 AlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAla 527  
DB 1320 GCGAACTGCAATATCTACATACAGGGAACACAAAGTCTCTCTCGGAAGGGCTAATGAAGCG 1379  
QY 528 ArgHisValLysArgLeuHisValGlyProCysArg 539  
DB 1380 AGCATGTCAAAGACTTTCAGTGGGACCATGCGCG 1415  
RESULT 12  
ADQ37148  
ID ADQ37148 standard; DNA; 1881 BP.  
XX  
AC ADQ37148;  
XX





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Db 940 GGTGTGGAGCTGCCAGTACATATCTGACCTGGGATTCACCTGAATGGTATGGAGCA 999
Qy 250 LeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaVal 269
Db 1000 TTAGAATGGGTGTTTCCAGAGTGGGCAAGCGCATGCCCTTGACAAAGGTCGAGGCAGTC 1059
Qy 270 AenPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyr 289
Db 1060 AATTTTTTAAAGGCGCAGTTGTGACAGCAGATCGAAATTTGTGACTGTCCAGCAGGGGTAT 1119
Qy 290 SerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArg 309
Db 1120 TCATGGGAGTCCACAACTGCTGAGGTGGCGAAGGCTCAATGAGCTCTTAAGCTCCCG 1179
Qy 310 LysSerValLeuAsnGlyIleValLeuGlyIleAspIleAsnAspTrpAsnProAlaThr 329
Db 1180 AAGAGTGTATTGAATGGAATTTGAAATGGAATTTGACATTAATGATTTGGAACCCATCCACA 1239
Qy 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349
Db 1240 GACAGATTCTCCCTTATCATTTATCTGTGTGATGACCTGTCCGGAAGGCCAAGTGTAAA 1299
Qy 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369
Db 1300 GCTGAATTGCAGAGGAGTGGGTTTACCTATAGGCCCGATGTGCTCTGATTGGCTTT 1359
Qy 370 IleGlyArgLeuAspTrpGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeu 389
Db 1360 ATTGGAAGATTGGACTATCAAAAGGCAATTGATCTAAATTAATTTGCCATTCAGATCTC 1419
Qy 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409
Db 1420 ATGCGGGAACAATTAATTCGTGCTGCTGTGATCTGGTGACCCAGGTTTGAAGATGG 1479
Qy 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429
Db 1480 ATGAGATCCACAGATCAGGTACAGGATATAATTTCTGGATGGTGGATTAGTGT 1539
Qy 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
Db 1540 CCAGTTTCCACCGAATAACTGCAGGTTGCGATATATTGTTGATGCCATCCAGATTCGAA 1599
Qy 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
Db 1600 CTTGTGGCTCAATCAGCTATGCTATGCAATATGGTACAGTGCCTGTTGTCATGGA 1659
Qy 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489
Db 1660 ACTGGAGGCTCAGAGATACAGTGGAGATTTTAACCCGTTTCTGAGAAAGGAGCAG 1719
Qy 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509
Db 1720 GGTACAGGTGGGCAATCTCGCACCTAACCATTTGAAAAAAATGCTGTGGGCATTCGGAT 1779
Qy 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529
Db 1780 GGCAATTTCCAGATACAGGGAACACAAAGTCTCTTGGGGGGTCTAATGAAGCGAGGCAT 1839
Qy 530 ValLysArgLeuHisValGlyProCysArg 539
Db 1840 GTCAGGCACTTACATGGGACCATGCCGC 1869
```

## RESULT 14

ADNR04094

ID ADNR04094 standard; DNA; 1881 BP.

XX AC ADNR04094;

XX AC ADNR04094;

DT 21-OCT-2004 (first entry)

XX DE Rice starch synthase 3 coding sequence.

XX

KW transgenic; plant; ds; gene; starch synthase 3; targeted expression;  
KW starch-containing tissue; feed; pathogen resistance; nutritional quality;  
KW SS3; rice.

OS Oryza sativa.

FH Key Location/Qualifiers

FT CDS 1..1881  
FT /tag= a  
FT /product= "starch synthase 3"

XX WO2004065537-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-EP000241.

XX 20-JAN-2003; 2003DE-01002324.

XX (SUNG-) SUNGENE GMBH &amp; CO KGAA.

PA Heim U, Herbers K, Sonnewald U, Glickmann E;

XX WPI; 2004-562151/54.

DR P-PSDB; ADNR04095.

XX Targeted transgenic expression in starch-containing plant tissue, useful  
PT e.g. for imparting pathogen resistance, comprises placing nucleic acid  
PT under the control of a promoter from a starch synthase 3 gene.

PS Claim 3; SEQ ID NO 9; 158pp; German.

XX The present invention relates to a method for the targeted transgenic  
CC expression of a nucleic acid in a starch-containing tissue of a plant,  
CC which comprises transforming plant cells and regenerating the cells to  
CC produce plants. The nucleic acid is contained on an expression cassette  
CC comprising at least one promoter of a gene encoding starch synthase 3  
CC (SS3) functionally linked to the nucleic acid. Transgenic organisms, or  
CC their products, that express the nucleic acid in their starch-containing  
CC tissues are useful for preparation of foods, animal feeds, seeds,  
CC pharmaceuticals and fine chemicals, e.g. enzymes, vitamins, amino acids,  
CC antibiotics, tocopherols and carotenoids; also they may have improved  
CC resistance to pathogens and abiotic stress, improved nutritional quality,  
CC better germination and storage properties, and better growth rate or  
CC harvest yield. The present sequence is an SS3 coding sequence.

SQ Sequence 1881 BP; 454 A; 398 C; 548 G; 481 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	2,79e-257	Length:	1881
Score:	2525.50	Matches:	475
Percent Similarity:	85.8%	Conservative:	31
Best Local Similarity:	80.5%	Mismatches:	33
Query Match:	87.3%	Indels:	51
DB:	13	Gaps:	3

US-10-628-525A-21 (1-539) x ADNR04094 (1-1881)

Qy 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 100 TGCCTGGCGGAGCTGAGCAGGACGCTGGTTCGGCGCAGCGCGCTGCGCGGCCG 159  
Qy 8 ----- 8  
Db 160 CTGGTGAAGCAGCCGCTCTGCGGACCTTCTCTGTCGGACGTCGACGCCACCCGCGCC 219  
Qy 9 -----AspLeuGly----- 11  
Db 220 AGCAGTCCCG 279  
Qy 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
Db 280 ATCGAGCCGATCTAGAAGGTCTCAGAGAAGATTCCATCGAAGAACCAATTTTGTGGCT 339

QY 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaAraGAlaLysValThrGln 49  
 DB 340 AGTGAAGAGGAGTCTGAGATCATGGATGTGAAGGAGCAAGCTCAAGCTAAAGTAACACGC 399  
 QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69  
 DB 400 AGCGTTGCTTTGTAACCGGTGAAGCTTCTCTTATGCAAGGTCAAGGTGGACTAGGAGAT 459  
 QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMet 89  
 DB 460 GTTGTGTTGCTTCACTGCGCAATGTCTTCTTCTTGTGTGTCATCTGTGTGTGTGTATG 519  
 QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109  
 DB 520 CCGAGATACATGAACGGGGCTTGAACAAATAATTTGCAACGCAATTTTACCTGAGAG 579  
 QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
 DB 580 CACATTAAAGATTCCATGCTTTGGCGGAGACATGAAGTTACTTTTTTTCAGAGTATAGG 639  
 QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149  
 DB 640 GATTCTGTGATTGGGTGTTGTGATCATCCCTCATATCATAGACCTGGAAATTTGTAT 699  
 QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
 DB 700 GAGAGATAAATTTGGTGTCTTTGGCGGATAATCAGTTTCAGATACACACTCTGTGTATGCG 759  
 QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMet 189  
 DB 760 GCCTGTGTAGACCCCATTAATCTTGAACCTGGAGGATATATCTATGGACAGAAATGCAATG 819  
 QY 190 PheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArg 209  
 DB 820 TTTGTTGTGAATGATTGGCATGCCAGTCTTGTGCGAGTCTTCTTGTGCAAAATATAGA 879  
 QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229  
 DB 880 CCATATGGTGTTTACAGGGATGCCCGCAGTGTCTTGTGCATACATAATCTAGCACATCAG 939  
 QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAla 249  
 DB 940 GGTGTGAGCTCCCAAGTACATATCTTGACCTGGGATTCACCTGAATGGTATGAGCA 999  
 QY 250 LeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaVal 269  
 DB 1000 TTAGAATGGTGTTCACAGATGGGCAAGGCGCATGCCCTTGACAAAGGTGAGGCAGTC 1059  
 QY 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
 DB 1060 AATTTTTTAAAGGCGCAGTTGTGACAGCAGATCGAATTTGTGACTGTGACCCAGGGGTAT 1119  
 QY 290 SerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGlnLeuLeuSerSerArg 309  
 DB 1120 TCATGGAGGTCAACACTGCTGAAGTGGCAGGCTCATAGTCTTAAAGCTTTAAAGCTCCCG 1179  
 QY 310 LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThr 329  
 DB 1180 AAGAGTGTATTGAATGGAATTTGAATGGAATTTGACATTAAATTTGGAACCCATCCACA 1239  
 QY 330 AspLysCysIleProCysHisTyrSerValAspLeuSerGlyLysAlaLysCysLys 349  
 DB 1240 GACAAAGTTTCTCCCTTATCATTAATCTGTGTGATGACCTGTCCGAAAGGCCAAGTGTAA 1299  
 QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProIleGlyPhe 369  
 DB 1300 GCTGAATTCAGAAAGGAGCTGGGTGTACCTATTAAGCCCGCATGTGCTCTGATTTGCTTT 1359  
 QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeu 389  
 DB 1360 ATTGGAAGATTGGACTATCAAAAGGCAATGATCTAATTAACCTTCCATTCAGATCTC 1419

QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409  
 DB 1420 ATCGGAGCAATATTTCAATTCGTCATGCTTGGATCTGTCACCCAGGTTTTGAAGGATGG 1479  
 QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429  
 DB 1480 ATGAGATCCACAGAATCAGGGTACAGGGATAAAATTTCTGTGATGGGTGGATTTAGTGT 1539  
 QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
 DB 1540 CCAGTTTCCACCCGATNACTCAGGTTGCGATATATTTGTGATGCCATCCAGATTGAA 1599  
 QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
 DB 1600 CCTTGTGGCTCAATCAGCTATATGCTATGCAATATGTTACAGTGCCTGTTGTTTCATGGA 1659  
 QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489  
 DB 1660 ACTGGAGGCTTCAGAGATACAGTGGAGAAATTTTAACCCGTTTGTGAGAAGGAGAGCAG 1719  
 QY 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
 DB 1720 GGTACAGGTGGGCATCTCTCGCCACTAACCATTTGAAAAAAATGCTGTGGCATTTGCCGAT 1779  
 QY 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
 DB 1780 GGCAATTTTCACATACAGGGAACAAGTCTCTTGGAGGGTCTAATGAAGCGAGGCAT 1839  
 QY 530 ValLysArgLeuHisValGlyProCysArg 539  
 DB 1840 GTCAGGACTTTTACATGGGACCATGCCGC 1869  
 RESULT 15  
 AAQ45183  
 ID AAQ45183 standard; cDNA to mRNA; 2533 BP.  
 XX AAQ45183;  
 AC AAQ45183;  
 DT 16-NOV-1994 (first entry)  
 XX Soluble rice starch synthetic enzyme.  
 DE Rice; starch synthetic enzyme; transit peptide; amyloplast; transition;  
 KW protoplast; expression; ss.  
 XX Oryza sativa.  
 OS  
 FH Key Location/Qualifiers  
 FT 5'UTR 1..113  
 FT /\*tag= a  
 FT CDS 114..1994  
 FT /\*tag= b  
 FT sig\_peptide 114..452  
 FT /\*tag= c  
 FT mat\_peptide 453..1991  
 FT /\*tag= d  
 FT 3'UTR 1992..2533  
 FT /\*tag= e  
 XX JP06070779-A.  
 XX 15-MAR-1994.  
 XX 07-JUL-1992; 92JP-00179947.  
 XX 07-JUL-1992; 92JP-00179947.  
 XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.  
 XX WPI; 1994-128678/16.  
 DR P-PSDB; AAR51231.  
 XX Soluble rice starch synthetic enzyme gene and transit peptide - for the





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XX ADA70523;
XX AC
XX DT 20-NOV-2003 (first entry)
XX DE
XX KW Rice gene, SEQ ID 3846.
XX KW Plant; bacterial infection; fungal infection; viral infection; rice;
XX KW Gene; ds.
XX OS
XX OS Oryza sativa.
XX PN W02003000898-A1.
XX PD 03-JAN-2003.
XX PF 22-JUN-2001; 2001WO-IB001105.
XX PR 22-JUN-2001; 2001WO-IB001105.
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX DR WPI; 2003-175290/17.
XX PT
XX PT Identifying at least one gene involved in plant resistance or response to
XX PT pathogenic infection for conferring resistance or tolerance to a plant to
XX PT bacterial, fungal or viral infection by determining or detecting plant
XX PT gene expression.
XX PS Claim 6; SEQ ID NO 3846; 899pp; English.
XX CC
XX CC The present invention relates to a method (M1) for identifying genes
XX CC involved in plant resistance or response to pathogenic infection. M1
XX CC comprises identifying a gene whose expression is significantly altered in
XX CC the incompatible interaction of plant gene expression relative to
XX CC expression of the gene in an uninfected plant, in a mutant plant that
XX CC does not express a gene associated with response to pathogenic infection,
XX CC or in a corresponding incompatible or compatible interaction. (M1) is
XX CC useful for conferring resistance to resistance or tolerance to a plant to
XX CC bacterial, fungal or viral infection. The present sequence was used to
XX CC illustrate the invention.
XX SQ
XX SQ Sequence 1926 BP; 467 A; 407 C; 557 G; 494 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 8.84e-256 Length: 1926
Score: 2511.50 Matches: 476
Percent Similarity: 85.9% Conservative: 31
Best Local Similarity: 80.7% Mismatches: 32
Query Match: 86.8% Indels: 52
DB: 8 Gaps: 3

US-10-628-525A-21 (1-539) x ADA70523 (1-1926)
QY 1 CysValAlaGluLeuSerArgGlu----- 8
DB 100 TGGTGGCGGAGTGTAGCAGGAGCGGTGGTGGCGCAGCGCCGCTGGCAGCGCGCGG 159
QY 8 ----- 8
DB 160 CTGGTGAAGCAGCGGCTCTCGCGACCTTCCTCGTGGCAGGTGCGACGCCCGCGGCC 219
QY 9 -----AspLeuGly----- 11
DB 220 ACGCAGTGGCGCGCGCGCGCGACCGCCCGCGCTTGGCGGACTCCGCGCGTGGGGAG 279
QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAenThrValValAla 29
DB 280 ATCGAGCCCGATCTAGAGGTCTCAGAGAGATTCCATCGACAAACAATTTTGTGGCT 339

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QY 30 SerGluGlnAaspSerGluIleValValGlyLysGluGlnAlaAraGAlaLysValThrGln 49
DB 340 AGTGAGCAGGAGTCTGAGATCATGATGTGAGGAGCAAGCTCAAGCTAAAGTAAACAGC 399
QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAasp 69
DB 400 AGCGTGTGCTTTGTAACCGGTGAAGCTTCTCTTATGCAAAAGTCAGGTGAGGAT 459
QY 70 ValCysGlySerLeuProValAlaLeuAlaAraGlyHisArgValMetValValMet 89
DB 460 GTTGTGTTCACTGCGCAATGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
QY 90 ProArgTyrLeuAenGlyThrSerAspLysAsnTyrAlaAenAlaPheTyrThrGluLys 109
DB 520 CCGAGATACATGAACGGGGCTTTGAACAAAAATTTTGCAAAACGCAATTTTACAC 579
QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
DB 580 CACATTAAGATTCCATGCTTTGGCGGAGAACATGAAGATTACTTTTTCACGATAGG 639
QY 130 AspSerValAaspTyrPheValAaspHisProSerTyrHisArgProGlyAenLeuTyr 149
DB 640 GATTCGTGTGATTTGGGTGTTTGTATCATCCCTCATATCATAGACCTGGAAATTT 699
QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169
DB 700 GGAGATAATTTTGGTCTTTTGGCGATATCATCAGTTCAGATACACATCTCTGTCTAG 759
QY 170 AlaCysGluAlaProLeuLeuLeuGluGlyGlyTyrIleTyrGlyGlnAenCysMet 189
DB 760 GCGTGTGAAGCCCCATTAATCTTGAACCTGGGAGGATATATCTATGGACAGAAATG 819
QY 190 PheValValAasnAaspTyrHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209
DB 820 TTTGTGTGATGATTTGGCATGCGCATCTGTGCCAGTCTCTTCTGTGCAAAATAGA 879
QY 210 ProTyrGlyValTyrLysAaspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229
DB 880 CCATATGGTGTTTACAGGAGTCCCGCAGTGTCTTGTGTATACATATCTTAGCACATCAG 939
QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAla 249
DB 940 GGTGTGGAGCTTCCAGTACATATCTGACCTGGGATTCACCTGAATGTGTATGGAGCA 999
QY 250 LeuGluTyrPheProGluTyrPheAlaArgAlaArgHisAlaLeuAspLysGlyGluAlaVal 269
DB 1000 TTAGATGGGTGTTTCCAGTGGGCGAGCGGCGATGCCCTTGACAAAGGTGAGGAGTC 1059
QY 270 AsnPheLeuLysGlyAlaValValThrAlaAaspArgIleValThrValSerLysGlyTyr 289
DB 1060 AATTTTTTAAAGGCGCAGTTGTGACAGCAGATCGAATTTGTGACTGTCTCAGCAGGGGTAT 1119
QY 290 SerTyrGluValThrThrAlaGluGlyGlyGlnGlyLeuAenGluLeuLeuSerArg 309
DB 1120 TCATGGGAGTCCACAACTGCTGAAGGTGGCGAGGCTCAATGAGCTCTTAAGCTCCCG 1179
QY 310 LysSerValLeuAasnGlyIleValAenGlyIleAaspIleAasnAaspTrpAenProAlaThr 329
DB 1180 AAGAGTGTATTAATGAATTTGTAATGAATTTGACATTAATTAATTTGGAACCCATCCAA 1239
QY 330 AspLysCysIleProCysHisTyrSerValAaspAspLeuSerGlyLysAlaLysCysLys 349
DB 1240 GACAAAGTTCTCCCTTATCATTTATCTGTTGATGACCTGTCCGGAAGGCCAAGTGTAA 1299
QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAaspValProLeuIleGlyPhe 369
DB 1300 GCTGAATTTGAGAGGAGCTGGGTTTACCTATAAGCCCGCATGTGCTCTGATTTGCTTT 1359
QY 370 IleGlyArgLeuAaspTyrGlnLysGlyIleAaspLeuIleGlnLeuIleIleProAaspLeu 389
DB 1360 ATGGAAGATTGGACTATCAAAAGGATTTGATTAATTAATTTGCTTCCCATTCAGATCTC 1419
QY 390 MetArgGluAaspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAaspTyr 409

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Db 1420 ATGGGGACAATATTCAATTCGTCATCTTGGATCTGGTGACCCAGGTTTGAAGATGG 1479  
Qy 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429  
Db 1480 ATGAGATCCACAGAATCAGGATACAGGATATAATTTTCGTGGATGGGTTAGTGT 1539  
Qy 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
Db 1540 CCAGTTTCCACCGAATAACTGAGGTTCGATATATTGTTGATGCCATCCAGATTCGAA 1599  
Qy 450 ProCysGlyLeuAsnGlnLeuTyzAlaMetGlnTyrGlyThrValProValValHisAla 469  
Db 1600 CCTTGTGGCTCAATCAGCTATATGCTATGCAATATGATGATGCTGCTGTTCATGGA 1659  
Qy 470 ThrGlyLeuArgAspThrValGluAsnPheAsnPropheGlyGluAsnGlyGluGln 489  
Db 1660 ACTGGAGGCTCAGAGATACAGTGGAGAAATTTTAACCCGTTTCTGCTGAGAAAGGAGAGCAG 1719  
Qy 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
Db 1720 GGTACAGGTGGGCATCTCGCCTACCTAACCATTTGAAAAATGCT-GTGGGCATTGCGGAT 1778  
Qy 510 CysAsnIleTyzIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
Db 1779 GGCATTTTCGACATACAGGGAACACAAAGTCTCTTGGGAGGCTCTAATGAAGGAGGCAT 1838  
Qy 530 ValLysArgLeuHisValGlyProCysArg 539  
Db 1839 GTCAAGCGACTTTACATGGGACCATGGCCG 1868

RESULT 17

ADT20132

ID ADT20132 standard; cDNA; 2747 BP.

XX ADT20132;

XX 13-JAN-2005 (first entry)

XX Plant cDNA, Seq ID 5458.

XX Plant; ss; gene; transgenic; cold tolerance; growth rate;  
KW drought tolerance; disease resistance; galactomannan production;  
KW plant growth regulator; heat tolerance; herbicide tolerance;  
KW lignin production; extreme osmotic condition tolerance;  
KW pathogens resistance; pest resistance; yield improvement; seed oil yield;  
KW seed protein yield.

XX Viridiplantae.

OS US2004216190-A1.

PN 28-OCT-2004.

XX 18-DEC-2003; 2003US-00739930.

XX 28-APR-2003; 2003US-00424599.

PR 28-APR-2003; 2003US-00425115.

XX (KOVA/) KOVALIC D K.

PA KOvalic DK;

PI WPI; 2004-757369/74.

DR New recombinant DNA constructs useful in the field of biochemistry and  
XX genetics, and in particular for producing transgenic plants with improved  
PT biological characteristics.  
PT  
XX Claim 1; SEQ ID NO 5458; 14pp; English.  
PS  
XX The invention relates a recombinant DNA construct comprising a  
CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:

CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences  
CC (SEQ ID NO: 5545-11098). The cDNAs and proteins are from corn, soybean,  
CC Arabidopsis, wheat and rape but the specification does not indicate which  
CC sequences is derived from which organism. Also included is a method of  
CC producing a plant having an improved property, comprising transforming a  
CC plant with a recombinant DNA construct comprising a promoter region  
CC functional in a plant cell operably joined to a polynucleotide encoding a  
CC polypeptide associated with the property, and growing the transform encoded a  
CC plant. The property is selected from improving plant cold tolerance, for  
CC manipulating growth rate in plant cells by modification of the cell cycle  
CC pathway, for improving plant drought tolerance, for providing increased  
CC resistance to plant disease, for galactomannan production, for production  
CC of plant growth regulators, for improving plant heat tolerance, for  
CC improving plant tolerance to herbicides, for increasing the rate of  
CC homologous recombination in plants, for lignin production, for improving  
CC plant tolerance to extreme osmotic conditions, for improving plant  
CC tolerance to pathogens or pests, for yield improvement by modification of  
CC photosynthesis, for modifying seed oil yield and/or content, for  
CC modifying seed protein yield and/or content, for yield improvement by  
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake  
CC and for yield improvement by providing improved plant growth and  
CC development under at least one stress condition. The polynucleotide may  
CC also encode a plant transcription factor. The methods and compositions of  
CC the present invention are useful in the field of biochemistry and  
CC genetics, in particular for producing transgenic plants with improved  
CC biological characteristics such as increased yield, improved nitrogen  
CC flow, increasing plant tolerance to cold or heat, improving plant  
CC tolerance to extreme osmotic and drought conditions, and improving plant  
CC tolerance to plant pests or pathogens. They can also be used in physical  
CC arrays of molecules, plant breeding markers, computer-based storage and  
CC analysis systems. The present sequence is one of the 5544 plant cDNA  
CC sequences of the invention. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX SQ Sequence 2747 BP; 661 A; 688 C; 759 G; 639 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.32e-251 Length: 2747  
Score: 2470.50 Matches: 465  
Percent Similarity: 91.8% Conservative: 29  
Best Local Similarity: 86.4% Mismatches: 41  
Query Match: 85.4% Indels: 4  
DB: 13 Gaps: 2

US-10-628-525A-21 (1-539) x ADT20132 (1-2747)

Qy 2 ValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySer 21  
Db 538 GTGGGGGAACCTCGCG---CCCGACCTCTCTGCTC-----GAAGGGATTGCTGAGGATTCC 598  
Qy 22 IleAspAsnThrValValAlaSerGluGlnAspSerGluIleValValGlyLysGlu 41  
Db 589 ATCGACAGCATAAATTGTGGCTGCAAGTGAGCAGGAGTTCTGAGATCATGATGCGAATGAG 648  
Qy 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
Db 649 CAACCTCAGCTAAAGTTACACGTAGCATCGTGTTGTGACTGGTGGTGAACCTCTCTTAT 708  
Qy 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg 81  
Db 709 GCAAAGTCAGGGGGCTGGGAGATGTTTGTGTTCTGTTACCAATTGCTCTTGTCTCGT 768  
Qy 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
Db 769 GGTCCACCGTGTGATGGTTGTAATGCCAGATACCTTGAATGGTCTCTGTATAAAACTAT 828  
Qy 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGluHisGlu 121  
Db 829 GCAAAAGGCATTATACACTGGGAAGACACATTGAATTCATGCTTTTGGGGGATCACAATGA 888  
Qy 122 ValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer 141



Query Match:	85.3%	Indels:	4
DB:	2	Gaps:	2
US-10-628-525A-21 (1-539) x AAX34651 (1-2662)			
QY	2	ValAlaGluLeuSerArgGluLeuGlyLeuGluProGluGlyLeuAlaGluGlySer	21
DB	539	GTGGGGAACTCGCG---CCCGACCTCTCTGCTC-----GAAGGATTCGTGAGGATTC	589
QY	22	IleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGlu	41
DB	590	ATCGACAGCATTAATGTGGCTGCAAGTCAGGAGGATTCGAGATCATGGATCGCAATGAG	649
QY	42	GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr	61
DB	650	CAACCTCAAGCTAAGTTACAGTACATCGTGTGTGCTGCTGCTGCTGCTGCTGCTGCT	709
QY	62	AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg	81
DB	710	GCAAAAGTCAGGGGGCTGGGAGATGTTGTGGTTCGTTACCAATGCTCTTGTGCTGCT	769
QY	82	GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr	101
DB	770	GGTCACCGTGTGATGGTTGTAATGCCAGATACCTTGAATGGGTCTCTCATAAACTAT	829
QY	102	AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu	121
DB	830	GCAAAAGCATTAACACTGGGAAGCACATTAGATTCATGCTTTGGGGGATCACATGAA	889
QY	122	ValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSer	141
DB	890	GTGACCTTTTTCATGAGTATAGAGCAACGTCGATGGGTGTTGTGCTCATCGTCA	949
QY	142	TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe	161
DB	950	TATCATAGACCAAGGAATTTATATGAGATAAATTTTGGTCTTTGGTGTATATCATGTT	1009
QY	162	ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly	181
DB	1010	AGATACACACTCTTTGCTATGCTGATCGATGGAGGCCCACTAATCTTGAAATGGGAGA	1069
QY	182	TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValPro	201
DB	1070	TATATTATAGCAGAAATTCATGCTGTTGTGTGAACGATGGCATGCCAGCCTTGTGCCA	1129
QY	202	ValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu	221
DB	1130	GTCCCTTCTTGTGCAAAATATAGACCATACGGTGTGTTACAGAGATTCCTCCGACGCC	1189
QY	222	ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly	241
DB	1190	GTTATACATAATTTAGCACATCAGGCTCTGGAGCTCGAAGTACATCTCTGATCTGGGA	1249
QY	242	LeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHis	261
DB	1250	TTGGCAACCTGAAATGGTATGAGCTTTAGAAATGGGTATTTCCAGAAATGGGAGGAGCAT	1309
QY	262	AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg	281
DB	1310	GCCCTTGAACAGGGTGAGGAGTAACTTTTGAAGAGGAGCAGTCTGTGACGACATCGA	1369
QY	282	IleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlnGly	301
DB	1370	ATTGTGACCGTCAGTCAGGCTTATTCATGGAGGTACAACTGCTGAAGGTGGACAGGGC	1429
QY	302	LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp	321
DB	1430	CTCAATGAGCTCTTAAGCTCCCGAAAGAGTATTTGAATGGAATTCGAAATGGAATGAC	1489
QY	322	IleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp	341
DB	1490	ATTAATGATTTGAACCCCAACCAAGAGTGTCTCCCTCATCATTAATTTCTGTGATGAC	1549
QY	342	LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg	361
DB	1550	CTCTCTGGAAAGGCCCAATGTAAGCTGAATTCGAGAAGAGCTGGTTACTCTGTAAGG	1609
QY	362	ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu	381
DB	1610	GAGGATGTTCTCTGATTTGTTGAGAGCTGGATTACAGAAAGGCATTTGATCTC	1669
QY	382	IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer	401
DB	1670	ATTAAATGGCCATTTCCAGAGCTCATGAGGAGGAGCTGCAGTTTGTGCTGTTGATCT	1729
QY	402	GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe	421
DB	1730	GGGGATCCCAATTTTGAAGGCTGGATGAGATCTACCGAGTCCGATTACAGGATAAATTC	1789
QY	422	ArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle	441
DB	1790	CGTGGATGGTGGATTTAGTGTTCAGTTTCCAGATAAATTAAGTCCAGGTTCCGATATA	1849
QY	442	LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr	461
DB	1850	TTGTTAATGCCATCCAGGTTTGAACCTTGTGTCTTAAATCAGCTATATGCTATGCAATAT	1909
QY	462	GlyThrValProValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn	481
DB	1910	GGTACAGTTCCTGTAGTTTCATGGAATCTGGGGCCCTCCGAGACACAGTCGAGACCTTCAC	1969
QY	482	ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu	501
DB	1970	CCTTTTGTGTCAAAAGGAGGAGGAGGTACAGGGTGGCGCTTCTCACCGCTAACCCGTGGAC	2029
QY	502	AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu	521
DB	2030	AGATGTTTGTGGGCATTCGGAACCCGATGCGATTCGACATTCAGGAGGACCAAGCCGCTCG	2088
QY	522	GlyArgAlaAsnGluAlaArgHisValLysValLysValGlyProCysArg	539
DB	2089	GGAGGGCTCATGAGCGGAGGATGACGAAAGCACCATACGTGGGACCATGCGCGC	2142
RESULT 19			
AAV01527	standard; cDNA to mRNA; 2239 BP.		
ID	AAV01527		
XX	AAV01527;		
XX	27-AUG-2003 (revised)		
XX	21-MAY-1998 (first entry)		
XX	Wheat soluble starch synthase partial cDNA sequence.		
XX	Starch synthase; wheat; transgenic plant; ss.		
XX	Triticum aestivum.		
XX	Key	Location/Qualifiers	
XX	CDS	3..2018	
XX		/*tag= a	
XX	WO9745545-A1.		
XX	04-DEC-1997.		
XX	28-MAY-1997; 97WO-EP002793.		
XX	29-MAY-1996; 96DE-01021588.		
XX	11-SEP-1996; 96DE-01036917.		
XX	(AGRE ) HOECHST-SCHERING AGREVO GMBH.		
XX	Block M, Loerz H, Luetticke S, Walter L, Froberg C, Kossmann J;		
XX	WPI; 1998-032652/03.		

DR P-PSDB; AAW23937.

XX Nucleic acid encoding starch synthase enzymes from wheat - for transgenic  
 PT plants that produce modified forms of starch, useful e.g. in foods, or  
 PT for production of packaging materials and disposable goods.

XX Claim 1; Page 47-51; 71pp; English.

XX This near full-length cDNA clone, designated TaSSS, codes for a soluble  
 CC starch synthase (see AAW23837) of summer wheat (cv. Florida). It was  
 CC isolated from a phage cDNA library of 21-day-old wheat caryopses by  
 CC screening with a PCR fragment derived from rice soluble starch synthase  
 CC (see also AAW01529-30). A second clone (see AAW01528), coding for wheat  
 CC granule-bound starch synthase (see AAW23938) is also claimed. These  
 CC isolated nucleic acids can be inserted into vectors for production of  
 CC transgenic plants, particularly starch-producing plants, specifically  
 CC wheat. Use of the isolated nucleic acids, or of antisense sequences,  
 CC allows starch metabolism to be regulated in transgenic plants.  
 CC Overexpression may result in improved crop yield, while modification of  
 CC starch in planta may eliminate the need for subsequent chemical/physical  
 CC modification. Plants with altered levels of the various isoforms of  
 CC starch synthase will produce starch of different chain length,  
 CC amylose/amylopectin ratio, degree of branching, phosphate content,  
 CC gelatinisation behaviour, granule size and shape, viscosity etc. The  
 CC starch produced by such plants is useful particularly in foods or to  
 CC produce packaging materials or disposable goods, as well as in any other  
 CC known use of starch. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 2239 BP; 611 A; 448 C; 590 G; 590 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 6.55e-251 Length: 2239  
 Score: 2466.50 Matches: 464  
 Percent Similarity: 91.8% Conservatives: 29  
 Best Local Similarity: 86.4% Mismatches: 41  
 Query Match: 85.3% Indels: 4  
 DB: 2 Gaps: 2

US-10-628-525A-21 (1-539) x AAW01527 (1-2239)

QY 2 ValAlaGluLeuSerArgGluAspLeuGluProGluGlyLeuAlaGluGlySer 21  
 DB 30 GTGGGGGAACTCGCG---CCGACCTCTCTC-----GAAGGATTGCTGAGGATTC 80  
 QY 22 IleAspAsnThrValValValAlaSerGluGlnAspSerGluLeuValGlyLysGlu 41  
 DB 81 ATCGACAGCATAATTGGCTGCAAGTGACGAGGATTCTCGAGATCATGGATGCAATGAG 140  
 QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
 DB 141 CAACCTCAAGCTAAGTTACACATGACATGCTGTTTGTGACTGGTGAAGCTGCTCTTAT 200  
 QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAArg 81  
 DB 201 GCNAAGTCAGGGGGTGGAGAGATTGTGGTTCGTTACCAANTGCTTGTGCTGCTGT 260  
 QY 82 GlyHisArgValMetValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
 DB 261 GGTCCAGAGTGTGTTGTAATGCCAAGATCTTAATGGGTCTCTGATNAAACTAT 320  
 QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
 DB 321 GCAAAAGCCATTATACATCGAAGACACATTAAAGATTCCATGCTTTGGGGATCACATGAA 380  
 QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSer 141  
 DB 381 GTGACCTTTTTCATGAGTATAGACACACGTCGATTTGGGTGTTGTGCGATCATCCGTCA 440  
 QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyValaPheGlyAspAsnGlnPhe 161  
 DB 441 TATCAGACACAGGAAGTTATATGAGATATAATTTTGGTGTCTTTTGTGATATACAGTTC 500  
 QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLeuGluGlyGly 181

DB 501 AGATACACACTCTCTTCTATGCTATGCTATGCGAGGCCCACTTAATCTCTGAATTTGGGAGA 560  
 QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValPro 201  
 DB 561 TATATTTATGACAGAAATTCATGTTTGTGTGAACGATTGGCATGTCAGCCTTTGTGCCA 620  
 QY 202 ValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221  
 DB 621 GTCTCTTCTGCTGCAAAATATAGACCATACGCGTGTTCACAGAGATTCCTCCGAGCACCTT 680  
 QY 222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
 DB 681 GTTATATACATAATTTAGCACATCAGGGGTGCGAGCCTGCAAGTACATATCTCTGATCTCGGA 740  
 QY 242 LeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrPheAlaAArgArgHis 261  
 DB 741 TTGCTCTCTGTAATGGTATGAGGCTTTAGAAATGGGTATTTCCAGAAATGGGCAAGGAGCAT 800  
 QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281  
 DB 801 GCCCTTGACAAGGGTGGCGAGTTAACTTTTGAAGGAGCAGTTGTGACAGCAGATCGG 860  
 QY 282 IleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlyGlnGly 301  
 DB 861 ATTGTGACCGTCACTCAGGGTTATTTCATGGGAGGTCACTGCTGAAGGTGGACAGGCG 920  
 QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321  
 DB 921 CTCATAGAGCTCTTAAAGTCCCCGAAAAGGTATTTGAATGGAATTTGAAATGGAATTGAC 980  
 QY 322 IleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341  
 DB 981 ATTAATGATTGGAACCCCAACACAGACAGTGTCTCCCTCATCATTTCTGTGCGATGAC 1040  
 QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361  
 DB 1041 CTCTCTGGAAGGCCAAATGTAAAGCTGAATTCGAGAAGGAGTTGGGTTTACCTGTGAAGG 1100  
 QY 362 ProAspValProLeuIleGlyPheIleGlyArgGlyLeuAspTyrGlnLysGlyIleAspLeu 381  
 DB 1101 GAGGATGTTCTCTGATTGGCTTTATTTGGAAGACTGGATTACCAAGAAAGGCATTTGATCTC 1160  
 QY 382 IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
 DB 1161 ATTAATAATGCGCAATTCACAGAGCTCATGAGGAGGAGCTGCAATTTGTCTGCTGATCT 1220  
 QY 402 GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe 421  
 DB 1221 GGGGATCCCAATTTTGAAGGCTGGATGAGATCTACCGAGTTCGAGTTACCAAGGATAAATTC 1280  
 QY 422 ArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
 DB 1281 CGTGGATGGGTGGATTAGTTAGTTTCCAGATTTCCACAGAAATACTGCGAGTTCCGATATA 1340  
 QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461  
 DB 1341 TTGTTAATGCCATCGAGATTGAACTTGGGCTTTAATCAGCTATATGCTATGCAATAT 1400  
 QY 462 GlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPheAsn 481  
 DB 1401 GGTACAGTTCCTGTAGTTTCATGGAACTGGGGGCTCCGAGACACAGTCGAGACCTTCAAC 1460  
 QY 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
 DB 1461 CTTTTTGGTGGCAAGAGGAGGGGTACAGGTGGGGCTTCTCAACCGTAAACCGTGGAC 1520  
 QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
 DB 1521 AAGATGTT-GTGGGCATTGCGAACCGGATGTGCGATTCAGGAGGACACAGCGGCTCTG 1579  
 QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538

Db	1580	GGAGGGGCTCATGACGAGGCGATGACGGAAGACCATATCGTGGGACCATGC	1630
RESULT 20			
AAZ24487			
ID	AAZ24487	standard; DNA; 2805 BP.	
XX			
AC	AAZ24487;		
XX			
DT	18-FEB-2000	(first entry)	
XX			
DE	Wheat soluble starch synthase DNA.		
XX			
KW	Soluble; starch synthase; wheat; transgenic plant; starch production; food; baking; pastry; packaging material; glucose; glucan; paper; pulp; adhesive; textile; building material; soil stabilizer; wetting agent; fertilizer; plant-protection; cosmetic; flocculant; ss.		
KW			
KW			
XX			
OS	Triticum aestivum.		
XX			
FF	Key	Location/Qualifiers	
FT	CDS	314..2584	
FT		/*tag= a	
FT		/product= "soluble starch synthase"	
XX			
PN	DE19820607-Al.		
XX			
PD	11-NOV-1999.		
XX			
XX			
PF	08-MAY-1998;	98DE-01020607.	
XX			
PR	08-MAY-1998;	98DE-01020607.	
XX			
PA	(AGRE ) HOECHST-SCHERING AGREVO GMBH.		
PI	Loerz H, Luetticke S, Block M;		
XX			
DR	WPI; 2000-024508/03.		
XX			
DR	P-PSDB; AAY50818.		
PT	New enzyme with starch synthase activity, useful for producing starch for foods and packaging materials.		
XX			
PS	Claim 1b; Page 15-19; 24pp; German.		
XX			
CC	This invention describes a novel protein (I) with the activity of wheat starch synthase. Transgenic plants, specifically wheat, that contain (I) are used for production of starch, used particularly in foods, particularly baked and pastry goods and for making packaging materials or disposable items. Starch may also be used as starting materials for glucose or glucan components (e.g. for fermentation or further chemical conversation); in paper and pulp production, as adhesives, in textiles, in preparation of gypsum-based building materials, as soil stabilizer, as wetting agent etc. in fertilizer and plant-protection compositions, as binder (in pharmaceuticals, cosmetics, coal briquetting and casting sand), as flocculant in soil or coal slurries, as rubber and leather additives, and for production of synthetic polymers, e.g. polyurethane films. Transgenic plants with increased/decreased production of (I) produce starches with altered physical and/or chemical properties such as amylose/amylopectin ratios, degree of branching, mean chain length, phosphate content, gelatinization properties, gel- or film-forming properties, or starch grain size or structure. This sequence encodes the soluble starch synthase isolated from wheat (Triticum aestivum L. cv. Florida)		
XX			
SQ	Sequence 2805 BP; 683 A; 703 C; 763 G; 656 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	9,1e-251	Length:	2805
Score:	2466.50	Matches:	464
Percent Similarity:	91.8%	Conservative:	29
Best Local Similarity:	86.4%	Mismatches:	41
Query Match:	85.3%	Indels:	4
DB:	3	Gaps:	2



Db 1607 CTCTCTGGAAGGCCAAATGTAAAGCTGAATTGCAGAGGAGTTGGGTTTACCTGTAAAGG 1666

Qy 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381

Db 1667 GAGGATGTTCTCTGATGGCTTTATTTGGAAGACTGGATTACCAAGAAAGGCAATTGATCTC 1726

Qy 382 IleGlnLeuIleLeuProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401

Db 1727 ATTAAATGGCCATTCCAGAGCTCATGAGGAGACGTGCAATTTGTTCATGCTTGGATCT 1786

Qy 402 GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe 421

Db 1787 GGGGATCCAAATTTTGAAGCTGGATGAGATCTACCGAGTCGAGTTTACAAGGATAAATTC 1846

Qy 422 ArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441

Db 1847 CGTGGATGGGTGGATTTAGTGTTCAGTTTCCAGTTTCCACAGATAACTGCAGGTTCGATATA 1906

Qy 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461

Db 1907 TTGTTAATGCCATCGAGATTGAACCTTGGCGTCTTAAATCAGCTATATGCTATGCAATAT 1966

Qy 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn 481

Db 1967 GGTACAGTTCCTGTAGTTTCATGGNACTGGGGGCTCCGAGACACATCGAGACCTTCAAC 2026

Qy 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501

Db 2027 CCTTTTGGTCAAAAGGAGAGGAGGTACAGGGTGGGCGTTCTCACCGCTAACCGTGGAC 2086

Qy 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521

Db 2087 AAGATGTT-GTGGGCAATTGCGAACCGCGATGTGACATTCAGGGAGCACAAAGCCGCTCTG 2145

Qy 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538

Db 2146 GGAGGGCTCATAGCGAGGCATGACGAAGACCATACGTGGGACCATGC 2196

RESULT 21

AAZ50642

ID AAZ50642 standard; cDNA; 1415 BP.

AC AAZ50642;

XX 23-MAY-2000 (first entry)

DT XX

DE XX

XX Corn soluble starch synthase gene fragment inserted in pSS64-C5.

KW Soluble starch synthase; starch fine structure; corn; transgenic plant;

KW amylose; amylopectin; amylose polymerisation;

KW non-granule bound starch synthase; non-GBSSI; altered starch; food;

KW paper; plastic; adhesive; ss.

XX Zea mays.

OS XX

XX WO200006755-A2.

PN XX

XX 10-FEB-2000.

PD XX

XX 26-JUL-1999; 99WO-US016296.

PF XX

XX 28-JUL-1998; 98US-0094436P.

PR XX

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

PA XX

XX Broglie KB, Lightner JE;

PI XX

XX WPI; 2000-195311/17.

DR XX

XX Producing transgenic cereal crops with altered starch structure useful

PT for preparing foodstuff, paper, plastic or adhesives, comprises

PT transforming crops with chimeric sense or antisense gene construct

PT encoding starch synthase.

XX

PS Claim 5; Page 52-53; 56pp; English.

CC The present sequence is the corn soluble starch synthase (SSI) DNA

CC sequence comprising the SSI coding region of amino acids 1-494 inserted

CC into plasmid pSS64-C5. The chimeric gene containing the zein promoter

CC followed by the SSI gene fragment is used as a sense construct for

CC preparation of transgenic corn expressing altered starch structure. The

CC starch fine structure derived from a grain of the cereal crop can be

CC altered in the transformed cereal crop by changes in amylose to

CC amylopectin ratio, amylopectin fine structure, increased abundance of

CC very short amylopectin chains and in the degree of polymerisation of

CC amylose. These modifications can be created by controlling the expression

CC of non-GBSSI (non-granule bound starch synthase) in transgenic plants.

CC Altered starches are useful in foods, paper, plastics or adhesives

XX

SQ Sequence 1415 BP; 317 A; 335 C; 397 G; 366 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2,87e-206 Length: 1415

Score: 2043.00 Matches: 388

Percent Similarity: 89.8% Conservative: 0

Best Local Similarity: 89.8% Mismatches: 0

Query Match: 70.6% Indels: 44

DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x AAZ50642 (1-1415)

Qy 1 CysValAlaGluLeuSerArgGlu-----8

Db 119 TGGCTCGCGAGCTGAGCAGGGAGGGCGCGCGCGCGCTGCCACCCGCGTCTG 178

Qy 8 -----8

Db 179 GCGCCCCCGCTCGTGGCCCGCTTCCTCGCGCGCGCGCGCGCGCGGTGAGCCGCCA 238

Qy 9 -----AspLeuGlyLeuGluProGluGly 16

Db 239 TCGACGCCCGCGCCCGTGGCCGACGCGCTGGGGGACCTCGGTCTCGAACCTGAAGGG 298

Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36

Db 299 ATTGCTGAAGGTTCCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 358

Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56

Db 359 GTGGTTGGAAAGAGGACGACCTCGAGCTAAGTAACAACAAAGCATTTGTCTTTGAACCGGC 418

Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76

Db 419 GAAGCTTCTCTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGTTTCATTGCCAGTT 478

Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValMetProArgTyrLeuAsnGlyThr 96

Db 479 GCTCTTGTCTGCTGCTGGTCAACGTTGATGGTTGTAATCCCAAGATATTAAATGTGTACC 538

Qy 97 SerAspLysAsnTyrAlaAlaAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116

Db 539 TCCGATAGAATTATGCAAAATGCAATTTTACACAGAAACACATTCGGATTCCATGCTTT 598

Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136

Db 599 GCGGTGGAACATGAAGTTACCTTCTCCATGATAGATATAGAGATTTCAGTTCAGTGGGTGTT 658

Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156

Db 659 GTTGATCATCCCTCATATCACAGACCTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT 718

Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176

Db 719 GGTGATATCATGTTTCAGATACACATCTCTTGTCTATGCTGATGAGGCTCTCTTGAATC 778

Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrPhe 196



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PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 23-JUL-1999; 99US-0145226P.
PR 26-JUL-1999; 99US-0145133P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 08-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.

PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159337P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 22-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 5,36e-172 Length: 1984
Score: 1722.00 Matches: 327
Percent Similarity: 76.4% Conservative: 59
Best Local Similarity: 64.8% Mismatches: 86
Query Match: 59.5% Indels: 34
DB: 3 Gaps: 5

US-10-628-525A-21 (1-539) x AAC46797 (1-1984)

QY 38 ValGlyLeuGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGlu 57
Db 506 GTTGGGATTCGAGTGGAAAGCTGAAGTTGTCAATAACCTGTTTCGTACATCCGAG 565
QY 58 AlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAla 77
Db 566 GCGGCTCCTTACTCGAAAACAGGAGGATTAGGAGATGTTTGTGGTCTCTTTGCCGATAGCT 625
QY 78 LeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr--- 96
Db 626 TTAGCTGGTCGTGGGCATCGTGTATGGTCATTTCTCCTCGGTACTTAATGAAGACTGCT 685
QY 97 SerAspLysAsnTyrAlaAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
Db 686 GCAGACAAGACTATGCCCGGGCTAAGGATTTGGGGATACGTACAGTAAGTAATTCCTTT 745
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136
Db 746 GGTGGTTCTCAAGAAGCTTTCCTTCTATCATGATATAGAGATGCTGCTGATTCGGTTTTT 805
QY 137 ValAsnHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156
Db 806 GTTGATCACAATCCTTACCATGACCTGGTAATCCTACGGAGATAGTAAGAGGACCTTT 865
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 866 GGTGACATCAGGTA-----CTACTG 886
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196
Db 887 TTGACATTG-----895
QY 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 896 TCCAAAGAAAGACTTTTGACTTTTGGCCCAAGATATCGCCCATATGAGGATTATAGGAT 955
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QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProHisSerThr 236
DB 956 GCAAGAGCATTCCTCATATCCATACCTCGCTCATCAGGGGTGAGCGACGATCA 1015
QY 237 TyrProAspLeuGlyLeuProGluTyrPyrGlyValAlaLeuGluTrpValPheProGlu 256
DB 1016 TACACCAACTGGGATGGCTTCGGAATGGTATGAGCAGCTGGGTGGTATTTCCACG 1075
QY 257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
DB 1076 TGGGCAAGAACTCATCCCTTGACACCGGTGAAGCGTTAATGTTCTCAAGGGTGTATT 1135
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
DB 1136 GTGACCTCTGACCGTATCATTTACTGTGACCGGGCTATGCTGGGAATCACTACTGTT 1195
QY 297 GluGlyGlyGlnGlyLeuAsnGlnLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316
DB 1196 GAAGGTGGTTATGGTCTTCAAGATTTGCTTTCTAGTCGGAAGTGTATATAATGGATC 1255
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
DB 1256 ACAATATGGAATTAATGTTGATGAATGGAATCCATCCACGGATGAACACATTTCTTCCAT 1315
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyValAlaLeuGlnLysGluLeu 356
DB 1316 TACTCTGCTGATGATGCTCCGGAAGATCAATGCAAGATGCATCAAAAGGAAATG 1375
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
DB 1376 GGTCTCCCATAGGCTCAATGCTCTATGATGGTTTATAGGAAGACTTGATTACCA 1435
QY 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396
DB 1436 AAGGGCAATGATCTGATCCAAACCGCTGCTGCTGATCTCATGCTGATGACATCAATTC 1495
QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
DB 1496 GTCATGCTTGGTTCGGGTGACCCAAATATGAAGCTGGATGAGAAGTATGGAGGAACA 1555
QY 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
DB 1556 TACAGAGCAAAATTCGGTGGTGGTGGTTCATGTCATCCCATCTCTCATCGAATCACA 1615
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
DB 1616 GCCGGCTGTGACATTTCTCTCATGCGTGCAGATTCGAGCCCTGTGTTTAAATCAGCTA 1675
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
DB 1676 TACGCATGAGATACGGAACCATTCAGTTGTTTCATGGCAGCTGGAGGACTCAGAGTACG 1735
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGlu---GlnGlyThrGlyTrpAlaPhe 495
DB 1736 GTTGAGAAATTCACCCCTTATGCAGAAAGTGCAGCTGCTGCTGCTGCTGCTGCTGCT 1795
QY 496 AlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGln 515
DB 1796 ACTCCCTTGTGAAAGATAGCATGGTCTCGGCTTTGAGGCTTGGCTGCAGCAAC-GTACAG 1854
QY 516 GlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisVal 535
DB 1855 AGAGTATAACAGTCAATGGAGGAGTGTATGAGAGAGGAATGACCCGAAACTACTCTTG 1914
QY 536 GlyPro---CysArg 539
DB 1915 GGAAGAACGCTGCCGT 1929
RESULT 23
AAT32325
ID AAT32325 standard; cDNA; 1758 BP.
XX
AC AAT32325;
```

```
XX 31-OCT-1996 (first entry)
DT Soluble starch synthase (Isoform B) coding sequence.
XX Soluble starch synthase; transformation; transgenic plant; starch;
KW amylose; amylopectin; ss.
XX Solanum tuberosum.
XX Key Location/Qualifiers
CDS 1..1377 /tag= a
FT /product= "Soluble starch synthase."
FT
XX DE4441408-Al.
XX 15-MAY-1996.
XX 10-NOV-1994; 94DE-04441408.
XX 10-NOV-1994; 94DE-04441408.
XX (GENB-) INST GENBIOLOGISCHE FORSCHUNG.
XX Kossmann J, Springer F, Abel GJ;
XX WPI; 1996-240218/25.
XX P-PSDB; AAR99540.
XX DNA encoding soluble starch synthase of potato - used to produce
XX transgenic plants with increased prodn. of starch or able to produce
XX modified starches.
XX Claim 2; Page 20-22; 32pp; German.
XX DNA sequences from the potato encoding soluble starch synthase having the
XX 459 C-terminal amino acid sequence encoded by this sequence or the 677 C-
XX terminal amino acid sequence given in AAR99539 can be used to identify
XX and isolate homologous sequences encoding soluble starch synthase and
XX enzymes with similar activities from plants or other organisms; to
XX transform prokaryotic or eukaryotic cells; to produce transgenic plants
XX which synthesise starch of altered structure or in increased yield
SQ Sequence 1758 BP; 529 A; 328 C; 413 G; 488 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,88e-164 Length: 1758
Score: 1645.50 Matches: 304
Percent Similarity: 81.7% Conservative: 63
Best Local Similarity: 67.7% Mismatches: 70
Query Match: 56.9% Indels: 13
DB: 2 Gaps: 5

US-10-628-525A-21 (1-539) x AAT32325 (1-1758)
QY 95 GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114
DB 1 GGCACGAGC-----AATGCTGTGTACCTTGATGTGGCGGCCACTGTCCAT 45
QY 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrp 134
DB 46 TCGTTTGGTGATGCACAGGAAGTAGCCTTCTACCATGATACAGGCGAGGTGTTGATTGG 105
QY 135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154
DB 106 GTATTGTGGACCACTCTTCTTACCGCAGACTCTGGAACGCCCATATGGTGATATTATGCT 165
QY 155 AlaPheGlyAspAsnGlnPheArgTyrThrIleLeuLeuCysTyrAlaAlaCysGluAlaPro 174
DB 166 GCATTTGGTGATAATCAGTTTCGTTTCATCTTTCCTCAGCAGCATGTGAAGCGCCA 225
QY 175 LeuIleLeuGluGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194
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Score: 1496.00 Matches: 284  
Percent Similarity: 99.6% Conservative: 0  
Best Local Similarity: 99.6% Mismatches: 1  
Query Match: 51.7% Indels: 1  
DB: 13 Gaps: 0

US-10-628-525A-21 (1-539) x ADX59939 (1-1294)

QY 255 ProGluThrAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
Db 2 CCTGAATGGCGAGGAGCATGCCCTTGACAGGGGTGAGCGAGTTAAATTTTGAAGGT 61  
QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294  
Db 62 GCAGTTGTGACACGACATCGATCGTGACTGTGCTGAGTAAAGGGTTATTCATGGGAGGTGACA 121  
QY 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314  
Db 122 ACTGCTGAAGGTGGACAGGCCCTCATGAGCTCTTAAGCTCCAGAAAGAGTGTATTTAAAC 181  
QY 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIlePro 334  
Db 182 GGAATTTGTAATGGAATTGACATTAATGATGGAACTCCGCCACACAAATGTATCCCC 241  
QY 335 CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354  
Db 242 TGTATATATCTGTTGATGACCTCTCTGGAAGGCCAAATGTAAGGTGCATTCGCAAG 301  
QY 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374  
Db 302 GAGCTGGTTCCTATATAAGGCTGATGTTCTCTGATTTGGCTTTATTCGAAGATTGGAT 361  
QY 375 TyrGlnLysGlyIleAspLeuLeuGlnLeuIleProAspLeuMetArgGluAspVal 394  
Db 362 TATCAAAAGGCGATGATCTCATCTCAACTTATCATACCAGATCTCATGCGGGAAGATGT 421  
QY 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGlu 414  
Db 422 CAATTTGTCATGCTTGATCTGTGTGCCAGAGCTTGAGATTTGGATGAGATCTACAGAG 481  
QY 415 SerIlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArg 434  
Db 482 TCGATCTTCAAGGATAAAATTCGTGATGGTGGATTTAGTGTTCAGTTCCTCCACCGA 541  
QY 435 IleThrAlaGlyCysAspIleLeuMetProSerArgPheGluProCysGlyLeuAsn 454  
Db 542 ATAACCTGCCGCTCGCATATATTTGTTAATGCCATCCAGATTCGAACCTTTGTGCTCAAT 601  
QY 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474  
Db 602 CAGCTATATGCTATGCGATGTCACAGTTCCTGTTGTCATGCACTGGGCGCTTAGA 661  
QY 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAla 494  
Db 662 GATACCGTGGAGAACTTCAACCTTCGTGAGATGGAGAGCAGGGTACAGGGTGGCA 721  
QY 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514  
Db 722 TTCGCACCCCTTAACACAGAAAACATGTT-TGGGACATTCGCAACTGCAATATCTACATA 780  
QY 515 GlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHis 534  
Db 781 CAGGGNACACAGTCTCTCTGGAGGGGCTATGAGCGGCGATGTCAAAAGACTTTCAC 840  
QY 535 ValGlyProCysArg 539  
Db 841 GTGGGACCATGCCG 855

RESULT 25

ADX08949

ID ADX08949 standard; cDNA; 1300 BP.

XX

AC ADX08949;

XX 21-APR-2005 (first entry)  
DT Plant full length insert polynucleotide seqid 3524.  
DE  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
DR  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 3524; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 1300 BP; 354 A; 268 C; 327 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,32e-144 Length: 1300  
Score: 1459.00 Matches: 278  
Percent Similarity: 99.6% Conservative: 0  
Best Local Similarity: 99.6% Mismatches: 1  
Query Match: 50.4% Indels: 1  
DB: 13 Gaps: 0

US-10-628-525A-21 (1-539) x ADX08949 (1-1300)

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Qy 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280
Db 3 CATGCCCTTGACAAAGGGTGAGCGAGTTAAATTTTGAAGGTCAGTTGTGCACAGCAGAT 62
Qy 281 ArgIleValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGln 300
Db 63 CGAATCGTGACTGTCAGTAAGGGTTATTTCATGGAGGTCACAACTGCTGAAGGTGGACAG 122
Qy 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320
Db 123 GGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAATGTAAATGGAAAT 182
Qy 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340
Db 183 GACATTAAATGATTGGAAACCTCGCCACACAGACAAATGTATCCCTGTCTATTATCTGTGAT 242
Qy 341 AspLeuSerGlyLysAlaLysCysLysGlyValAlaLeuGlnLysGluLeuGlyLeuProIle 360
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Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380
Db 303 AGGCTGATGTTCTCTGATTGGCTTTATTGGAGATTGGATTATCAGAAAGGCATTGAT 362
Qy 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400
Db 363 CTCATTCAACTTATCATACAGATCTCATCGGGAAGATGTTCAATTTGTTCATGCTTGA 422
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Qy 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440
Db 483 TTTTGGTGGATGGGTGGATTAGTTTCCAGTTTCCACCGAATACTGCGGCTGGAT 542
Qy 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460
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Qy 461 TyrGlyThrValProValHisAlaThrGlyLeuArgAspThrValGluAsnPhe 480
Db 603 TATGGCACAGTTCCTGTGTCCATGCAACTGGGGGCTTAGAGTACCGTGGAGAACTTC 662
Qy 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThr 500
Db 663 AACCTTTTCGGTGGATGGAGAGCAGGGTACAGGGTGGGCATTCGACCCCTAACACA 722
Qy 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520
Db 723 GAAACATGTT-GTGGACATTGGCAACTGCAATATCTACATACAGGGAACACAAGTCTTC 781
Qy 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db 782 CTGGGAAGGGCTAATGAGCGAGGCAATGTCAAAGAATTTCACGTGGGACCATGCCGC 838

RESULT 26
ID AAX34652
XX AAX34652 standard; DNA; 10336 BP.
AC AAX34652;
XX
DT 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX
DE Wheat starch soluble synthase I (SSS I) gene sequence.
XX
KW Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS;
KW starch branching enzyme; starch soluble synthase; debranching enzyme;
KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
KW grain softness protein I; bacterial isomylase; glycogen synthase;
KW WSB1 I-D4 gene; db.

```

```

XX Aegilops tauschii.
OS
XX
FH Key Location/Qualifiers
CDS 1..9713
FT /*tag= a
FT /product= "SSS I"
FT /note= "contains introns"
FT
FT exon 1..316
FT /*tag= b
FT /number= 1
FT 317..1471
FT /*tag= c
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 FT 8916. .8991  
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 FT 8992. .9104  
 FT /\*tag= z  
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 FT 9161. .9199  
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 FT /number= 14  
 FT 9200. .9497  
 FT /\*tag= ac  
 FT /number= 14  
 FT 9498. .9713  
 FT /\*tag= ad  
 FT /number= 15

WO9914314-A1.

25-MAR-1999.

11-SEP-1998; 98WO-AU000743.

12-SEP-1997; 97AU-00009108.

20-MAR-1998; 98AU-00002509.

(CSIR ) COMMONWEALTH SCI & IND RES ORG.

(AUSU ) UNIV AUSTRALIAN NAT.

(GOOD-) GOODMAN FIELDER LTD.

(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

Li Z, Morell M, Rahman S;

WPI; 1999-229525/19.  
 P-PSDB; AAY09004.

New isolated cereal plant enzyme genes used for, e.g. expression of  
 antiense sequences of granule bound synthase.

Claim 10; Page 87-94; 171pp; English.

The invention relates to a novel enzyme of starch biosynthetic pathway in  
 a cereal plant, where the enzyme is selected from starch branching enzyme  
 (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme  
 (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of  
 rice or maize. The methods and products can be used for targeting  
 expression specifically to the endosperm of the seeds of cereal plants  
 such as wheat or barley. They can be used for the expression of e.g.  
 antiense sequences of granule-bound synthase (GBSS), SBE II, low mol.  
 wt. glutenin, grain softness protein I, bacterial isomylase, bacterial  
 glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be  
 used for modifying the characteristics of starch produced by a plant. The  
 present sequence represents the wheat SSS I gene sequence. (Updated on 17  
 -OCT-2003 to standardise OS field)

Sequence 10336 BP; 2733 A; 2055 C; 2625 G; 2921 T; 0 U; 2 Other;

#### Alignment Scores:

Pred. No.:	4.68e-124	Length:	10336
Score:	1280.00	Matches:	346
Percent Similarity:	29.2%	Conservative:	19
Best Local Similarity:	27.7%	Mismatches:	20
Query Match:	44.2%	Indels:	864
DB:	2	Gaps:	9

US-10-628-525A-21 (1-539) x AAX34652 (1-10336)

QY	12	LeuGluProGluGlyIleAlaGluGlySerIleAspAsnThrValValValAlaSerGlu	31
DB	1463	TTGCAACCA---GGATTGCTGAGGATTCATCGACAGCATATATCTGGCTGCAAGTGAG	1519
QY	32	GlnAspSerGluIleValValGlyLyysGluGlnAlaAraGAlaLysValThrGlnSerIle	51
DB	1520	CAGGATTCAGATCATGGATCGAATGAGCAACCTCAAGCTAAAGTTACACGTAGCATC	1579
QY	52	ValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCys	71
DB	1580	GTGTTTGTGACTGGTGAAGCTGCTCTTATGCAAAAGTCAGGGGGGCTGGAGATGTTGT	1639
QY	72	GlySerLeuProValAlaLeuAlaAraGlyHisAraGValMetValValMetProAraG	91
DB	1640	GGTTGTTTACCAATTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1699
QY	92	TyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIle	111
DB	1700	TACTTGAATGGGTCTCTGATTAATAACTATGCAAGGCATTTATACACTGCAAGCACATT	1759
QY	112	ArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSer	131
DB	1760	AAGATTCCATGCTTTGGGGGATCACATGAAGTGACCTTTTTTCATGAGTATAGAGCAAC	1819
QY	132	ValAspTyr-----	134
DB	1820	GTGCAATGGTGGGTACACAATCACCTTCTTATTCTCTGTTGAAATGTAGCAACTGTTTA	1879
QY	134	-----	134
DB	1880	TCCTTGTTTACACTTCTTTTAGCCCTGCAAGACATATGTGATTTCCATACTACTTTTGT	1939
QY	134	-----	134
DB	1940	ATTTCCCTTGTACTCTTGCTCATGAAGGTCAAAATATCATATATCCATGGAAGTCATGCA	1999
QY	134	-----	134
DB	2000	TGTGCTAGTATTTTGGTGTGGTGGCTTTAACTTTTCAGGGATTAATACGTGGAAATTG	2059
QY	134	-----	134
DB	2060	ATAACTAAAGTTTATTATTATTGAAAAAATTTAGTGTGGTGAGCCACAGCCACGAGT	2119
QY	134	-----	134
DB	2120	GGCACCACTGCTTGCACATGATTTTGCATTTCTGTTTGCACCGACATTCATGTGAATA	2179
QY	134	-----	134
DB	2180	AGGTGTAAATCATAAAGTACCATTTTATTCTGCCAATTGCACCTTAAGAGTATATACAT	2239
QY	134	-----	134
DB	2240	TTATCTTGGCTCAATCATGGGAGTACTGTGCATTCAGTGCCACCATCATTTGTTCTAAGA	2299
QY	134	-----	134
DB	2300	GAAAATGTTGGTGGCAAGGAAGACACTTTTGTCCCTTAATAAAAGGAGGCACTCTGTTGT	2359
QY	134	-----	134
DB	2360	CATATAGTAGAAAGCAACAACACTTTATTTCAGAGACTAACATGCAAAAGNACCACAA	2419
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DB	2420	AAAGCATGCTAAGCGGTGCACACAAAGGTGAGGGGGGCTTTGTGACTGACAGCACCC	2479
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Qy 134 ----- 134  
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Qy 135 ----- Val PheValAspHisProSerTyrHisArgProGlu 146  
Db 2720 CATTTCAATCAACTTTTGTGTCAGGTGTTGTGCGATCCCGTCATATCATAGACCAGG 2779  
Qy 146 YAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsn----- 159  
Db 2780 AAGTTATATGGAGATAATTTTGGTGCTTTTGGTGATAATCAGGTACACTACACTATACT 2839  
Qy 159 ----- 159  
Db 2840 AAGTCCTAGTTGACTAAGTCGTAAGTTGTACTCTCTCGCTACCGGCTGCTCTATGTCG 2899  
Qy 160 --GlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluL 179  
Db 2900 TGCAGTTTCAGATACACACTCTTTGCTATGCTGCATCGAGGCCCCACTAATCCTTGAAT 2959  
Qy 179 euGlyGlyTyrIleTyrGlyLysCysMetPheValValAsnAspTyrHisAlaSerL 199  
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Qy 199 euValProVal----- 202  
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Qy 202 ----- 202  
Db 3079 TTGCAGTGCCTCCANGTCTACATTTCTTTTATGCTTTTTCATGTCGTCTTATATGTC 3138  
Qy 202 ----- 202  
Db 3139 ATATATGCTTATGGAGTCTAAAGTTACCGAGGGGATAACTCTTAAGGATTTCTCTCAAT 3198  
Qy 202 ----- 202  
Db 3199 CAATTATCTTTAGCTTTAGTTAAATTTACTGTGGCAACATATAATGTGTTTTCAGATTTA 3258  
Qy 202 ----- 202  
Db 3259 CAAGTTCAGAGATTGCATTTCACTAGTTTCGTAGCTAATCTGATGTTTTTCCCGAGAAAT 3318  
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Db 3319 GCCTAAAGCTTTGTGCTTGATGCAATTTAGATAAGAAAGATTATGTACACTCCCAAGA 3378  
Qy 202 ----- 202  
Db 3379 GGGGACCCAAAATTACAAACCACACCCCTCGAGAACTAGGCGTGCAGGAAGAGCGATG 3438  
Qy 202 ----- 202  
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Db 3499 GCTAGCAGTCTAGATTGCCAAGTGCATTCGTCGNAGATGACAGTTGGCCTGCTTC 3558  
Qy 202 ----- 202  
Db 3559 CAAATCCACCACCAACTATGACATGATCACTGGAGAGTACCTTTTCTCGGGCTGAGGGG 3618  
Qy 202 ----- 202

Db 3619 GTGGACTGGTGGTCTGCTGCTGCCAGTTTTCAGATAATCTGAAAAATGCATGTTTTGATG 3678  
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Qy 218 rGSerIleLeuValIleHisAsnLeuAlaHisGln----- 229  
Db 4159 GCAGCACCTTGTGTATACATAATTTAGCACATCAGGTTTGGGTCTATCACCTTTTCATTAT 4218  
Qy 229 ----- 229  
Db 4219 CCGTACATGGCTTTGTAAAGTCGGTTCACAGTATCGTACTACTGTATGTTATTTTCAATGT 4278  
Qy 230 ----- GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyr 247  
Db 4279 CATTAGGTTGTGGAGCTGCAAGTACATATCTCTGATCTGGGATGCCACCTGAATGTA 4338  
Qy 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGlu 267  
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Db 4399 GCAGTTAACTTTTGAAGGAGCAGTTGTGACAGCAGATCGAATTTGACCGTCAGTCAG 4458  
Qy 287 ----- 287  
Db 4459 GTGAATACTCAATACTTCTCTTTTCTTTGGGATGTTCTTCAGTTCAATTTGCCCTG 4518  
Qy 288 ----- GlyTyrSerTyrGluVal 293  
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Qy 294 ThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeu 313  
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Qy 314 Asn----- 314  
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Qy 315 ----- GlyIleValAsnGlyIle 320  
Db 4699 GATGGGTTCAGAAATAAATTCAGTTTGTCTCTTTTCGGTATGAAGGAATTTGTAATGGAAT 4758

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 QY 346 -----AlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuPr 359  
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 RESULT 27  
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 AC ADX13652;  
 DT 21-APR-2005 (first entry)  
 XX  
 DE Plant full length insert polynucleotide seqid 8227.  
 KW plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content; gene; ss.  
 OS Unidentified.  
 XX  
 XX US2004034888-A1.  
 FN  
 PD 19-FEB-2004.  
 XX  
 PF 28-APR-2003; 2003US-00425114.  
 XX  
 PR 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX  
 PA (LIU//) LIU J.  
 PA (ZHOU//) ZHOU Y.  
 PA (KOVA//) KOVALIC D K.  
 PA (SCRE//) SCREEN S E.  
 PA (TAB//) TABASKA J E.  
 PA (CAO//) CAO Y.  
 XX  
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 DR WPI; 2004-180133/17.

XX  
 PT New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX  
 PS Claim 1; SEQ ID NO 8227; 15pp; English.  
 XX  
 CC The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.seqdata.upto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This sequence represents a plant full length insert  
 CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC invention.  
 XX  
 SQ Sequence 1860 BP; 529 A; 337 C; 481 G; 513 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7,51e-115 Length: 1860  
 Score: 1183.00 Matches: 264  
 Percent Similarity: 62.2% Conservative: 67  
 Best Local Similarity: 49.6% Mismatches: 167  
 Query Match: 40.9% Indels: 36  
 DB: 13 Gaps: 11  
 US-10-628-525A-21 (1-539) x ADX13652 (1-1860)  
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 Db 31 GAAGCTTTGAGTGAATCAAGT-----ACAAAGGAGGTGTGCTAATGAAGCCGACAA 81  
 QY 35 GluIleValValGlyLysGluGln-----AlaArgAlaLysValThrGlnSerIle 51  
 Db 82 GTGGAGAGTAAAGGTGAAACCCGCCACCGTGGTGGGCCCAATGTC---ATGATATGTC 138  
 QY 52 ValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLysGlyLeuGlyAspValCys 71  
 Db 139 ATATTGGTTGCAGCAGAAATGTCTCCCTCGTCAAAACAGAGGTGCTTGGAGATGTTGCT 198  
 QY 72 GlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValValMetProArg 91  
 Db 199 GGATCATTTACCTAAGGCTTTGGCTAGCGGTGACACAGATTATGGTTGTAGTACCTCGG 258  
 QY 92 TyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIle 111  
 Db 259 TAT-----AGTCATTATGCTGACGACAGATATAGGATATGGAAA 300  
 QY 112 ArgIleProCysPheGlyGlyLysGluValThrPhePheHisGlyLysArgAspSer 131  
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 QY 132 ValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeuTyrGly 150  
 Db 361 GTTGATCTTCGTTTTTATTGACAGCTCCAAACTTCCCACTTTACAGGATAACATATATGG 420  
 QY 151 AspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAla 170  
 Db 421 -----GGNAACCGAGAGGATATTCTAAACCGCATGGTGTGTTTTGCAAGCAGCT 471  
 QY 171 CysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln---AsnCysMet 189

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Db 472 GCTGAGGTTCTTGGCATGTTCTTGGTGGAGTTGCTATGAGATGGAAATTTGGCC 531
Qy 190 PheValValAenAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyArg 209
Db 532 TTTCATGCCAATGATGGCATACTGCTTGGTGGCAGTGATCTGAAAGCATATATCGT 591
Qy 210 ProTyArgValTyLeuAspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229
Db 592 GACCATGGTTTAATGAAGTACACAGATCTGTTCTTGGATTTCATACATAGCACACAG 651
Qy 230 GlyValGluProAlaSerThrTyProAspLeuGlyLeuProGluTyTrpTyGlyAla 249
Db 652 GGACGGGGCCCAATGATGATTTCCGCTACACAGATTTACTTGACACTACATAGACCTT 711
Qy 250 LeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaVal 269
Db 712 TTCAAATATATATGACCGGTT-----GGAGGTGAGCACTTC 747
Qy 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTy 289
Db 748 AATATCTTTTCGGCTGGTTTAAAGGCAGCTGACCGGATTTGCTGTGAGTCTATGGAT 807
Qy 290 SerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAenGluLeuSerSerArg 309
Db 808 GCATGGGAGATTAACACTTCTGAAGTGGTGGGTTTGGATGGGATCAATAATGAGAA 867
Qy 310 LysSerValLeuAenGlyIleValAsnGlyIleAspIleAenAspTrpAenProAlaThr 329
Db 868 GACTGGAAATTTGAGAGAAATTTGAATGAATTGACACCAAGATTCGAACCCAGATT 927
Qy 330 AspLysCysIlePro-----CysHisTySerValAspLeu----SerGly 344
Db 928 GATGTTCACTTGAATCAGATGATACACTAACTACACCTTGAGACCCCTGCAAGTGGC 987
Qy 345 LysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspVal 364
Db 988 AAGCTCAGTGCAAGCGCTTGCMAAGAGCTCGTTGCTGCTGCTGAGGATTT 1047
Qy 365 ProLeuIleGlyPheIleGlyArgLeuAspTyArgLysGlyIleAspLeuIleGlnLeu 384
Db 1048 CCGTTACTTGAATTCGATGGAAGCTGATCAACAGAAAGGCAATTCATCTCATAGCGAA 1107
Qy 385 IleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspPro 404
Db 1108 GCAATTCCTTGGATAGTGGCCAGGATGTCACCTAGTCTATGTTGGAACTGGAAGCGC 1167
Qy 405 GluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrp 424
Db 1168 GACTTAGAGATATGCTTAGCGAGTTTGTAGTCCACACCGTGACAAAGTCAGAGGATGG 1227
Qy 425 ValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMet 444
Db 1228 GTTGGCTTTTCGGTCAAGATGGCTCCCGGATTAACAGCAGGTGCAGACATATTTGCTG 1287
Qy 445 ProSerArgPheGluProCysGlyLeuAenGlnLeuTyAlaMetGlnTyThrVal 464
Db 1288 CCATCAAGATTTGAGCCATGTGGATGAAATCAACTCTATGCCATGAATACGGAACAAT 1347
Qy 465 ProValValHisAlaThrGlyGlyLeuArgAspThrValGluAenPheAenProPheGly 484
Db 1348 CCAATTTGATACATGCTGCTGGTGAATGAGGATACAGTGAAGCCTTTTATCATTTGAA 1407
Qy 485 GluAenGlyGluGlnGlyThrGlyTyTrpAlaPheAlaProLeuThrThrGluAenMetPhe 504
Db 1408 GAGTCG-----GGCCTTGGTGGACATTTGACAGTGCAGAACTAACAGTTAATA 1458
Qy 505 ValAspIleAlaAenCysAenIleTyIleGlnGlyThrGlnValLeuLeuGlyArgAla 524
Db 1459 AATGCATATAGGAACACTGCTT-GTTGACCTTCAGCAGATATAAGCAGCTGGGAGGCT 1517
Qy 525 AsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 1518 CCNACGGCGAGGATGA-CGCAGATCTTAGTTGGG 1552
```

```
RESULT 28
AAV29755
ID AAV29755 standard; DNA; 2097 BP.
XX
XX
AC AAV29755;
XX
XX 11-SEP-1998 (first entry)
XX
DE Zea mays soluble starch synthase IIb gene.
XX
XX SSR; starch-encapsulating region; fusion vector;
KW soluble starch synthase IIb; glucosyl transferase; ss.
XX
XX Zea mays.
XX
XX Key Location/Qualifiers
XX CDS 1..2097
XX /tag= a
XX /product= "soluble starch synthase IIb"
XX
XX WO9814601-A1.
XX
XX 09-APR-1998.
XX
XX 30-SEP-1997; 97WO-US017555.
XX
XX 30-SEP-1996; 96US-0026855P.
XX
XX (EXSE-) EXSEED GENETICS LLC.
XX
XX Keeling P, Guan H;
XX
XX WPI; 1998-240100/21.
XX P-PSDB; AAW56487.
XX
XX Hybrid polypeptide comprising starch-encapsulating region and protein -
XX useful for, e.g. producing protein(s) resistant to degradation by stomach
XX acids.
XX
XX Example 2; Page 36-38; 156pp; English.
XX
XX The sequence is that of the soluble starch synthase IIb gene. It can be
XX used in the production of a hybrid polypeptide comprising a starch-
XX encapsulating region (SSR) fused to a payload protein. The hybrid
XX polypeptide can be used to make modified starches comprising the payload
XX protein, selected from, e.g. hormones, growth factors, antibodies,
XX enzymes, dyes, immunoglobulins, etc. The modified starch can also be used
XX to provide grain feeds enriched in amino acids. By encapsulating the
XX payload protein in starch, it is more resistant to degradation by stomach
XX acids.
XX
XX Sequence 2097 BP; 409 A; 575 C; 696 G; 417 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,32e-109 Length: 2097
Score: 1130.50 Matches: 254
Percent Similarity: 57.2% Conservative: 64
Best Local Similarity: 45.7% Mismatches: 159
Query Match: 39.1% Indels: 80
DB: 2 Gaps: 11

US-10-628-525A-21 (1-539) x AAV29755 (1-2097)
Qy 3 AlaGluLeuSerArgGluAspLeuGluProGluGlyIleAlaGluGlySerIle 22
Db 565 GCTCCTTATGACAGGAGGAT-----AATGAACCTGGCCCTTTGGCTGGCCTAATGTG 618
Qy 23 AspAenThrValValValAlaSerGluGlnApsSerGluIleValValGlyLysGluGln 42
Db 619 ATGAACGTCGTGCTGGTGGCTTCT----- 642
Qy 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyAla 62
```



CC polypeptides including starch synthase enzymes as fusion proteins with  
 CC improved affinity to starch and modified catalytic capabilities and to  
 CC the in vivo and in vitro synthesis of glucan chains of modified lengths  
 CC as compared to plants producing native starch or starch produced with  
 CC native starch synthases. Expression of the starch synthase fusion  
 CC proteins along with granule bound starch synthase (GBSS) will lead to a  
 CC modified starch having an altered or improved morphology, retrogradation,  
 CC waterbinding, or swelling potential of the granules, gel strength,  
 CC adhesiveness, cohesiveness, hardness, elasticity, increased or decreased  
 CC granule size, degree of branching, crystallinity, degree of cross-  
 CC linking, and increased or decreased glucan chain lengths. This sequence  
 CC encodes a starch synthase used in the invention  
 XX

SQ Sequence 2480 BP; 477 A; 673 C; 827 G; 503 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 4,24e-109 Length: 2480  
 Score: 1130.50 Matches: 254  
 Percent Similarity: 57.2% Conservative: 64  
 Best Local Similarity: 45.7% Mismatches: 159  
 Query Match: 39.1% Indels: 80  
 DB: 8 Gaps: 11

US-10-628-525A-21 (1-539) x ABX09934 (1-2480)

QY 3 AlaGluLeuSerArgGluAspLeuGlyLeuProGluGlyLeuAlaGluGlySerIle 22  
 DB 622 GCTCCTTATGACAGGAGGAT-----AATGAACCTTGGCCCTTTGGCGCCATAATGTG 675  
 QY 23 AspAsnThrValValAlaLaserGluGlnAspSerGluIleValValGlyLysGluGln 42  
 DB 676 ATGAACTGCTGCTGGTGGCTTCT----- 699  
 QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62  
 DB 700 -----GAATGTGCTCTTCTGTC 717  
 QY 63 LysSerGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGly 82  
 DB 718 AGACAGGTGGCTTGGAGATGTCGTGGGTGCTTTCCTAAGGCTCTGGCGAGGAGGA 777  
 QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102  
 DB 778 CACCGTGTATGTGCTGATACCAAGATAT-----GGAGAGTATGCC 819  
 QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122  
 DB 820 GAAGCCCGGATTTAGGTGTAAAGAGACGTTACAAAGGTAGCTGGACAGATTTCAGAGTT 879  
 QY 123 ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyr 142  
 DB 880 ACTTATTTTCACTCTTACATTGATGAGTGTGATTTGTATTCGTAGAGCCCTCCCTTC 939  
 QY 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
 DB 940 CGGACCCGGACAAATAATATTATGGG-----GGAGAAAGATTGATATTTTGAAG 990  
 QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGly 181  
 DB 991 CGCATGATTTTGTCTGCAAGGCCGCTGTGTAGTTCATGTTGATGCTCCATGTCGGGT 1050  
 QY 182 TyrIleTyrGlyGln---AsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200  
 DB 1051 ACTGTCTATGGTGATGGCAACTTAGTTTCATTGCTAATGATGGCATACCGCACTTCG 1110  
 QY 201 ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 DB 1111 CCTGTCTATCAAGGCCCTATTACCGGCAACATGTTTGTATGATGATGCTCGCTCTGTG 1170  
 QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 DB 1171 CTTGTGATACACACATTGCTCATAGGTGCTGGCCCTGTAGACGACTTCGTCATATTTT 1230

QY 241 GlyLeuProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArg 260  
 DB 1231 GACTTGCCT-----GAA 1242  
 QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272  
 DB 1243 CACTATCATGACACCTTCAAACTGTATGACAAACATTGGTGGGATCACAGCAACGTTTTT 1302  
 QY 273 LysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292  
 DB 1303 GCTGCGGGCTGAAGACGGCAGACCCGGTGTGACCGTTAGCAATGGCTACATGTGGAG 1362  
 QY 293 ValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerVal 312  
 DB 1363 CTGAAGACTTCGAAGCGCGGTGGGCTCCACGACATCATATAACCAAGACGACTGGAAG 1422  
 QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332  
 DB 1423 CTGACGGCATCTGTGAACGGCATCGACATGAGCGAGTGAACCCCGCTGTGGAC----- 1476  
 QY 333 IleProCysHisTyrSerValAspAspLeu-----Ser 343  
 DB 1477 -----GTGCACCTCCACTCCGACGACTACCACTACACGTTTCGAGCGCTGGACAC 1530  
 QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363  
 DB 1531 GGCNAGCGCAGTCAAGCGCCCTGACGCGCAGCTGGCCCTGAGGTCCGCGACGAC 1590  
 QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383  
 DB 1591 GTGCCACTGATCGGGTTCATCGGGCGGCTGGACACCAAGAGCGCTGGACATCATCGCC 1650  
 QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403  
 DB 1651 GACGCGATCCACTGGATCGGGGCGAGAGCTGCAGCTCGTGTGTTGGCACCAGGCGG 1710  
 QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423  
 DB 1711 GCCGACCTCGAGGACATGCTGGCGCGGTTCGAGTCGAGCAGCAGCAGCAAGGTGCGCG 1770  
 QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443  
 DB 1771 TGGGTGGGGTTCCTGGGTGCCCTCGCGCACCGCATCACGGCGGCGCGGACATCTGCTG 1830  
 QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463  
 DB 1831 ATGCGCTCGGGTTCGAGCGCTGCGGGCTGAACAGCTCTACGCCATGGCGTACGGGACC 1890  
 QY 464 ValProValValIleAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483  
 DB 1891 GTGCCGTGGTGACGCGCTGGGGGGCTCCGGGACACGCTGGCGCGCTTCGACCCGTTCC 1950  
 QY 484 GlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMet 503  
 DB 1951 AACGACACC-----GGGCTCGGGTGGAGCTTCGACCCGCGGAGCGCAACCGGATG 2001  
 QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523  
 DB 2002 ATCGACCGCTCTCGCACTGCTT-CACACAGTACCGGAACACTACAGGAGAGCTGGCGCG 2060  
 QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
 DB 2061 CTGCAGGGCGCGCGCATGGCGGAGACCTCAGCTGGGAGACCAACCGCGC 2108  
 RESULT 30  
 AAV70958  
 ID AAV70958 standard; DNA; 2423 BP.  
 XX  
 AC AAV70958;  
 XX  
 DT 26-AUG-1999 (first entry)  
 XX  
 DE DNA encoding maize starch soluble synthase I1b.

XX Non-glycogen-like polysaccharide production; fermentation;  
 KW starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;  
 KW non-starch branching gene; amylopectin; amylose; plant-like starch;  
 KW maize starch soluble synthase IIB; ss.  
 XX  
 OS Zea mays.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1632  
 FT /tag= a  
 FT /note= "this base represents a nucleotide missing from  
 FT the sequence given in the specification. It is included  
 FT to maintain the nucleotide numbering given in the  
 FT specification for this sequence"  
 XX  
 PN W09844780-A1.  
 XX  
 PD 15-OCT-1998.  
 XX  
 PP 03-APR-1998; 98WO-US006660.  
 XX  
 PR 04-APR-1997; 97US-0042939P.  
 XX  
 PA (EXSE-) EXSEED GENETICS LLC.  
 XX  
 PI Guan H, Keeling PL;  
 XX  
 DR WPI; 1998-568285/48.  
 DR P-PSDB; AAW70892.  
 XX  
 PT Producing non-glycogen-like polysaccharides in bacteria, fungi or plants  
 PT - transformed with genes for enzymes involved in starch or glycogen  
 PT synthesis allows fermentative production of starches with engineered  
 PT properties.  
 XX  
 PS Disclosure; Fig 50; 150pp; English.  
 XX  
 CC The specification describes a method for the production of non-glycogen-  
 CC like polysaccharides in a host. The method comprises transforming a host,  
 CC suitable for fermentation, with genes encoding starch- or glycogen-  
 CC synthesis enzymes, and fermenting the transformants. The specification  
 CC also describes hosts transformed with a gene active in glycogen synthesis  
 CC and at least one non-starch branching gene, involved in production of  
 CC amylopectin or amylose in its original host. The method is used to  
 CC produce plant-like starches by fermentation and new starches in plants.  
 CC These starches are useful for all food and non-food applications of  
 CC starch. The present sequence is used in the course of the invention  
 XX  
 SQ Sequence 2423 BP; 466 A; 656 C; 804 G; 496 T; 0 U; 1 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 1.39e-108 Length: 2423  
 Score: 1125.50 Matches: 253  
 Percent Similarity: 57.0% Conservative: 64  
 Best Local Similarity: 45.5% Mismatches: 160  
 Query Match: 38.9% Indels: 80  
 DB: 2 Gaps: 11  
 US-10-628-525A-21 (1-539) x AAV70958 (1-2423)  
 QY 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyLeuAlaGluGlySerIle 22  
 DB 565 GCTCTTATGACAGGAGAT-----AATGAACCTGGCCCTTTGGCTGGGCTATATG 618  
 QY 23 AspAsnThrValValAlaSerGluGlnAspSerGluIleValValGlyLeuGluGln 42  
 DB 619 ATGAACGTGCTGCTGCTTCT----- 642  
 QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62  
 DB 643 -----GAATGTGCTCTCTTCTGC 660

QY 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAaArgGly 82  
 DB 661 AAGACAGGTGGCTTGGAGATGTCGTGGTGTCTTTGCCCTAAGCTCTGCGGAGGAGGA 720  
 QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102  
 DB 721 CACCGTGTATGTCGTGATACCAAGATAT-----GGAGAGTATGCC 762  
 QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122  
 DB 763 GAAGCCCGGATTTAGGTGTAAGGAGACGTTCAAGGTAGCTGGACAGATTCAGAAGTT 822  
 QY 123 ThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSerTyr 142  
 DB 823 ACTTATTTTCACTCTTACATTGATGAGTTGATTTGATTCTGTAGAACCCCTCCCTTC 882  
 QY 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
 DB 883 CGGCACCGGCACATAATATTTATGG-----GGAGAAAGATTGGATATTTGAAG 933  
 QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly 181  
 DB 934 CGCATGATTTTGTCTCAAGCCCGCTGTGAGGTTCATGCTGCTCCATGTGCGGT 993  
 QY 182 TyrIleTyrGlyGln---AsnCysMetPheValValAsnAspTyrHisAlaSerLeuVal 200  
 DB 994 ACTGTCTATGTCATGGCACTTAGTTTCATGTCATGTCATGTCATGTCATGTCATGTC 1053  
 QY 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 DB 1054 CCGTCTATCTAAAGCCCTATTACCGGACATGTTGATCGCATGATGCTCGTCTGTG 1113  
 QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 DB 1114 CTTGTGATACACACATTCCTCATCGGTCGTGGCCCTGTAGACGACTTCCTCAATTT 1173  
 QY 241 GlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260  
 DB 1174 GACTTGCCT-----GAA 1185  
 QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272  
 DB 1186 CACTACATCGACCTCAAACTGTATGACAACTGTTGGGGGATCACAGCAACGTTTTT 1245  
 QY 273 LysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292  
 DB 1246 GCTGGGGGCTGAAGACGCGACGCGGTGGTACCGTTAGCAATGGCTACATGTGGGAG 1305  
 QY 293 ValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312  
 DB 1306 CTGAAGACTTCGAAGGGGGGGTGGGGCTCCACGACATCATAAACAGACGACTGGAAG 1365  
 QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCys 332  
 DB 1366 CTGCAGGGCATCGTGAACGGCATCGACATGACGAGCGAGTGAACCCGCTGTGGAC----- 1419  
 QY 333 IleProCysHisTyrSerValAspAspLeu-----Ser 343  
 DB 1420 -----GTGCACCTCCACTCCGACGACTACACCAACTACACTTCGAGACGCTGGACACC 1473  
 QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363  
 DB 1474 GCAAGCGGAGTGCAGGCGCCCTGACGGCGAGCTGGGGCTGAGCTCGCGACGAC 1533  
 QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383  
 DB 1534 GTGCCACTGATCGGTTTCATCGGGCGGTGGACCAACAGAGGGCGTGACATCATCGCC 1593  
 QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403  
 DB 1594 GACGCGATCCACTGATCGGGGCGGACGAGCTGTGATCGTGGCGACCGCGCG 1653  
 QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423



```
Db      1654  GCGACCTGGAGGACATGCTCGCGGGTTCCAGTCGGAGACACAGCGACAAGTTCGCGCG 1713
Qy      424   TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443
Db      1714  TGGGTGGGGTTCTCGGTGCCCTCGCGCACCGCATCACGGCGGCGCGGACATCCTGCTG 1773
Qy      444   MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
Db      1774  ATGCCGTGCGGGTTTCGAGCCGTGCGGGCTGAACAGCTCTACGCCATGGCGTACGGACC 1833
Qy      464   ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProphe 483
Db      1834  GTGCCCGTGTGCACGCGGTGCGGGGCTCCGGGACACGGTGGCGCGCTTCGACCCCGTTC 1893
Qy      484   GlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503
Db      1894  AACGACACC-----GGGCTCGGGTGGACGTTTCGACCGCGCGGAGCGAACCGGATG 1944
Qy      504   PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523
Db      1945  ATCGACGCGCTCTCGCACTGCCT-CACCACGTACCGGAACCTACAAGGAGAGCTGGCGCGC 2003
Qy      524   AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db      2004  CTGCAGGGCGCGGCGCATGGCCGAGGACCTCAGCTGGGACCAACGCGCG 2051
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Job time : 1358 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 8692.03 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

Title: US-10-628-525A-21

Perfect score: 2893

Sequence: 1 CVABLGRDGLRPEGIAG.....LLGRANEARHVXRLHVGPCR 539

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Ygapop 10.0 , Ygapext 0.5  
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Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Database :

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2: gb\_est2:\*  
3: gb\_est3:\*  
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5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1558	53.9	877	6	CD435568
4	1424	49.2	815	7	CN147393
5	1266.5	43.8	983	6	CA252614
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7	1235	42.7	769	7	CK123179
					BBS182410

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9	1125	38.9	805	7	CO442565
10	1066	36.8	2959	10	CL951041
11	1054	36.4	639	3	BI953855
12	1053	36.4	833	8	CV760941
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14	1044	36.1	782	3	BM111144
15	1036.5	35.8	695	6	CD463762
16	1035	35.8	630	5	BQ472054
17	1031.5	35.7	877	6	CA818188
18	1028	35.5	609	5	CA020001
19	1021	35.3	621	3	BJ481805
20	1020	35.3	704	5	BU027679
21	1017	35.2	727	3	BM412062
22	1015	35.1	2498	4	AY109714
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24	1010	34.9	3248	4	AY111778
25	999	34.5	710	6	CA923834
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CB003951	VVB034B02
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CD443174	EL01N0422
BE434991	EST406069
CD440915	EL01N0562
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CK007984	28959F81C
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85	693	24.0	472	7	CK064995	CK064995 7000ArbC
86	686	23.7	798	10	CG362560	CG362560 OG3CP68TV
87	685.5	23.7	688	8	DN677214	DN677214 PP YBa002
88	684	23.6	611	3	CF759861	CF759861 DSaF1.52
89	683	23.6	611	3	BM377030	BM377030 ERem05_SQ
90	681.5	23.6	602	6	CD482588	CD482588 atr01-2ma
91	681.5	23.6	761	7	CO113875	CO113875 GR Eb014
92	677.5	23.4	623	5	BU045439	BU045439 PP Lda002
93	668	23.1	834	7	CO461599	CO461599 M2CCS2002
94	666	23.0	436	6	CA7113871	CA7113871 wdk3C.dk0
95	664.5	23.0	649	7	CV053030	CV053030 EST 12478
96	664.5	23.0	785	6	CD443882	CD443882 EU01N0432
97	650.5	22.5	699	6	CA072449	CA072449 SCEPAM101
98	650	22.5	616	7	CM013203	CM013203 WHE3357.H
99	642.5	22.2	1003	10	CG037054	CG037054 PUKB330TD
100	641.5	22.2	481	3	BP892026	BP892026 BP892026
101	641.5	22.2	618	1	AW759559	AW759559 BL45A09.Y
102	640.5	22.1	654	5	BU925670	BU925670 MCS012B09
103	639	22.1	1100	7	CK163628	CK163628 FGAS01625
104	638.5	22.0	623	1	AW759946	AW759946 BL56B01.Y
105	637	22.0	420	1	AJ479519	AJ479519 AJ479519
106	636	22.0	437	3	BP744439	BP744439 BP744439
107	636	22.0	566	8	DR996565	DR996565 Mdlr7004G
108	634.5	21.9	585	2	BG226847	BG226847 40-53.Sce
109	634	21.9	454	1	AV832689	AV832689 AV832689
110	631.5	21.8	694	6	CA289589	CA289589 SCAGPL800
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132	591	20.4	396	1	AU075475	AU075475 AU075475
133	587	20.3	677	3	BI934232	BI934232 EST554121
134	586.5	20.3	595	10	CM037057	CM037057 104_268.1
135	584	20.2	539	3	BI935620	BI935620 EST55509
136	582	20.1	1280	7	CN831271	CN831271 EL948.Bra
137	580	20.0	557	3	BI934660	BI934660 EST554549
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139	578	20.0	773	7	CV470324	CV470324 43164.1.C
140	577.5	20.0	518	9	BZ642783	BZ642783 OGCA052FM
141	577	19.9	874	6	CF330054	CF330054 NACL--05-
142	573	19.8	362	5	BU974575	BU974575 HB28G06r
143	571.5	19.8	735	6	CA295339	CA295339 SCAC1V102
144	570	19.7	509	3	BM493903	BM493903 NXLY.071
145	570	19.7	631	3	BI531619	BI531619 1024115B1
146	570	19.7	900	6	CD433792	CD433792 ELOIN0315
147	568	19.6	699	10	CM299555	CM299555 104_782.1
148	565	19.5	401	2	BG050773	BG050773 FM1_70.D0
149	564	19.5	849	8	DR924417	DR924417 EST111595
150	564	19.5	887	8	CX712740	CX712740 RTPQ1_4_A

ALIGNMENTS

RESULT 1	CNS09YPE	2287 bp	mRNA	linear	HTC 06-FBB-2004
LOCUS	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
DEFINITION	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
ACCESSION	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
VERSION	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
KEYWORDS	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
SOURCE	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
ORGANISM	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
REFERENCE	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
AUTHORS	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
TITLE	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
JOURNAL	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
AUTHORS	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
TITLE	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
JOURNAL	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
COMMENT	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
FEATURES	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
ORIGIN	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
Alignment Scores:	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
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Score:	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
Percent Similarity:	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
Best Local Similarity:	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
Query Match:	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
DB:	Arabis thaliana Full-length cDNA Complete sequence from clone				Arabis thaliana (thale cress).
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ACCESSION AY104834.1 GI:21207912
VERSION HTC.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1530)
Gardner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H.,
Fang, Z., Morgante, M., Landewe, T., Fongler, K., Ueche, F.,
Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H.
Jr.
Anchoring 9,371 maize expressed sequence tagged unigenes to the
bacterial artificial chromosome contig map by two-dimensional
plant hybridization
Plant Physiol. 134 (4), 1317-1326 (2004)
15020742
2 (bases 1 to 1530)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
3 (bases 1 to 1530)
Coe, E.H.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schubale, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
FEATURES
Location/Qualifiers
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/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Corneaus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
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contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."

## ORIGIN

## Alignment Scores:

Pred. No.: 1.42e-202 Length: 1530  
 Score: 1858.00 Matches: 350  
 Percent Similarity: 99.7% Conservatives: 0  
 Best Local Similarity: 99.7% Mismatches: 1  
 Query Match: 64.2% Indels: 1  
 DB: 4 Gaps: 0

US-10-628-525A-21 (1-539) x AY104834 (1-1530)

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 DB 101 AGACCATATGGTGTATTAAGACTCCCGACGACATTCCTTGTATATCATTAATTTAGCACAT 160  
 QY 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGly 248  
 DB 161 CAGGGGTGTAGAGCTGCAAGCACATATCTGACCTTGGGTGGCCACTGAATGTTATGCA 220  
 QY 249 AlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAla 268  
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 QY 289 TyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSer 308  
 DB 341 TATTTCAGGAGGTACAACTGCTGAAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCC 400  
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 DB 401 AGAAGAGGTATTAACCGAATTTGAAATGGAATTGACATTAATGATTGGAACCTGTC 460  
 QY 329 ThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCys 348  
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 QY 409 TrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSer 428  
 DB 701 TGGATGAGATCTACAGAGTCGATCTTCAAGGATAAATTTTCGTGGATGGGTTGATTTAGT 760  
 QY 429 ValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPhe 448  
 DB 761 GTTCCAGTTTCCACCGAATAATCTCCGGTTCGGATATATTTGTTAATGTCATCCAGATTC 820  
 QY 449 GluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHis 468  
 DB 821 GAACCTTGTGGTCTCAATCAGCTATATGCTATGCTAGTATGACACAGCTTCTCTGTTCCAT 880  
 QY 469 AlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlu 488

DB 881 GCAACTGGGGGCTTAGAGATACCGTGGAGAACCTTCAACCCCTTCGGTGAATGGAGAG 940  
 QY 489 GlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAla 508  
 DB 941 CAGGGTACAGGGTGGGCATTCGACCCCTTAACACAGAAAACATGTT-GTGGACATTGGC 999  
 QY 509 AsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArg 528  
 DB 1000 AACTGCATATCTATCATCAGGGAACACAAAGTCTCTCTGGGAAGGCTAATGAAGCAGG 1059  
 QY 529 HisValLysArgLeuHisValGlyProCysArg 539  
 DB 1060 CATGTCNAAAGACTTCACGTGGGACCATGCGCG 1092

RESULT 3  
 CD435568 877 bp mRNA linear EST 03-JUN-2003  
 LOCUS ELO1N0362G08.b Endosperm\_3 Zea mays cDNA, mRNA sequence.  
 DEFINITION CD435568  
 ACCESSION CD435568  
 VERSION CD435568.1 GI:31351211  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 877)  
 AUTHORS Lai, J., Dey, N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,  
 Larkin, B., Bera, P. and Messing, J.  
 TITLE Characterization of the maize endosperm transcriptome and its  
 comparison to the rice genome  
 JOURNAL Genome Res. 14 (10), 1932-1937 (2004)  
 PUBMED 15466231  
 COMMENT Contact: Lai, Jinsheng  
 Dr. Joachim Messing's lab  
 Wakeman Institute, Rutgers University  
 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA  
 Tel: 732-445-3801  
 Fax: 732-445-5735  
 Email: jlai@waksman.rutgers.edu  
 Seq primer: T3.  
 FEATURES  
 source  
 1. .877  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cui="W22"  
 /db\_xref="taxon:4577"  
 /tissue\_type="Endosperm of 7-23DAP"  
 /clone\_lib="Endosperm 3"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.4e-168 Length: 877  
 Score: 1558.00 Matches: 287  
 Percent Similarity: 99.3% Conservatives: 1  
 Best Local Similarity: 99.0% Mismatches: 1  
 Query Match: 53.9% Indels: 1  
 DB: 6 Gaps: 0  
 US-10-628-525A-21 (1-539) x CD435568 (1-877)

QY 101 TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIle-ProCysPheGlyGlyGluHi 120  
 DB 9 TATGCAAAATGCAATTTTACACAGAAAACACATTCCTGATCTCCATGCTTTGGCGGTGAACA 68  
 QY 120 sGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisPr 140  
 DB 69 TGAAGTTACCTTCTTCCATGAGTATAGAGATTCAGTTGAGTGGGTGTTGTTGATCATCC 128  
 QY 140 oSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAsnGlu 160

```

Db      129  CTCAATACAGAGACTGGAAATTTATATGGAGATAAGTTTGGTCTTTTGGTGATAATCA 188
Qy      160  nPheArgTyrThrLeuLeuCysTyrAlaAaCysGluAlaProLeuLeuLeuGluLeuG1 180
Db      189  GTTCAGATACACACTCTCTTGTCTATGCTGTCATGTGAGGCTCTCTTGGTCTTGAATTGGG 248
Qy      180  yGlyTyrIleTyrGlyGlnAenCysMetPheValValAlaAsnAspTrpHisAlaSerLeuVa 200
Db      249  AGGATATATTTATGGACAGAAATTCATGTTTGTGTCAATGATTGGCATGCCAGTCTAGT 308
Qy      200  iProValLeuLeuAlaAlaTyrArgProTyrGlyValTyrLysAspSerArgSerI1 220
Db      309  GCCAGTCTCTTCTGCAAAATATAGACCATATGGGTGTTTATTAAGACTCCCGACGAT 369
Qy      220  eLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLe 240
Db      369  TCTTGTAATACATAATTTAGCACATCATGGGTGTAGAGCTGCAAGCACATATCTGACCT 428
Qy      240  uGlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgAr 260
Db      429  TGGGTTCGCCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTCCTCGAATGGCGAGGAG 488
Qy      260  gHisAlaLeuAspLysGlyGluAlaValAlaAsnPheLeuLysGlyAlaValThrAlaAs 280
Db      489  GCATGCCCTTGACAGGGTGAGCGGTATATTTTGAAGGTGCGTGTGACAGCAGA 548
Qy      280  pArgIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyG1 300
Db      549  TCGAATCGTCACTGCTCAGTAAGGTTATTATCATGGAGGTCAACACTGCTGAGGTGACA 608
Qy      300  nGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyI1 320
Db      609  GGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAATGTAATGGAAT 668
Qy      320  eAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAs 340
Db      669  TGACATTTAATGATTGGAACTTCGCCACAGACAAATGATCCCTGTCAATTATCTGTGA 728
Qy      340  pAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProI1 360
Db      729  TGACCTCTCTGGAAGGCCAAATGTAAGGTGCAATGTCAGAGGAGGTGGGTTTACCTAT 788
Qy      360  eArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyLeAs 380
Db      789  AAGGGCTGATGTTCTCTGATGGCTTTATTTGAAGATTGGATTATCAGAAAGGCATTGA 848
Qy      380  pLeuIleGlnLeuIleProAspLeu 389
Db      849  TCTCATCAACTTATCATACCATCTC 876

RESULT 4
CN147393
LOCUS      815 bp mRNA linear EST 01-APR-2004
DEFINITION WOUND1_49 All_1A002 Wounded leaves Sorghum bicolor cDNA clone
            WOUND1_49 All_1A002 5', mRNA sequence.
ACCESSION  CN147393.1 GI:45987913
VERSION     CN147393.1
KEYWORDS    EST.
SOURCE      Sorghum bicolor (sorghum)
ORGANISM    Sorghum bicolor
            Sukariyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
            1 (bases 1 to 815)
REFERENCE   Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
AUTHORS     Sun, F., Sullivan, R., Brady, J., Eastman, A., Miller, V., Gonzalez, M.,
            Anfuco, C., Chhabra, D., Johnson, H., Kaman, D. and Pratt, L.H.
            A Sorghum EST database: mechanically damaged and methyl
            Jasmonate-treated leaves
            Unpublished (2003)
TITLE       Other ESTs: WOUND1_49 All_1A002
JOURNAL
COMMENT     Contact: Cordonnier-Pratt MM

```

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The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
the Human Genome Center, University of Tokyo Institute of Medical  
Science; plant material and RNA prepared at Texas A & M University;  
sequencing done in the Laboratory for Genomics and Bioinformatics,  
University of Georgia. Sequence ends have been trimmed to exclude  
vector and regions below Phred quality 16. Three-prime sequences  
are presented as their reverse complement and have been trimmed to  
exclude polyA.

Seq primer: Sug5 (CTTCTGCTCTAAAGCTGGG).

#### FEATURES

Location/Qualifiers

1..815

/organism="Sorghum bicolor"

/mol\_type="mRNA"

/cultivar="BTx623"

/db\_xref="taxon:4558"

/clone="WOUND1\_49 All\_1A002"

/lab\_host="DH10B-T1 phage-resistant E. coli"

/clone\_lib="Wounded leaves"

/notes="Organ: Leaf; Vector: pME18S-FL3; Site\_1: XhoI;  
Site\_2: XhoI; The library was prepared from polyA+ RNA  
harvested from 8-day-old hydroponically grown, BTx623  
sorghum seedlings. For some plants, one-half of the second  
leaf was crushed without damaging the midvein. For others,  
methyl jasmonate was added to the growth medium to a final  
concentration of 100 uM. Leaves were harvested 3 and 27 hr  
after treatment and pooled. Double-stranded cDNA was  
cloned unidirectionally into different DraIII sites of the  
pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,  
3-prime DraIII site is CACCATGTG). XhoI excises the cDNA  
insert."

#### ORIGIN

Alignment Scores:

Pred. No.: 6,17e-153 Length: 815

Score: 1424.00 Matches: 266

Percent Similarity: 98.9% Conservative: 2

Best Local Similarity: 98.2% Mismatches: 3

Query Match: 49.2% Indels: 0

DB: 7 Gaps: 0

US-10-628-525A-21 (1-539) x CN147393 (1-815)

Qy 189 MetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyr 208

Db 1 ATGTTTGTGTAATGATTGGCATGCCAGTCTAGTGCCAGTCTTCTTGTGCAAAATAT 60

Qy 209 ArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHis 228

Db 61 AGACCATATGGGTGTTTATTAAGACTCCCGACGATCTTGTGTAATACATAATTTAGCACAT 120

Qy 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGly 248

Db 121 CAGGGGTGAGAGCTGCAAGCACATATCTGACCTTGGGTGGCCACTGAATGGTATGGA 180

Qy 249 AlaLeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspLysGlyGluAla 268

Db 181 GCTCTGGAGTGGGTATTCCTGAATGGGCAAGGAGCATGCCCTTGCAAGGCTGAGGCA 240

Qy 269 ValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGly 288

Db 241 GTTAATTTTTCAGAGGTGCGTGTGACAGCAGATCGAATTTGTGACTGTCTAGTAAGGCT 300

Qy 289 TyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuSerSer 308

Db 301 TATTCAATGGAGGTCACAACTGCTGAGGTGACAGGGTCTCATGAGCTCTTAAGCTCC 360

Qy 309 ArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAla 328



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Db CGAAGAGTGTATTAACCGAATGTAATGGAATGACATTAATGATTGGAACCTCGG 420
QY ThrAspLysCysIleProCysHisTyrSerValAspLeuSerGlyLysAlaLysCys 348
Db ACGGACAAATGATCCCTTGTCTATTAATCTGTGATGACCTCTCTGGAAGCCAAATGT 480
QY LysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGly 368
Db AAAAGTGCATTCGACAGAGAGCTGGGTACCTATTAAGCCCTGAATTCCTCTGATTGT 540
QY PheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAsp 388
Db TTTATTTGGAAGATTGGATTATCAGAAGCAATGATCTCATTCATCACTATCACCACAT 600
QY LeuMetArgLysAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAsp 408
Db CTCATCGCGGACGACGCTCAATTTGTCATCTGGATCTGGTGACCCAGAGCTCGAAGAC 660
QY TrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSer 428
Db TGGATGAGATCTACAGAGTCGAGCTTCAGAGTAATAATTTCTGGATGGGTTGATTAAT 720
QY ValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPhe 448
Db GTTCCAGTTTCCACCGCAATACTGCGCGCTGCGATATATTGTTAATGCAATCCAGATTC 780
QY GluProCysGlyLeuAsnGlnLeuTyrAlaMet 459
Db GAACCTTGTGGTCTCAATCAGCTATATGCTATG 813
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RESULT 5
CA252614
LOCUS SCVPFL1139H12.9 FL1 Saccharum officinarum cDNA clone SCVPFL1139H12
DEFINITION 983 bp mRNA linear EST 25-SEP-2003
5', mRNA sequence.
ACCESSION CA252614
VERSION CA252614.1 GI:35338653
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1 (bases 1 to 983)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 139 row: H column: 12
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..983
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCVPFL1139H12"
/lab_host="DH10B"
/clone_lib="FL1"
(note="Organ: Inflorescence at beginning of development
(ncm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;
An unidirectional cDNA library generated from
[inflorescence at beginning of development (1cm-long)]).
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## FEATURES

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source
1..983
/organism="Saccharum officinarum"
/mol_type="mRNA"
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/lab_host="DH10B"
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(note="Organ: Inflorescence at beginning of development
(ncm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;
An unidirectional cDNA library generated from
[inflorescence at beginning of development (1cm-long)]).
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cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucst.lad.ic.unicamp.br/public>

## ORIGIN

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Alignment Scores:
Pred. No.: 1.23e-134 Length: 983
Score: 1266.50 Matches: 263
Percent Similarity: 85.5% Conservative: 20
Best Local Similarity: 79.5% Mismatches: 34
Query Match: 43.8% Indels: 14
DB: 6 Gaps: 7
US-10-628-525A-21 (1-539) x CA252614 (1-983)
QY 116 PheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrVal 135
Db 2 TTTGGCGGTGAACACGAAAGTTACCTTTTCCATGAGTACAGAGATTCAGTTGACTGGGTG 61
QY 136 PheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAla 155
Db 62 TTTGTTGATCATCCCTCATATCACAGACCTGGAATTTATATGAGATAAGTTTGGTGCT 121
QY 156 PheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeu 175
Db 122 TTTGGTGAATAATCAGTTTACAGATACACGCTCTCTTCTATGCTGATGTAGAGCTCTCTTTG 181
QY 176 IleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyr 195
Db 182 GTCCTTGTAATTTGGAGAGATATATTTATGGCGAGAATTCATGCTTTGTTGTGAATGATGG 241
QY 196 HisAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLys 215
Db 242 CATGCCAGTCTAGTGCCAGTCTCTTCTGCTCAAAATATAGACCATATGCTGTTATATAA 301
QY 216 AspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSer 235
Db 302 GACTCCCGCAGCATTTCTTTGTAATACATAATTTAGCACATCAGGGGTGTAGAGCTCGCAAG 361
QY 236 ThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPhePro 255
Db 362 ACATATCTGACCTTGGGTGGCCACTGAATGGTATGAGGCTCTCGAGTGGGTATTCCT 421
QY 256 GluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAla 275
Db 422 GAATGGGCAAGGAGCATGCTCTTCAAGAGGTGAGGCAGCTTTAATTTTGAAGGTGCA 481
QY 276 ValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThrThr 295
Db 482 GTTGTGACAGCAGATCGAATCGTGTGATAGAGGGTTATTCATGGGAGGTCAACT 541
QY 296 AlaGluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGly 315
Db 542 GCTTGAAGTGAACAGGGCTCAATGAGCTCTTAAGCTTCAGAAAGAGGTGTATTAACGGA 601
QY 316 IleValAsnGly-IleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro-- 334
Db 602 ATGGTAAATGGAAATTGACATTAATGATTGGAACCTCGCACGGACAAATGATTCTCTTT 661
QY 335 -CysHisTyrSerValAspAspLeuSerGly-LysAlaLysCysLysGlyAlaLeu--G 353
Db 662 GGCATTATTCTGGGTGATGAACCTTTTGGAAAAAGCAAAATGTAATAATTGCATTGGCA 721
QY 353 LnlLysGluLeuGlyLeuPro--IleArgProAspValProLeu--IleGlyPheIleG 371
Db 722 AAAAGGAACCTGGGGTTTAACCTTTTAAGCCCTAGAAATTCCTCTGAAATGGCTTTT 781
QY 371 Iy-ArgLeuAspTyr-GlnLysGlyIle---AspLeuIleGlnLeuIleIleProAsp-- 388
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```

DB      828 GTTAATG 834
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CK123179      769 bp mRNA linear EST 01-MAR-2004
BES1824102f21 BES1824 Hordeum vulgare subsp. vulgare cDNA clone
MPMGp2010F212 5-PRIME, mRNA sequence.
CK123179
CK123179.1 GI:44806181
EST.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 769)
Kramer,A., Fellner,T., Possling,A., Radchuk,V., Weschke,W.,
Buerkle,L. and Kersten,B.
Application of the protein microarray technology for the
identification of expression library derived target proteins for
barley protein kinase CK2
Unpublished (2003)
Contact: Birgit Kersten* and Winfriede Weschke**
*Plant Protein Chip Group, Department Lehrach, **Department
Molecular Genetics, Gene Expression Group
**Max-Planck-Institute for Molecular Genetics, **Institute of Plant
Genetics and Crop Plant Research Gatersleben
*Inhnestr. 73 , D-14195 Berlin, Germany, **Corrensstrasse 3, D-06466
Gatersleben, Germany
Tel: **49 (0)30/84131648, **449 (0) 394825500
Fax: **49 (0)30/84131128, **449 (0) 394825237
Email: *kersten@molgen.mpg.de, **weschke@ipk-gatersleben.de
Insert Length: 769 Std Error: 0.00
Plate: 2 row: F column: 21
Seq primer: pQES65.
FEATURES
source
Location/Qualifiers
1..769
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/mol_type="mRNA"
/cultivar="Barke"
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/db_xref="taxon:112509"
/clone="WPMGP2010P212"
/tissue_type="embryosac"
/dev_stage="0-10 DAF (days after flowering)"
/lab_host="E. coli, SCS-1/pSE111"
/clone_lib="BES1824"
/note="Vector: pQES30NST (AF074376); Site 1: SalI; Site 2:
NotI; 0-10 DAF (days after flowering), cDNA synthesis
using pBluescript II XR cDNA-library construction kit
(Stratagen) with an oligo(dT)-primer containing NotI
restriction site and a SalI adapter (Invitrogen). The main
library of 21500 clones was rearrayed into the sublibrary
BES 1824 containing 4100 putative expression clones. Note:
Due to a cloning artefact caused by the kit, in most cases
the SalI site is NOT present, as well as the SalI Adapter
used for cloning. To excise the insert, restriction sites
upstream SalI should be used (e.g. BamHI). Average insert
size is 1 kb. Library generation and sequencing was
granted in context of GABI; data are also accessible at
https://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.: 3.59e-131 Length: 769
Score: 1235.00 Matches: 228
Percent Similarity: 93.0% Conservative: 10
Best Local Similarity: 89.1% Mismatches: 17
Query Match: 42.7% Indels: 1
DB: 7 Gaps: 0

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US-10-628-525A-21 (1-539) x CK123179 (1-769)
QY      15  GluGlyIleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSer 34
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DB      4  GAAGGGATTCCTGAGGATTCATCGACACCATAGTGTGGCTGCAAGTGAGCAGGATTCCT 63
QY      35  GluIleValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheVal 54
      |||||
DB      64  GAGATCATGGATGCCAAGCACCACCTCTAGCTAAAGTTACACGTAGCATCGTGTGTTG 123
QY      55  ThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeu 74
      |||||
DB      124  ACTGTGTAAGCTGCTCTTATGCAAGTCAGGGGGCTGGGAGATGTTTGTGTTGTTG 183
QY      75  ProValAlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsn 94
      |||||
DB      184  CCAATTCCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
QY      95  GlyThrSerAspLysAsnTyrAlaAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114
      |||||
DB      244  GGGACCTCTGATATAAAACCTATGCAAGGCATTTATACCCGGGAGCACATTAAGATTCCA 303
QY      115  CysPheGlyGlyGluHisGluValThrPhePheHisGlyTyrArgAspSerValAspTrp 134
      |||||
DB      304  TGCCTTCGGGGGATCATGTAAGTCACCTTTTTCATGAGTATAGAGACAACGTCGATTGG 363
QY      135  ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154
      |||||
DB      364  GTGTTTGTTCATTCATCCATCATATATACACGAGGAGTTTGTATGGAGATTAATTTTGT 423
QY      155  AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174
      |||||
DB      424  GCTTTTGTGTATATCAGTTTCAGATACACATCTTTGCTATGCTGCTGCTGAGGCCCA 483
QY      175  LeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194
      |||||
DB      484  CTAATCCTTGAATTCGGAGGATATATTTATGACAGAGTTGTCATGTTTGTGTAACGAT 543
QY      195  TrpHisAlaSerLeuValProValLeuAlaAlaLysTyrArgProTyrGlyValTyr 214
      |||||
DB      544  TGGCATGCCAGCCTTGTGCCAGTCCTTCTTGTCTGCAAAAGTATAGACCATATGAGATTAC 603
QY      215  LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234
      |||||
DB      604  AGAGATTTCGACGACCATCTTGTATATATATATTTAGACATCAGGGTGTGGAGCTGCA 663
QY      235  SerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTrpValPhe 254
      |||||
DB      664  AGTACATATCCTGATCTGGATTGCCACCTGAATGTTATGGAGCTTTAGATGGGTATTT 723
QY      255  ProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaVal 269
      |||||
DB      724  NCCANAATGGGCAAGAGGCATGCCCNTGACAAGGGGAGGCGGTT 769

RESULT 8
CA199168      672 bp mRNA linear EST 25-SEP-2003
LOCUS SCRFL1010G05.g FL1 Saccharum officinarum cDNA clone SCRFL1010G05
5', mRNA sequence.
VERSION CA199168
CA199168.1 GI:35231161
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1 (bases 1 to 672)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P

```

Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089

Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccenter.fcav.unesp.br  
Plate: 010 row: G column: 05  
Seq primer: T7 Promoter Primer.  
Location/Qualifiers

#### FEATURES

1..672  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clones="SCRLFL1010G05"  
/lab\_host="DH10B"  
/clone\_lib="FL1"

/notes="Organ: Inflorescence at beginning of development (1cm-long); Vector: pSport1; Site 1: Salt; Site 2: NotI; An unidirectional cDNA library generated from [Inflorescence at beginning of development (1cm-long)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"

#### ORIGIN

Alignment Scores:  
Pred. No.: 1.85e-121 Length: 672  
Score: 1150.00 Matches: 217  
Percent Similarity: 97.3% Conservative: 2  
Best Local Similarity: 96.4% Mismatches: 6  
Query Match: 39.8% Indels: 3  
DB: 6 Gaps: 0

US-10-628-525A-21 (1-539) x CA199168 (1-672)

QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102  
DB 1 CACCGTGTGATGGTGTGAATGCCAGCATATTAAATGGTACCTCTGTAGAAATTATGCA 60  
QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGluHisGluVal 122  
DB 61 AATGCAATTTACACAGAAAGCACATTCGGATTCATGCTTTGGCGGTGACACGAAGTT 120  
QY 123 ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyr 142  
DB 121 ACCTTTTCCATGAGTACAGAGATTTCAGTTGACTGGGTGTTTGTTCATCATCTCATAT 180  
QY 143 HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArg 162  
DB 181 CACAGACCTCGAAATTTATATGAGATAAGTTGGTGCTTTTGGTGATAATCATGTTTCTG 240  
QY 163 TyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyr 182  
DB 241 TACACGCTCTCTTGGCTATGCTGATGATGAGGCTCTTTGGTCTCTGAATGGGAGATAT 300  
QY 183 IleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProVal 202  
DB 301 ATTTATGGGCAGAAATTCATGTTTGTGTGAATGATTGGCATGCCAGTCTAGTCCAGTC 360  
QY 203 LeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuVal 222  
DB 361 CTTCTTCTGCGCAAAATATAGACCATATGGTGTATATAAGACTCCCGCAGCATTTCTTGA 420  
QY 223 IleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeu 242  
DB 421 ATACATAATTTAGCACATCAGGGGTAGAGCCTGCAGCACATATCTGACCTTGGGGTTG 480

QY 243 ProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAla 262  
DB 481 CCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTCCTCGAATGGGACGAGCATGCC 540  
QY 263 LeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIle 282  
DB 541 CTTTGACAAGGGTGGGCGAGTTAAATTTTGAAGAGTGCAGTTGTGACAGCAGATCGAATC 600  
QY 283 ValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeu 302  
DB 601 GTGAATTGCAGTAAGGGTTATCA-TGGGAGGGCACCACTGCTGTAAGG-GGACAGGGCCT- 657  
QY 303 AsnGluLeuLeuSer 307  
DB 658 AATGAGCTTTTAGCT 672

RESULT 9  
CO442565  
LOCUS  
DEFINITION MZCCL10045D02.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
ACCESSION CO442565  
VERSION CO442565.1 GI:67013816  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 805)  
AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,P.R. and Arruda,P.  
TITLE Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags  
JOURNAL Plant Mol. Biol. (2005) In press  
COMMENT Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br.

#### FEATURES

1..805  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="F-352 near isogenic line"  
/db\_xref="taxon:4577"  
/sex="hermaphrodite"  
/tissue\_type="endosperm"  
/dev\_stage="multiple stages (10 to 25 days after pollination, see publication for more information)"  
/lab\_host="E. coli DH10B"  
/clone\_lib="Maize Endosperm cDNA Library"  
/note="Organ: seed; Vector: pSPORT1; Site 1: Salt; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -80o C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dt. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001). The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, L20, L25). Unamplified





<http://www.genome.clemson.edu/projects/barley/>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinjof A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

## ORIGIN

Alignment Scores:  
Pred. No.: 2,04e-110 Length: 639  
Score: 1054.00 Matches: 193  
Percent Similarity: 97.1% Conservative: 9  
Best Local Similarity: 92.8% Mismatches: 6  
Query Match: 36.4% Indels: 1  
DB: 3 Gaps: 0

US-10-628-525A-21 (1-539) x BF953855 (1-639)

QY 109 LysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyr 128  
Db 14 AGGACATTAAGATTCATGCTTCGGGGATCATAGAGTACCTTTTTCATGAGTAT 73  
QY 129 ArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeu 148  
Db 74 AGAGACAACGTCGATGGGTGGTGTGTGATCATCATATCATAGACCGAAGTTTG 133  
QY 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168  
Db 134 TATGGAGATAATTTTGGTCTTGGTGGGCGGTGCAGATACACACTACTTTCCTAT 193  
QY 169 AlaAlaCysGluAlaProLeuIleLeuGluGlyTyrIleTyrGlyGlnAsnCys 188  
Db 194 GCTGCTGTGAGCCCCACTAATCTTGTAATGGGAGGATATATTTATGGACAGAGTGC 253  
QY 189 MetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyr 208  
Db 254 ATGTTTGTGTGAACGATGGCATGCCGCTTGTGCCAGTCTCTTCTGTCAGAGTAT 313  
QY 209 ArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHis 228  
Db 314 AGACCATATGGAGTTTACAGAGATCTCGCAGCAGTCTTGTATATACATAATTTAGCACAT 373  
QY 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyrGly 248  
Db 374 CAGGGTGTGAGCCTCGAGTACATATCTGATCTGGATGCCACTCGAATGGTATGGA 433  
QY 249 AlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAla 268  
Db 434 GCTTTAGATGGTATTTCCAGATGGGCAAGAGCATGCCCTTGACAAGGTGAGGCG 493  
QY 269 ValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGly 288  
Db 494 GTTAACCTTTTGAAGAGTGCAGTTGTGACAGCAGATCGAATTTGTGACCTCAGTCAGGG 553  
QY 289 TyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSer 308  
Db 554 TATTCATGGAGGTCAACAATCTGCTGAAGTGGACAGGCGCTCAATGAGCTCTTAAGCTCC 613  
QY 309 ArgLysSerValLeuAsnGlyIle 316  
Db 614 CGAAAAGT-GTCTTGAGTGGATTT 636

## RESULT 12

CV760941  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CV760941  
FGAS05328  
CV760941  
CV760941.1  
EST.  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

833 bp mRNA linear EST 09-NOV-2004  
Triticum aestivum FGAS: Library 2 Gate 3 Triticum  
aestivum cDNA, mRNA sequence.

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.

## REFERENCE

1 (bases 1 to 833)  
Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,  
Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,  
Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D.,  
Penniket,C., Roach,J.L. and Sarhan,F.

## TITLE

Functional Genomics of Abiotic Stress In Wheat and Canola Crops  
Unpublished (2003)

## JOURNAL

## COMMENT

Contact: Wm L Crosby  
Bioinformatics  
University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033  
Email: fgas.estecs.usask.ca

This sequence is the direct result of the Base calling software  
Phred (default parameters). It is the raw base calls. To aid in the  
identification of the high quality insert the software Lucy  
(default parameters) has been run on this sequence. Lucy identified  
the region [98,710].

Plate: WEF025 row: I column: 21.

## FEATURES

source

1..833  
Location/Qualifiers

/organism="Triticum aestivum"

/mol\_type="mRNA"

/db\_xref="taxon:4565"

/clone\_lib="Triticum aestivum FGAS: Library 2 Gate 3"

/note="Organ: Crown and leaf; Vector: pCMV.SPORTS; Aerial  
parts (crown and leaf) of wheat cultivar Norstar from  
control and long exposure times to low temperature. 4 mRNA  
populations were combined before constructing the library;  
7 days non-acclimated plants and 1, 23, and 53 days  
cold-acclimated at 4C. Non-acclimated and cold-acclimated  
plants were grown in vermiculite This is the only library  
that was done according to the Invitrogen manual, and  
therefore, a percentage of clones will not have the 3  
prime end because of NotI digestion within the cDNA."

## ORIGIN

## Alignment Scores:

Pred. No.: 4,04e-110 Length: 833  
Score: 1053.00 Matches: 203  
Percent Similarity: 89.7% Conservative: 14  
Best Local Similarity: 83.9% Mismatches: 24  
Query Match: 36.4% Indels: 2  
DB: 8 Gaps: 0

US-10-628-525A-21 (1-539) x CV760941 (1-833)

QY 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314  
Db 111 ACTGCTGAAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCCGAAAAAGTGTATTGAAT 170  
QY 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIlePro 334  
Db 171 GGAATTTGTAATGGAATTTGACATTAATGATTGGAACCCACCACAGACAAGTGTCTCCCT 230  
QY 335 CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354  
Db 231 CATCATATTCTGTCGATGACCTCTCTGGAAAGGCCAATGTAAAGCTGAATTCAGAG 290  
QY 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374  
Db 291 GAGCTGGGTTTACCTTAAGGGAGGATGTTCTCTGATTGGCTTTTATTGGAAGACTGGAT 350  
QY 375 TyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspVal 394  
Db 351 TACCAGAAAGGCATTGATCTCAATTAATGATGGCCATTCCAGAGCTCATGAGGGAGGACG 410  
QY 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGlu 414



Db 411 CAGTTTGTGATGCTTGGATCCAAATTTTGAAGGCTGGATCAGATCCAG 470  
 Qy 415 SerlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArg 434  
 Db 471 TCGAGTTTACAGGATAAATTCGGTGGATGGGTTGGATTTAGTGTCCAGTTTCCACAGA 530  
 Qy 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454  
 Db 531 ATAACTGCAGGTTCCGATATATTGTAATGCCATCCAGGTTTGAACCTTGGTGTCTTAAT 590  
 Qy 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474  
 Db 591 CAGCTATATGCTATGCAATATGTTACAGTTCCTCTAGTTCATGCAATCTGGGGGCTCGA 650  
 Qy 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAla 494  
 Db 651 GACACAGTCGAGACCTTTCAACCTTTTGGTGCAAAAGGAGAGAGGCTACAGGTTGGGCG 710  
 Qy 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514  
 Db 711 TTCTACCGCTAACCGTGGACAGATGTT-GTGGGCATTGGCAACCGCATGTCCACATT 769  
 Qy 515 GlnGlyThrGlnValLeuLeuGlyArg-AlaAsnGluAlaArgHisValLysArgLeuHi 534  
 Db 770 CAGGAGCACACAGCGCTCTGGGAGGGGCTCATGAGAGGAGGATCACAAGACATA 829  
 Qy 534 sVal 535  
 Db 830 CGTG 833

## RESULT 13

## BM410663

LOCUS 787 bp mRNA linear EST 22-JAN-2002  
 DEFINITION EST584990 tomato breaker fruit Lycopersicon esculentum cDNA clone  
 cLEG54M19 5' end, mRNA sequence.

## ACCESSION

VERSION

KEYWORDS

SOURCE

## ORGANISM

BM410663.1 GI:18262293  
 EST.  
 Lycopersicon esculentum (Solanum lycopersicum)  
 Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

## REFERENCE

## AUTHORS

Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S. A.,  
 Tsai, J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S.,  
 Ronning, C. M., Fraser, C. M., Martin, G. B., Tanksley, S. D. and  
 Giovannoni, J.

## TITLE

## JOURNAL

## COMMENT

Generation of ESTs from tomato fruit tissue, breaker stage (2002)  
 Unpublished (2002)  
 Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 This clone is available through the Clemson University Genomics  
 Institute

Seq primer: T3.

## FEATURES

## source

1..787  
 Location/Qualifiers  
 /organism="Lycopersicon esculentum"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:4081"  
 /clone="cLEG54M19"  
 /tissue\_type="Pericarp"  
 /dev\_stage="breaker"  
 /lab\_host="SOLR"  
 /clone\_lib="tomato breaker fruit"  
 /note="Vector: pBluescriptSKmCuadapt; Site 1: EcoRI;  
 Site 2: XhoI; supplier: Boyce Thompson Institute;  
 sequencing: The Institute for Genomic Research. Fruit  
 were harvested at the breaker stage (first sign of

lycopene accumulation on the blossom end of fruit). Fruit  
 were cut in half and the seeds and locules were discarded  
 prior to freezing the pericarp."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.07e-109 Length: 787  
 Score: 1049.00 Matches: 190  
 Percent Similarity: 86.6% Conservative: 36  
 Best Local Similarity: 72.8% Mismatches: 35  
 Query Match: 36.3% Indels: 1  
 DB: 3 Gaps: 0

US-10-628-525A-21 (1-539) x BM410663 (1-787)

Qy 161 PheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 180  
 Db 1 TTTGCGTCTCACTTGTCTTCTCAGCAGCATGTGAAGCGCATTTGGTTCCTTCCACTGGGA 60  
 Qy 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuVal 200  
 Db 61 GGCTTCACCTTATGGAGAGAAGTGTCTTCTCGCTAATGATTTGGCATGCTTCCCTGGTT 120  
 Qy 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 Db 121 CCTTACTTTTAGCAGCAAGTATCGTCTTATGGTGTTTTACAAGGATGCTCGTAGTATT 180  
 Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 Db 181 GTCGCAATACCAACATTCACATCAGGAGTGGAGCTCGACCACTACCAATAAATTG 240  
 Qy 241 GlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaIleArg 260  
 Db 241 GGATTGCTCTCAATGGTATGATGAGCATTGAATGATATTTCCACATGGCAAGGGCC 300  
 Qy 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280  
 Db 301 CATGCGCTTGACACTGGTGAACAGTGAATGTTTGAAGGGGCAATCTCAGTTGCTGAT 360  
 Qy 281 ArgIleValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGlyGlyGln 300  
 Db 361 CGGATCTAGCAGTTAGCCAGGGATCTCATGGGAATAACAACCTCTCTGAAGGGGGATAT 420  
 Qy 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
 Db 421 GGCTACATGAGCTGCTGAGCAGTACAGTCACTTCTTAATGGAATTACTAATGGATA 480  
 Qy 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
 Db 481 GATGTTAATGATTGGAACCCGTCGACAGATGAGCATATTGCTTCGCATTACTCCATCAAT 540  
 Qy 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuLeuProIle 360  
 Db 541 GACCTCTCTGGAAGGCTCAGTGCAAGACTGATCTGCAAAAGGAATCTGGGCCCTTCCAAT 600  
 Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
 Db 601 CGACCTGATTGCGCTGATTGGATTATTATGGGAAGCTGGACTACCAAGAAAGTGTGTGAC 660  
 Qy 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 Db 661 ATAATCTCTCAGCAATTCAGAACTTTTTCGCAAAAGGATGTCCATTCTGTAATGCTTGA 720  
 Qy 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420  
 Db 721 TCTGGTGAGAAACATAT-GAAGACTGGATGAGACATACAGAGAAATCTTTTAAAGACAAAT 779  
 Qy 421 Phe 421  
 Db 780 TTC 782

## RESULT 14

BM111144

LOCUS BM111144 782 bp mRNA linear EST 10-MAR-2003  
 DEFINITION EST558680 potato roots Solanum tuberosum cDNA clone cPRO10K18 5' end, mRNA sequence.  
 ACCESSION BM111144  
 VERSION BM111144.1 GI:17073444  
 KEYWORDS EST.  
 SOURCE Solanum tuberosum (potato)  
 ORGANISM Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.  
 1 (bases 1 to 782)  
 van der Hoeven, R., Sun, H., Karamycheva, S.A., Teai, J., Van Aken, S., Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.  
 TITLE Generation of ESTs from potato roots  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Robin Buell  
 The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: potato-array@tigr.org  
 This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:  
 http://genome.arizona.edu/orders/  
 Seq primer: T3.  
 FEATURES  
 Location/Qualifiers  
 1..782  
 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec"  
 /db\_xref="taxon:4113"  
 /clone="cPRO10K18"  
 /tissue\_type="roots"  
 /dev\_stage="in vitro grown stem cuttings"  
 /lab\_host="SOLR"  
 /clone\_lib="potato roots"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University, Tanksley lab; sequencing: The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3,99e-109 Length: 782  
 Score: 1044.00 Matches: 186  
 Percent Similarity: 84.1% Conservative: 31  
 Best Local Similarity: 72.1% Mismatches: 41  
 Query Match: 36.1% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-628-525A-21 (1-539) x BM111144 (1-782)  
 QY 115 CysPheGlyGlyGluHisGluThrPhePheHisGluTyArgAspSerValAspTrp 134  
 Db 5 TGCTTTGGTGATGCACAGGAAGTAGCTTCTACCATGATACAGGCGAGGTGTGATGG 64  
 QY 135 ValPheValAspHisProSerTyHisArgProGlyAsnLeuTyGlyAspLysPheGly 154  
 Db 65 GTATTTGTGGACCACTCTTCTTACTGCAGACCTGGAGCCCATATGTTGATATTATGGT 124  
 QY 155 AlaPheGlyAspAsnGlnPheArgTyThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 174  
 Db 125 GCATTTGGTGATGATACAGTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 184  
 QY 175 LeuLeuLeuGluLeuGlyGlyTyTrileTyGlyGlnAsnGlyMetPheValValAsnAsp 194  
 Db 185 TTGGTTCTTCCACTGGAGGGTTCACTTATGATGAGAGAGTGTCTTGTCTCGCTATGAT 244  
 QY 195 TrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyArgProTyGlyValTy 214  
 Db 245 TGGCATGTGCGCCCTGTTCTTCTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 304

QY 215 LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234  
 Db 305 AAGGATGCTCGTAGTATTGTCGAATACACACATTCGCATCAGGAGTGGAGCCTGCA 364  
 QY 235 SerThrTyProAspLeuGlyLeuProGluTrpTyTrGlyAlaLeuGluTrpValPhe 254  
 Db 365 GTAACCTACAATAATTTGGTTTGGCTCCACATGGTATGGAGCAGTTGAATGATATT 424  
 QY 255 ProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
 Db 425 CCACATGGCGAAGGCGCATGCGTTGACACTGGTGAACAGTGAACGTTTGAAGGG 484  
 QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyTrSerTrpGluValThr 294  
 Db 485 GCAATAGCAGTTGCTGATCGGATCTACAGTTAGCCAGGATCTCATCGGGAATAACA 544  
 QY 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314  
 Db 545 ACTCTGGAAGGGGATATGGCTACATGAGCTGTTGAGCAGTAGACAGTCTGTCTTAAT 604  
 QY 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIlePro 334  
 Db 605 CGAATTACTAATGGAATAGATGTTAATGATTGGAACCCGTCGACAGATGAGCATATTGCT 664  
 QY 335 CysHisTyTrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354  
 Db 665 TCGCATTTACTCTCAATCAATGACCTCTCCGAGAGTTTCAGTCGAGACTGATCTGCAAAAG 724  
 QY 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArg 372  
 Db 725 GAACCTGGGCTTCCCATCCGAACCTGATGTCCTCTGATTTGATTTATTGGAAGG 778  
 RESULT 15  
 CD463762  
 LOCUS  
 DEFINITION ETH1\_46\_D07.g1\_A002 Ethylene-treated seedlings Sorghum bicolor cDNA clone ETH1\_46\_D07\_A002 5', mRNA sequence.  
 ACCESSION CD463762  
 VERSION CD463762.1 GI:31385030  
 KEYWORDS EST.  
 SOURCE Sorghum bicolor (sorghum)  
 ORGANISM Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 695)  
 Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R., Chua, Tan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P., Olaseinde, O., Eastman, A. and Pratt, L.H.  
 TITLE An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid (ACC)-treated seedlings  
 JOURNAL Unpublished (2003)  
 COMMENT Other ESTs: ETH1\_46\_D07.b1\_A002  
 Contact: Cordonnier-Pratt, MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmpratt@uga.edu  
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
 Seq primer: Sugs (CTTCTGCTCTAAAGCTGCG).  
 Location/Qualifiers  
 1..695  
 FEATURES  
 source



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Db      87  GGAGATGTTTGTGTTGGTTCGTTGCAATGCTCTGCTCGTGGTCAACGTCGTGATGTT 146
Qy      88  ValMetProArgTrpLeuAenGlyThrSerAspLysAsnTyRalaAsnAlaPheTyThr 107
Db      147  GTAATCCCGAGATACCTTAATGAGGACCTCTGATAAAACATGTCAAAGCATTTATACAC 206
Qy      108  GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127
Db      207  GGGAGCACATTAAGATTCATGCTTCGGGGATCACATGAGTCACCTTTTTCATGAG 266
Qy      128  TyrArgAspSerValAspTrpValPheValAspHisProSerTyRHisArgProGlyAsn 147
Db      267  TATAGAGACACGCTCGATTTGGTGTGTTGTTGATCATCCATCATATCATAGACCAGGA 326
Qy      148  LeuTyGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyThrLeuLeuCys 167
Db      327  TTGTATGGAGATAAATTTTGGTCTTTGTGTGATAATCAGTTTCAGATACACACTACTT 386
Qy      168  TyrAlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyGlyTyRileTyRileTyR 187
Db      387  TATGCTGCTTGTGAGGCCCACTAATCTTGAATGGGAGATATATTTATGGACAGAT 446
Qy      188  CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLys 207
Db      447  TGCATGTTTGTGTGAACGATTTGGCATGCCAGCTTGTGCCAGTCTTCTTGTGCAAG 506
Qy      208  TyrArgProTyGlyValTyRysAspSerArgSerIleLeuValIleHisAsnLeuAla 227
Db      507  TATAGACCATATGGAGATTTACAGAGATTTCTCCAGCATCTCTGTTATATACATAAT 566
Qy      228  HisGlnGlyValGluProAlaSerThrTyRProAspLeuGlyLeuProGluTrpTyR 247
Db      567  CATCAGGTGTGGAGCTGCAAGTACATATCTGATCTGNGATGCGACCTGATGTTAT 626
Qy      248  Gly 248
Db      627  GGA 629

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RESULT 17
LOCUS   CA12E1302IIR
DEFINITION CA12E1302IIR_B02 Cabernet Sauvignon Leaf - CA12E1 linear EST 09-DEC-2002
ACCESSION CA181818
VERSION   CDNA clone CA12E1302IIR_B02 3', mRNA sequence.
KEYWORDS  CA181818.1 GI:26267125
SOURCE    EST:
ORGANISM  Vitis vinifera
          Vitis vinifera
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 877)
AUTHORS   Goes da Silva,F., Lim,H., Iandolo,A., Baek,J., Leslie,A., Xu,J.,
          Jones,K., Walker,M.A. and Cook,D.R.
TITLE      Transcriptional responses of Vitis vinifera to infection by the
JOURNAL    bacterial pathogen Xylella fastidiosa
COMMENT    Unpublished (2003)
          Contact: Doug Cook
          CAES Genome Facility
          UC Davis Department of Plant Pathology
          1 Shields Ave., Davis, CA 95616, USA
          Tel: 530 754 6561
          Fax: 530 754 6617
          Email: drcook@ucdavis.edu
          Seq primer: GCCAACGAATGGTCTAG.
          Location/Qualifiers
            1..877
              /organism="Vitis vinifera"
              /mol_type="mRNA"
              /cultivar="Cabernet Sauvignon"
              /db_xref="taxon:29760"
              /clone="CA12E1302IIR_B02"
FEATURES
source

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/ssex="hermaphrodite"
/dev_stage="Mid-season leaf material"
/lab_host="DH5alpha"
/clone_lib="Cabernet Sauvignon Leaf - CA12E1"
/note="Organ: Leaf; Vector: pDNR; Site 1: SfiI; Site 2:
SfiI; CA12E1 is a cDNA library of Cabernet Sauvignon
leaves. The leaves were collected on July 25, 2001, in
Napa Valley, California, and represent leaves in
mid-season development. These leaves were verified to be
infected with the bacterial pathogen, Xylella fastidiosa,
based on a diagnostic assay using PCR and Xylella-specific
primer pairs. The plants were asymptomatic at the time of
collection, but later developed symptoms. cDNAs were made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGAGATGGCCATTACGCCGGG-3' and
5'-ATTCTAGAGCGGCGCCGACATG-dt(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."

ORIGIN
Alignment Scores:
Pred. No.:      1,32e-107      Length:      877
Score:          1031.50      Matches:    190
Percent Similarity: 83.2%      Conservative: 38
Best Local Similarity: 69.3%      Mismatches: 45
Query Match:    35.7%      Indels:      1
DB:              6              Gaps:        1

US-10-628-525A-21 (1-539) x CA818188 (1-877)
Qy      264  AspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleVal 283
Db      8   GACACGGGCCAAGCTGTCAATCTCTGAAGGTGCTATTGTGACAGTTGATCGGATAC 67
Qy      284  ThrValSerLysGlyTyR-SerTrpGluValThrAlaGluGlyGlnGlyLeuAsn 303
Db      68  ACAGTTAGCAAGGGCTATGCTTGGGAGTAACAACCTCCGAAGTGGATATGTCGTCAT 127
Qy      304  GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323
Db      128  GAGCTCTCTGACACGTCGAAAAGCTGTATAATGGGATCACAATGGTATTGATTTTCC 187
Qy      324  AspTrpAsnProAlaThrAspLysCysIleProCysHisTyR-SerValAspAspLeuSer 343
Db      188  GAATGGATCCATCTCTCAGATGAGCATATTCCTTCCATTACTCTGCTGAAGATCTCT 247
Qy      344  GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363
Db      248  GGGAGGTTCAATGCAAGATGCTTTGCAAGGAATTAGGCTTCCCATTAGGCCGGAT 307
Qy      364  ValProLeuIleGlyPheIleGlyArgLeuAspTyRTrpGlnLysGlyIleAspLeuGln 383
Db      308  TGTCCATTGATGGATTCATTGGGAGATGGGACTACCAAGAAAGGAATCGATGTGATCG 367
Qy      384  LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403
Db      368  TTGGCACTCCAGAGCTTATGGAGAGGACGTCCTCAATTTGGTCTGCTGGGCTCGGAAC 427
Qy      404  ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423
Db      428  CCAGAGGACGAAGAGTGGATGAGAGTGAATCAACATACACAGGACCAAGTTCCCGGT 487
Qy      424  TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443
Db      488  TGGGTGGATTTAATGTCTCCCAATTTTCATAGATAACTGCAAGCTGTGACATCTCTGT 547
Qy      444  MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyRAlaMetGlnTyRThr 463
Db      548  ATGCCATCAGATTCGAACCTTGTGATTAACCAAGCTCTATGCAATGATATGGGGT 607
Qy      604  ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483

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Db      608 GTACCAGTTGTACATGCGACTGGAGGACTCAGAGATACAGTAGAGAAATTTCAATCCATAT 667
Qy      484 GlyGluAenGlyGlu----GlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAen 502
Db      668 GCTGGAGGAGCGCGGTGAAGGACCGGGTGGACGTTTCTCCCTGTCCAAAGACAC 727
Qy      503 MetPheValAspIleAlaAenCysAenIleTyriLeGlnGlyThrGlnValLeuLeuGly 522
Db      728 TATGTCGGCGCACTGAGAGTGTCTATCAGGACATACCGGGAACACAAAGCCCTCTCGGA 787
Qy      523 ArgAlaAenGluAlaArgHisValIleArgLeuHisValGly 536
Db      788 GAGGTTGATGAGAGAGGAGGATGCAAGAGATTATACATGGA 829

RESULT 18
CA020001
LOCUS   HV14A20r HV Hordeum vulgare subsp. vulgare cDNA clone HV14A20
DEFINITION
5-PRIME, mRNA sequence.
CA020001
VERSION 609 bp mRNA linear EST 23-OCT-2002
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 609)
Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
Graner,A.
Barley ESTs from germinating seeds
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 609 Std Error: 0.00
Plate: 14 row: A column: 20
Seq primer: M13rev.
Location/Qualifiers
1..609
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
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/db_xref="GABI:270043"
/db_xref="taxon:112509"
/clone="HV14A20"
/tissue_type="germinating seeds"
/dev_stage="germinating seeds (48-96 h)"
/lab_host="Xl10-Gold"
/clone_lib="HV"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Roots were grown for
two days on filter paper at room temperature. Due to a
cloning artefact caused by the kit, in most cases the
EcoRI site is NOT present as well as the EcoRI adapter
used for cloning. To excise the insert, restriction sites
upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white
selection for recombinants is not 100% reliable.Average
insert size is 1 kb"

Alignment Scores:
Pred. No.: 1.89e-107 Length: 609
Score: 1028.00 Matches: 189
Percent Similarity: 97.5% Conservative: 5
Best Local Similarity: 95.0% Mismatches: 5
Query Match: 35.5% Indels: 0

FEATURES
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1..609
Location/Qualifiers
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/db_xref="taxon:112509"
/clone="HV14A20"
/tissue_type="germinating seeds"
/dev_stage="germinating seeds (48-96 h)"
/lab_host="Xl10-Gold"
/clone_lib="HV"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Roots were grown for
two days on filter paper at room temperature. Due to a
cloning artefact caused by the kit, in most cases the
EcoRI site is NOT present as well as the EcoRI adapter
used for cloning. To excise the insert, restriction sites
upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
NOTE: Also due to the cloning system used Blue/white
selection for recombinants is not 100% reliable.Average
insert size is 1 kb"

ORIGIN
1.89e-107 Length: 609
Score: 1028.00 Matches: 189
Percent Similarity: 97.5% Conservative: 5
Best Local Similarity: 95.0% Mismatches: 5
Query Match: 35.5% Indels: 0

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DB:
US-10-628-525A-21 (1-539) x CA020001 (1-609) Gaps: 0

Qy      161 PheArgTyThrIleuLeuCysTyTrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 180
Db      12 TTCAAGATACACACTACTTTCATGCTATGCTGTGTGTGAGGCCCCCTAAATCCTTGAATTGGGA 71
Qy      181 GlyTyriLeTyGlyGlnAenCysMetPheValValAenAspTrpHisAlaSerLeuVal 200
Db      72 GGATATATTTATGACAGAGATTGCATGTTTGTGTGAACGATGGCATGCCAGCCTTGTG 131
Qy      201 ProValLeuLeuAlaAlaTyTrArgProTyTrGlyValTyTrLysAspSerArgSerIle 220
Db      132 CCAGTCCCTTCTTGCTGCTCAAAAGTATAGACCATATGGAGTTTACAGAGATTCCTCGCAGCACT 191
Qy      221 LeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerThrTyTrProAspLeu 240
Db      192 CTTGTTATATACATAATTTAGCACATCATCAGGGGTGTCAGGCTGCAAGTACATATCCTGTATCTG 251
Qy      241 GlyLeuProProGluTrpTyTrGlyAlaLeuGluTrpValPheProGluTrpAlaAaArg 260
Db      252 GGATTGCCACCTGAATGGTATGAGGCTTTAGAAATGGTATTTCCAGANTGGCGCAAGAGG 311
Qy      261 HisAlaLeuAspLysGlyGluAlaValAenPheLeuLysGlyAlaValValThrAlaAsp 280
Db      312 CATGCCCTTGACAAAGGTGAGGGGTAACTTTTGAAGGTGCAGTTGTGACAGCAGAT 371
Qy      281 ArgIleValThrValSerLysGlyTyTrSerTrpGluValThrThrAlaGluGlyGln 300
Db      372 CGAATTGTGACCGTCACTGAGGCTTATTCATGGGGGTGCACACTGCTGGAAGTGGACAG 431
Qy      301 GlyLeuAenGluLeuLeuSerSerArgLysSerValLeuAenGlyIleValAenGlyIle 320
Db      432 GGCTCAATGAGGCTCTTAAGCTCCCGAAAAGTGTCTTGANTGAATTTGAAATGGAAAT 491
Qy      321 AspIleAenAspTrpAenProAlaThrAspLysCysIleProCysHisTyTrSerValAsp 340
Db      492 GACATTAATGATTGGAACCCACACCGGACAAAGTGTCTCCCTCATCATTTCTGTGAC 551
Qy      341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuPro 359
Db      552 GACCTCTCTGGAAGGCGCAATGTAAAGCTGAATTCAGAGGAGGCTGGGTTTACCT 608

RESULT 19
BJ481805
LOCUS   BJ481805 K. Sato unpublished cDNA library, strain H602 adult,
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
cDNA clone bah61p3 5', mRNA sequence.
BJ481805
ACCESSION BJ481805.1 GI:21160269
VERSION
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare subsp. spontaneum
Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 621)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..621
/organism="Hordeum vulgare subsp. spontaneum"
/mol_type="mRNA"

FEATURES
source
1..621
Location/Qualifiers

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/sub_species="spontaneum"
/db_xref="taxon:77009"
/clone="bah61p3"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"

ORIGIN
Alignment Scores:
Pred. No.: 1.25e-106 Length: 621
Score: 1021.00 Matches: 188
Percent Similarity: 97.0% Conservative: 8
Best Local Similarity: 93.1% Mismatches: 6
Query Match: 35.3% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-21 (1-539) x BU481805 (1-621)
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Db 14 ATTTATGGACAGAGTTCAGATTTGTGTGAACGATTGGCATGCCAGCCTTGTGCCAGTC 73
QY 203 LeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuVal 222
Db 74 CTTCTGCTGCAAGATATAGACCATATGAGTTTACAGAGATCTTCGACGACTCTTGT 133
QY 223 IleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeu 242
Db 134 ATACATAATTTAGCACATCAGGCTGTGGAGCTGCAAGTACATATCTCTGATCTGGGATTG 193
QY 243 ProProGluTTPTrpTyrGlyAlaLeuGluTTPValPheProGluTTPAlaArgHisAla 262
Db 194 CCACCTGAAATGATGAGCTTTAGAAATGGGTATTTCCAGATGGGCAAGAGGCATGCC 253
QY 263 LeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIle 282
Db 254 CTTGACAGGGGTGAGCGGTAACTTTTGAAGGTGCAAGTTGTGACAGCATCGAATT 313
QY 283 ValThrValSerGlyGlyTyrSerTrpGluValThrThrAlaGlnGlyGlyGlnGlyLeu 302
Db 314 GTGACCGTCAGTCAGGGTTATTCATGGGAGGTCAACAATGCTCTGAAGGTGGACAGGCCTC 373
QY 303 AsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIle 322
Db 374 AATGAGCTCTTAAGCTCCCGAAAGAGTGTCTTGAATGGAATTGTAAATGGAATTGACATT 433
QY 323 AsnAspTTPAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeu 342
Db 434 AATGATTGGAACCCACACCGACAGAGTGTCTCCCTCATCATATTCTGTGACGACCTC 493
QY 343 SerGlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362
Db 494 TCTGGAAGGCCCAATTAAGCTGAATTCAGAGAGGAGCTGGTTTACCTGTAAGGGAG 553
QY 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIle 382
Db 554 GATGTTCACACTGATGGCTTTATTGGAAGCTGGATTACCAAGAGGCATTGATCTCAT 613
QY 383 GlnLeu 384
Db 614 AAAATG 619

RESULT 20
BU027679
LOCUS
DEFINITION
BU027679, yq ab1 OH EFHJ sunflower RHA280 Helianthus annuus cDNA
clone OHG7B12, mRNA sequence.
ACCESSION
BU027679
VERSION
BU027679.1 GI:22463199
KEYWORDS
Helianthus annuus (common sunflower)
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ORGANISM Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Helianthus.
REFERENCE 1 (bases 1 to 704)
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Leveille,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,W.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
singleton, see http://cgpdb.ucdavis.edu/ for details.
Plate: OHG7 row: B column: 12.
FEATURES
Location/Qualifiers
1..704
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/note="Vector: pBRCDNA5fiAB: The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG LIB=OH EFHJ sunflower RHA280
TAG_SEQ=TCGCAACGGG"

ORIGIN
Alignment Scores:
Pred. No.: 1.99e-106 Length: 704
Score: 1020.00 Matches: 184
Percent Similarity: 89.3% Conservative: 25
Best Local Similarity: 78.6% Mismatches: 25
Query Match: 35.3% Indels: 0
DB: 5 Gaps: 0

US-10-628-525A-21 (1-539) x BU027679 (1-704)
QY 234 AlaSerThrTyrProAspLeuGlyLeuProGluTTPTrpGlyAlaLeuGluTTPVal 253
Db 1 GCATCACTTACGGCAATTTGGATTGCCCGAATGGTACGAGCTTTGGGTGGGTA 60
QY 254 PheProGluTTPAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLys 273
Db 61 TTTCTCTACTTGGGCAAGAACACATGCTTTGACACCGCGAGGCTGTTAATGTTCTATAA 120
QY 274 GlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluVal 293
Db 121 GGTGCAATTTGTCACCTGCTGACCGGATCTGACAGTTAGCCAGGCTATTCTTGGGAAAT 180
QY 294 ThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeu 313
Db 181 ACACACACAGAGGTGGAAATGGTCTAGACGAGCTTCTTGGTAGTCCGAAGACTGTTTA 240
QY 314 AsnGlyIleValAsnGlyIleAspIleAsnAspTTPAsnProAlaThrAspLysCysIle 333
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Db 241 AATGGATCACAATGGCATTCATTAATGACTGGATTCATCTCTAGATGCCATATC 300  
 Qy 334 ProCysHisTyrSerValAspLeuSerGlyValAlaCysGlyAlaLeuGln 353  
 Db 301 CCTTCTCATTAATCTCTTGTGATGACCTTTTCAGGGAAGATTGAATGCAAGATTGCTCTTCAA 360  
 Qy 354 LysGluLeuGlyLeuProLeuArgProAspValProLeuLeuGlyPheLeuGlyArgLeu 373  
 Db 361 AGGAAATAGGCTCTTCAGTTCGGCCAGATTGTCTCATTTGATGAGTTTATTTGGAGATTG 420  
 Qy 374 AspTyrGlnLysGlyLeuAspLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 393  
 Db 421 GACTACCAAGAGGTATTGACATAATTTCTATCGGAATCCAGAAATTTGTCAGAGATGAT 480  
 Qy 394 ValGlnPheValMetLeuGlySerGlyAspProGluLeuGluLeuLeuLeuLeuLeuLeuLeuLeu 413  
 Db 481 GTTCAGTTTAAATGCTTGGATCCGAGAAATATATATATATATATATATATATATATATATATAT 540  
 Qy 414 GluSerLeuPheLysAspLeuGlyTyrValGlyPheSerValProValSerHis 433  
 Db 541 GAAGCAACGTTTAAAGATAAATTCGCGGATGGTTCGATTCACCGTCCCATATCTCAC 600  
 Qy 434 ArgIleThrAlaGlyCysAspLeuLeuLeuMetProSerArgPheGluProCysGlyLeu 453  
 Db 601 CGATAACACAGAGATGATATATTTACTAATGCCCTCGAGATTCGAGCCATGTGGTTTA 660  
 Qy 454 AsnGluLeuTyrAlaMetGlnTyrGlyThrValProValVal 467  
 Db 661 AATCAGCTGTATGCAATGAGATACGGAACCGTACCAGTGTA 702

## RESULT 21

BM412062 727 bp mRNA linear EST 22-JAN-2002  
 LOCUS tomato breaker fruit Lycopersicon esculentum cDNA clone  
 DEFINITION cLEGS8J10 5' end, mRNA sequence.

ACCESSION BM412062

VERSION 1

KEYWORDS 1 GI:18263692

SOURCE EST.

ORGANISM Lycopersicon esculentum (Solanum lycopersicum)

REFERENCE Lycopersicon esculentum

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 727)

Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A.,

Tsai, J., Bougri, O., Kirkness, E., Uterback, T., Van Aken, S.,

Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and

Giovannoni, J.

Generation of ESTs from tomato fruit tissue, breaker stage (2002)

Unpublished (2002)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics

Institute

Seq primer: T3.

Location/Qualifiers

1. 727

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="cLEGS8J10"

/issue\_type="Pericarp"

/dev\_stage="Breaker"

/lab\_host="SOLR"

/clone\_lib="tomato breaker fruit"

/notes="Vector: pBluescriptSKmCuadapt; Site 1: EcoRI;

Site 2: XhoI; supplier: Boyce Thompson Institute; Fruit

sequencing: The Institute for Genomic Research. Fruit

were harvested at the breaker stage (first sign of

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,64e-106 Length: 727  
 Score: 1017.00 Matches: 181  
 Percent Similarity: 88.4% Conservatives: 33  
 Best Local Similarity: 74.8% Mismatches: 28  
 Query Match: 35.2% Indels: 0  
 DB: 3 Gaps: 0

US-10-628-525A-21 (1-539) x BM412062 (1-727)

Qy 161 PheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLeuLeuGly 180  
 Db 1 TTTGGTTCACCTTGTCTTCTCAGCAGCATGTGAGCGCCATTTCTTCCATCGGA 60  
 Qy 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuVal 200  
 Db 61 GGGTTCACCTTATGAGAGAGTCTGTTTCTCGCTAATGATTGGCATGCTTCCCTGGTT 120  
 Qy 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 Db 121 CCTTTACTTTTAGCAGCAAGTATCGTCTTATGGTGTTTTACAAGGATGCTCGTAGTATT 180  
 Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 Db 181 GTCGCAATACACAACATTCACATCAGGGAGTGGAGCTTCGACCAACCTTCAATATTG 240  
 Qy 241 GlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260  
 Db 241 GGATTGCTCTCAATGATGATGGAGCATTTGAATGATATTTCCACATGGGCAAGGCC 300  
 Qy 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAsp 280  
 Db 301 CATGCGCTTGACACTGCTGTAACAGTGAATGTTTGAAGGGGCAATCTCAGTTGCTGAT 360  
 Qy 281 ArgIleValThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGlyGln 300  
 Db 361 CGATTAATGATGAGTATGAGGAGTACTCATGGGAATTAACAATCTCTGAAGGGGATAT 420  
 Qy 301 GlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
 Db 421 GGGCTACATGAGCTGCTGAGCAGTAGACAGTCACTTCTTAATGATTTACTAATGATTA 480  
 Qy 321 AspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
 Db 481 GATGTTAATGATGGAACCCGTCGACAGATGAGCATATTGCTTCGCATTTACTCCATCAAT 540  
 Qy 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGluLysGluLeuProIle 360  
 Db 541 GACCTCTCTGGAAGAGCTCAGTGCAAGACTGATCTGCAAAAGAACTGGGCTTCCAATT 600  
 Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
 Db 601 CGACCTGATTTGCGCTGATTGGATTATTATGGAAGGCTGAGCTACCAAGAAAGTGTGAC 660  
 Qy 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 Db 661 ATAATCTCTGACCAATTCAGAACTTTTTCAGAGAGGATGTCAATTTGTATGCTTGA 720  
 Qy 401 SerGly 402  
 Db 721 TCTGGT 726

## RESULT 22

AY109714

LOCUS

DEFINITION

AY109714

VERSION

AY109714 2498 bp mRNA linear HTC 25-FEB-2005  
 Zea mays C1171\_2 mRNA sequence.  
 AY109714  
 AY109714.1 GI:21213541

FEATURES  
 source





1710 GGGCGGCGGACCTGGAGGACATCTGGCGGTTTCGAGTGGAGCACAGCAGCANNNNN 1769  
 QY 422 ArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
 Db 1770 NNN  
 QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAlaGlnLeuTyrAlaMetGlnTyr 461  
 Db 1830 CTGCTGATGCGCTCGCGGTTTCGAGCCGTCGGGCTGAACACAGCTCTACGCCATGGCGTAC 1889  
 QY 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn 481  
 Db 1890 GGGACCGTGGCGGTGGTGGCGCGTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  
 QY 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGlu 501  
 Db 1950 CCGTTCAACGACACC-----GGGCTCGGGTGGAGCTTCGACCGCGGGCGGCGAAC 2000  
 QY 502 AsnMetPheValAspIleAlaAsnCys-----AsnIleTyrIleGlnGlyThr 517  
 Db 2001 CGATGATCGACCGGCTCTCGACTGCTCCTCACACGTTACCGGAACCTACAGAGAGAGCTGG 2060  
 QY 518 GlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyPro 537  
 Db 2061 CGCGGCTCGAGGSC-----GGCGGATGCGGCCAGGACCTCAGCTGGGACCA 2108  
 QY 538 CysArg 539  
 Db 2109 CGCGCG 2114

RESULT 23  
 CV765737  
 LOCUS  
 DEFINITION FGAS060124 Triticum aestivum FGAS: Library 2 Gate 3 Triticum  
 aestivum cDNA, mRNA sequence.  
 CV765737  
 EST: CV765737.1 GI:55608403  
 Triticum aestivum (bread wheat)  
 Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 808)  
 Allard, F., Crosby, W.L., Danyluk, J., Rudes, P., Frick, M., Gaudet, D.,  
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Larocche, A.,  
 Linke, M.G., McCarthy, E.L., Montoy, A., Muzak, I., Nilson, D.,  
 Penniket, C., Roach, J.L. and Sarhan, P.  
 Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
 Unpublished (2003)  
 Contact: Wm L Crosby  
 Bioinformatics  
 University of Saskatchewan, Department of Computer Science  
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
 Saskatchewan, S7N 5A9, Canada  
 Tel: 306 966 1769  
 Fax: 306 966 2033  
 Email: fgas\_est@cs.usask.ca  
 This sequence is the direct result of the Base calling software  
 Phred (default parameters). It is the raw base calls. To aid in the  
 identification of the high quality insert the software Lucy  
 (default parameters) has been run on this sequence. Lucy identified  
 the region [97,720].  
 Plate: WEP044 row: L column: 14.  
 Location/Qualifiers  
 1. . 808  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4565"  
 /clone\_lib="Triticum aestivum FGAS: Library 2 Gate 3"  
 /notes="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial  
 parts (crown and leaf) of wheat cultivar Norstar from  
 control and long exposure times to low temperature. 4 mRNA

populations were combined before constructing the library;  
 7 days non-acclimated plants and 1, 23, and 53 days  
 cold-acclimated at 4C. Non-acclimated and cold-acclimated  
 plants were grown in vermiculite. This is the only library  
 that was done according to the Invitrogen manual, and  
 therefore, a percentage of clones will not have the 3  
 prime end because of NotI digestion within the cDNA."

ORIGIN  
 Alignment Scores: 2.07e-105 Length: 808  
 Pred. No.: 1012.00 Matches: 196  
 Score: 89.3% Conservative: 13  
 Best Local Similarity: 83.8% Mismatches: 25  
 Query Match: 35.0% Indels: 2  
 DB: 8 Gaps: 0

US-10-628-525A-21 (1-539) x CV765737 (1-808)

QY 304 GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323  
 Db 108 GAGCTCTTAAGTTCGCCGAAAAGTGTATTGAATGGAATTGTAATGGAATTGATTAAT 167  
 QY 324 AspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSer 343  
 Db 168 GATTGGAAACCCCAACCGGCAAGTGTCTCCCTCATCATTAATTCTGTGATGACCTCTCT 227  
 QY 344 GlyLysAlaLysCysValLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363  
 Db 228 GGAAGGCCAATGTAAAGCTGAATTCAGAGAGCTGGGTTTACCTGTAAAGGAGAT 287  
 QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383  
 Db 288 GTTCTCTGATTGGCTTTATTGGAAGACTGGATTACCAAGAAAGCATTCATTAATAA 347  
 QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403  
 Db 348 ATGCCCATTCAGATCTCATGAGGAGGACGTCAGTTTGTCTGATCTGGATCTGGGGAT 407  
 QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheAspGly 423  
 Db 408 CCAAGTTTGAAGCTGGATGAGATCTACCGAGTCGAGCTACAGGATAAATTCGCGGT 467  
 QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443  
 Db 468 TGGTTTGGATTAGTGTTCAGTTTCCACAGATAAATTCGAGTTTGGATATATTGTTA 527  
 QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463  
 Db 528 ATGCCATCCAGATTCGAACCTTGGCGTCTTAATCAGCTATATCTATGCAATATGGCACA 587  
 QY 464 ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483  
 Db 588 GTTCTCTGATTCATGGAACCTGGGGCCCTCCGAGACACAGTCGAGACCTTCAACCCCTTT 647  
 QY 484 GlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMet 503  
 Db 648 GGTGCAAAAGGAGAGGAGGTACAGGTTGGCGTCTCACCGCTAACCGTGGACAGATG 707  
 QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523  
 Db 708 TT-GTGGGATTCGCAACCGGATGTGACATTCAGGAGGACACAGCCGCTCTGGGAGGG 766  
 QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyPro 537  
 Db 767 GCTCATGAAGGAGGAGCATGACAAAAGACA-TAGCTGGGACCA 807

RESULT 24  
 AV111778  
 LOCUS  
 DEFINITION Zea mays CU171\_1 mRNA sequence.  
 AV111778  
 ACCESSION  
 VERSION  
 Y1111778.1 GI:21216368

KEYWORDS	HTC.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 3248)
AUTHORS	Gardiner,J., Schroeder,S., Polacco,M.L., Sanchez-Villeda,H., Fang,Z., Morgante,M., Landewe,T., Fengler,K., Useche,P., Hanafey,M., Tingey,S., Chou,H., Wing,R., Soderlund,C. and Coe,E.H. Jr.
TITLE	Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization Plant Physiol. 134 (4), 1317-1326 (2004) 15020742
PUBMED	2 (bases 1 to 3248)
REFERENCE	Kainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
AUTHORS	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes Unpublished (2002)
JOURNAL	3 (bases 1 to 3248)
REFERENCE	Coe,E.H.
AUTHORS	Direct Submission
TITLE	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
JOURNAL	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
FEATURES	Location/Qualifiers 1..3248 /organism="Zea mays" /mol_type="mRNA" /db_xref="maizeDB:630529" /db_xref="taxon:4577" /clone_lib="Maize Mapping Project/DuPont Cornsensu Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACS in conjunction with the Maize Mapping Project"
ORIGIN	
Alignment Scores:	
Pred. No.:	3,168-104 Length: 3248
Score:	1010.00 Matches: 232
Percent Similarity:	56.0% Conservative: 73
Best Local Similarity:	42.6% Mismatch: 179
Query Match:	34.9% Indels: 62
DB:	Gaps: 12
US-10-628-525A-21 (1-539) x AY111778 (1-3248)	
QY	10 LeuGlyLeuLnuProGluGlyAlaGluGlySerTleAspAnThrValValala 29 ::: ::: :::
Db	1308 GTTGTCAGATGATGCTGTCTTTTGAACATTATGGGACAAT-----1352
QY	30 SerGluGlnAspSerGluLeuValValGlyLysGluGlnAlaArgAlaLysValThrGln 49         
Db	1353 -----GATCTCGGCCTTTGCCGGGAGAAT-----GTTATG 1385
QY	50 SerIleValPheValThrGlyGluAlaSerProTyrrAlaLysSerGlyGlyLeuGlyVasp 69 ::: ::: :::
Db	1386 AACTGATCGTGGTGGTCTGATGTTCTCATGTGTCGCAAAACAGGTGCTTGGAGAT 1445
QY	70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89 ::: ::: :::



PCR Primers  
 FORWARD: T3 20mer  
 BACKWARD: T7 21mer  
 Plate: 033 row: A column: 05  
 Seq primer: T3 20mer  
 High quality sequence stop: 678.  
 Location/Qualifiers  
 1. .678  
 /organism="Mesembryanthemum crystallinum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3544"  
 /clone="MCT033A05"  
 /tissue\_type="leaf"  
 /dev\_stage="five-week-old"  
 /clone\_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Craesulacean acid metabolism, phase IV (5:30 PM)."  
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

## FEATURES

source

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,15e-103 Length: 678  
 Score: 991.00 Matches: 176  
 Percent Similarity: 88.9% Conservatives: 24  
 Best Local Similarity: 78.2% Mismatches: 25  
 Query Match: 34.3% Indels: 0  
 DB: 6 Gaps: 0

US-10-628-525A-21 (1-539) x CA839938 (1-678)

QY 128 TyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsn 147  
 DB 3 TATAGGATGGTGTTCATTTGGTGGTGTTCATCTCTCTATCAGCGACCTGGAAAT 62  
 QY 148 LeuTyrGlyAspPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys 167  
 DB 63 CCTATGGTGTAGTGTTCCTTGGTGTATATCAGTTCCTGGTTCACCTGCTGTTCG 122  
 QY 168 TyrAlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn 187  
 DB 123 CATGCAGCATGTGAAGCTCTCTGTCTCTCCACTTGGAGGTACACTTATGGGGAAG 182  
 QY 188 CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLys 207  
 DB 183 TGTATGTTCTTGTATATGATGGCATGCAGGCTTGTGCCAGTACTTTTGGCAGCGAAA 242  
 QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227  
 DB 243 TACCTGCTTCAGGAGTATATAAGATGCAAGACTGTACTTGTATACAACTTTT 302  
 QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyr 247  
 DB 303 CATCAAGTGTGGAGCTGCAGTACATATGATACTTAGGACTTCCCGGACCTGGTAC 362  
 QY 248 GlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGlu 267  
 DB 363 GGGTCACCTGGAATGGTGTTCCTGGAGTGGGCAAGACACATGAACTTGACAAAGGTGAA 422  
 QY 268 AlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287  
 DB 423 GCTGTCAATATTTCTTAAGGAGCCATTGTGACTCGGATAGATAATCTACAGTTAGCCAG 482  
 QY 288 GlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307  
 DB 483 GGATATTTCATGGGAATAACAACCTGACAGGTGTGATACGGCTTGCATGAGTTACTAAGC 542  
 QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327  
 DB 543 AGTCGAAAGTTTCGTAAGTGGGATGTAATGGAATTAATPACTTCTGAATGCGACCCA 602

QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLys 347  
 DB 603 TCTACTGTATGACATATTGCAGCTCACTACACTGTTCAGATCTCTCTGTGAAGGCTCAA 662

QY 348 CysLysGlyAlaLeu 352

DB 663 TGCNAAAGCTGACCTG 677

## RESULT 27

BU571816

LOCUS

DEFINITION

946185B04.y1 946 - tassal

mays cDNA, mRNA sequence.

ACCESSION

BU571816

VERSION

BU571816.1

SOURCE

EST.

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 629)

AUTHORS

Walbot,V.

TITLE

Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL

University

COMMENT

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 946185 row: B column: 04.

FEATURES

Location/Qualifiers

1. .629

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="OH43"

/db\_xref="taxon:4577"

/tissue\_type="tassels"

/dev\_stage="just after the transition from vegetative to inflorescence development"

/lab\_host="XLOLR"

/clone\_lib="946 - tassal primordium prepared by Schmidt lab"

/note="Organ: tassels; Vector: HybrizAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybrizAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,02e-102 Length: 629  
 Score: 982.00 Matches: 188  
 Percent Similarity: 99.5% Conservatives: 0  
 Best Local Similarity: 99.5% Mismatches: 1  
 Query Match: 33.9% Indels: 1  
 DB: 5 Gaps: 0

US-10-628-525A-21 (1-539) x BU571816 (1-629)

QY 351 AlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIle 370

DB 6 GCATTGCAGAGGAGCTGGGTTTACCTATAGGCTGATGTTCTCTGATTGGCTTTATT 65

QY 371 GlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMet 390

DB 66 GGAAGGTTGGATTATTCAGAAAGGCGATTATCTCATTCACATTATCATACAGATCTCATG 125

QY 391 ArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMet 410

Db 126 CGGAGAGATGTTCAATTGTCATGCTGGATCTGGTGACCCAGAGCTTGAAGATTGGATG 185

Qy 411 ArgSerThrGluSerIlePheLeuAspLysPheArgGlyTyrPValGlyPheSerValPro 430

Db 186 AGATCTACAGAGTCGATCTTCAAGGATAAATTTCTGGATGGTTGGATTAGTTGTCCA 245

Qy 431 ValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluPro 450

Db 246 GTTTCCTCCACCAATTAACCTGCGGCTGGCATATATTTGTTAAATGCCATCCAGATTCCGAACCT 305

Qy 451 CysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThr 470

Db 306 TGTGCTCTCATACGATATATGCTATGCGATATGCGACAGTTCTTGTTCATGCAACT 365

Qy 471 GlyGlyLeuArgAspThrValGluAenPheAenProPheGlyGluAenGlyGluGlnGly 490

Db 366 GGGGGCTTACAGATACCGTGAGAACTTCAACCTTTCGGTGAGATGGAGACGGGT 425

Qy 491 ThrGlyTyrAlaPheAlaProLeuThrThrGluAenMetPheValAspIleAlaAenCys 510

Db 426 ACAGGGTGGGCAATTCGACCCCTAACACACAGAAACATGTT-GTGGACATTTGCCAATGTC 484

Qy 511 AsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAlaAenHisVal 530

Db 485 AATATCTACATACAGGAGACACAGTCTCTCTGGAGAGGCTAATGAGCGAGCAATGTC 544

Qy 531 LysArgLeuHisValGlyProCysArg 539

Db 545 AAAAGACTTCACGTGGGACCATGCGC 571

## RESULT 28

## BM412224

LOCUS EST586551 tomato breaker fruit Lycopersicon esculentum cDNA clone

DEFINITION cLEGS9110 5' end, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

BM412224 747 bp mRNA linear EST 22-JAN-2002

BM412224.1 GI:18263854

EST.

Lycopersicon esculentum (solanum lycopersicum)

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

## REFERENCE

## AUTHORS

Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S. A., Teai, J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning, C. M., Fraser, C. M., Martin, G. B., Tanksley, S. D. and Giovannoni, J.

Generation of ESTs from tomato fruit tissue, breaker stage (2002)

Unpublished (2002)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

## TITLE

## JOURNAL

## COMMENT

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics Institute

Seq primer: T3.

## FEATURES

## source

1..747

Location/Qualifiers

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="cLEGS9110"

/tissue\_type="Pericarp"

/dev\_stage="breaker"

/lab\_host="SOLR"

/notes lib="tomato breaker fruit"

/clone lib="pBluescriptSKmCuadapt; Site 1: EcoRI; Site 2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of

lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

## ORIGIN

Alignment Scores: 7.86e-102 Length: 747

Pred. No.: 980.50 Matches: 180

Score: 980.50 Conservative: 27

Percent Similarity: 83.1% Mismatches: 41

Best Local Similarity: 72.3% Indels: 2

Query Match: 33.9% Gaps: 1

DB: 3

US-10-628-525A-21 (1-539) x BM412224 (1-747)

Qy 60 ProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAla 79

Db 2 CCATATCTAAGACTGGTGGATAGGAGATGTTTGTGGCTCTTTGCCAATGGCACTAGCT 61

Qy 80 AlaArgGlyHisArgValMetValMetProArgTyrLeuAen---GlyThrSerAsp 98

Db 62 GCTCGGGTTCATCGTGTAAATGGTCTTTACCTAGGTATTTGAATGGAGGTCTCTTCAGAT 121

Qy 99 LysAsnTyrTrlAlaenAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGly 118

Db 122 GAAAAATATGCCAATGCTGTGTACCTTGTGACCTTGTATGTGGGCCACGGTCCATTTGGTGCAT 181

Qy 119 GluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrPheValAsp 138

Db 182 GCACAGAGTAGCTCTTACCATGAATACAGGCGAGGTGTGATGGGTATTTTGTGGAC 241

Qy 139 HisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAsp 158

Db 242 CACTCTCTTACCAGACAGCTGGAACGCCATATGGTGATATTTATGGTGCATTTGGTGAT 301

Qy 159 AsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGlu 178

Db 302 AATCAGTTTGGCTTCACTTTTGTCTTCTCAGCAGCATGTGAAGCGCATTTGGTCTTCCA 361

Qy 179 LeuGlyGlyTyrIleTyrGlyGlnAenCysMetPheValValAenAspTyrHisAlaSer 198

Db 362 CTGGAGAGGTTCACTTATGGAGAGAGTGTCTTCTCTCCTAATGATGGCATGCTTCC 421

Qy 199 LeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArg 218

Db 422 CTGGTTCCTTACTTTTAGCAGCAAGTATCGTCTTATGGTGTTTTACAGAGGATGCTCGT 481

Qy 219 SerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrPro 238

Db 482 AGTATTGTCCCATACACAACTTGCACATCAGGAGTGGAGCTTGCAGCAACCTACAT 541

Qy 239 AspLeuGlyLeuProGluTyrPyrGlyAlaLeuGluTyrValPheProGluTyrAla 258

Db 542 AATTGGGATGCTCTCTCAATGGTATGGAGCACTTGAATGGATATTTTCCACATGGGCA 601

Qy 259 ArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThr 278

Db 602 AGGGCCCATGGCTTGCACACTGCTGGAACAGTGAATGTTTGAAGAGGCAATCTCAGTT 661

Qy 279 AlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGly 298

Db 662 GCTGATCGGATACAGTACAGTTAGCCAGGATACCTCGTGGGAAT-ACAACTCTCTGAAGG 720

Qy 299 GlyGlnGlyLeuAenGluLeuLeuSer 307

Db 721 GGATATGGGCTACATGAGCTGTGAGC 747

## RESULT 29

## LOCUS

## DEFINITION

## ACCESSION

BQ466504 616 bp mRNA linear EST 30-MAY-2002

HT02L1S1r HT Hordeum vulgare subsp. vulgare cDNA clone HT02L1S

5-PRIME, mRNA sequence.

BQ466504

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BQ466504.1 GI:21274286
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
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/lab_host="XL10-Gold"
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/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN
Alignment Scores:
Pred. No.: 1.23e-100 Length: 616
Score: 969.00 Matches: 178
Percent Similarity: 92.6% Conservative: 9
Best Local Similarity: 88.1% Mismatches: 15
Query Match: 33.5% Indels: 0
DB: 5 Gaps: 0

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Db ATTGACATTAATGATTTGAACCCACCGACAAAGTGTCTCCCTCATCATTTCTGTC 125
QY 340 AspAspLeuSerGlyValAlaLysCysValysGlyAlaLeuGlnLysGluLeuGlyLeuPro 359
Db GACGACCTCTCTGGAAGGCCAAATGTAAGCTGAATTCAGAGGAGCTGGGTTTACT 185
QY 360 IleArgProAspValProIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIle 379
Db GTAAGGAGGAGTGTTCACATGATTGGCTTTATTTGGAGACTGATACCAAGAGGCATT 245
QY 380 AspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeu 399
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QY 400 GlySerGlyAspProGluLeuGluAspTTPMetArgSerThrGluSerIlePheLysAsp 419
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QY 420 LysPheArgGlyTTPValGlyPheSerValProValSerHisArgIleThrAlaGlyCys 439
Db AAATTCCTGGATGGGTGGATTTAGTGTTCAGTTTCCACAGATAACTGCGAGGTGC 425
QY 440 AspileLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMet 459
Db GATATATTGTTAATGCCATCCAGATTGAACCTTGGCGTCTTAAATCAGCTATATGCTATG 485
QY 460 GlnTyrGlyThrValProValHisAlaThrGlyGlyLeuArgAspThrValGluAsn 479
Db CAATATGGTACAGTTCCTGTTGTTATGAACTGGGGGCTTCGAGACACGGTGGAGACC 545
QY 480 PheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTTPAlaPheAlaProLeuThr 499
Db TTCAACCTTTTGGTGCAGAGGAGGAGGTACAGGGTGGCGGCTTCACACCTATACC 605
QY 500 ThrGlu 501
Db GTGGAA 611

RESULT 30
CK045789
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ORIGIN
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library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.
CK045789
CK045789.1 GI:58657109
EST.
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 593)
Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
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Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
The Genomes of Oryza sativa: A History of Duplications
PLOS Biol. 3 (2), e38 (2005)
15685292
Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 593
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ORIGIN

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Best Local Similarity:	88.3%	Mismatches:	10
Query Match:	33.3%	Indels:	0
DB:	7	Gaps:	0

US-10-628-525A-21 (1-539) x CK045789 (1-593)

Qy	31	GlulnAspSerGluIleValValGlyLysGluAlaArgAlaLysValThrGlnSer	50
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Qy	51	IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspVal	70
Db	62	GTTGTCTTTCTAAACCGGTGAAGCTTCTCTATGCAAGTCAGGTGAGCTAGGAGATGTT	121
Qy	71	CysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMetPro	90
Db	122	TGTGGTTTCATGCGCAATTGCTTGTCTTCTGTCATCATGTCGTGATGTTGTAATGCCG	181
Qy	91	ArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHis	110
Db	182	AGATACATGACGGGGCTTGAACAAAAATTTTGCACCGCATTTTACACTGAGAGCAC	241
Qy	111	IleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAsp	130
Db	242	ATTAAGATTCCATGCTTTGGCGGAGAACATGAAGTTACTTTTTTTCACGAGTATAGGAT	301
Qy	131	SerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGly	150
Db	302	TCTGTTGAATGGGTGTTTGTGTATCATCCCTCATATCATAGACCTGGAAATTTGTATGGA	361
Qy	151	AspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAla	170
Db	362	GATAATTTTGTGCTTTTGGCGATATACATTGATATACACTCTCTGTCTATGCGCGC	421
Qy	171	CysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPhe	190
Db	422	TGTGAAGCCCATTAATCTTGAACCTGGGAGGATATATCTATGACAGAAATGCATGTTT	481
Qy	191	ValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArgPro	210
Db	482	GTTGTGAATGATGGCATGCCAGTCTTGTGCCAGTCTCTTGTCTGCAAAATATAGACCA	541
Qy	211	TyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla	227
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Search completed: April 1, 2006, 19:23:27

Job time : 8717.03 secs





GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 31, 2006, 22:47:42 ; Search time 720.847 Seconds  
(without alignments)  
1329.139 Million cell updates/sec

Title: US-10-628-525A-21

Perfect score: 2893

Sequence: 1 CVAELSRDLGLPEGIAEG.....LLGRNARHVKLHVGPGR 539

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-LIST=150 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30  
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-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
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Database :

Issued Patents NA:\*

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- 6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/ina/pp COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2861	98.9	1752	3	US-08-941-445A-12
3	2832	97.9	2008	3	US-09-345-214-12
4	2832	97.9	2008	3	US-09-345-214-12
5	2832	97.9	2491	3	US-09-345-214-5
6	2832	97.9	2491	3	US-09-345-214-5
7	2818	97.4	2383	3	US-09-192-909-1
8	2818	97.4	2383	3	US-09-931-297-1
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91	456.5	15.8	6027	3	US-09-554-467A-1	Sequence 1, Appli
92	398.5	13.8	4121	3	US-09-538-524A-1	Sequence 1, Appli
93	394.5	13.6	4122	3	US-10-197-220-84	Sequence 84, Appli
94	392	13.5	1275	3	US-10-163-214-9	Sequence 9, Appli
95	386	13.3	310	3	US-09-118-990A-31	Sequence 31, Appli
96	379.5	13.1	1431	3	US-10-197-220-53	Sequence 53, Appli
97	379.5	13.1	123025	3	US-09-198-452A-1	Sequence 1, Appli
98	379.5	13.1	1230230	3	US-09-438-185A-1	Sequence 1, Appli
99	336.5	11.6	1664976	3	US-08-916-421B-1	Sequence 1, Appli
100	336.5	11.6	1664976	3	US-09-692-570-1	Sequence 1, Appli
101	249.5	8.6	384	3	US-09-118-990A-32	Sequence 32, Appli
102	244.5	8.5	1180	3	US-10-197-220-39	Sequence 39, Appli
103	198	6.8	1664976	3	US-08-916-421B-1	Sequence 1, Appli
104	198	6.8	1664976	3	US-09-692-570-1	Sequence 1, Appli
105	193	6.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
106	193	6.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
107	176.5	6.1	266	3	US-09-313-294A-3737	Sequence 3737, Ap
108	174	6.0	264	3	US-09-107-433-890	Sequence 890, Ap
109	164	5.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
110	164	5.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
111	152.5	5.3	3785	3	US-09-899-718A-1	Sequence 1, Appli
112	151.5	5.2	1293	3	US-09-602-787A-175	Sequence 175, App
113	142.5	4.9	763	3	US-10-197-220-8	Sequence 8, Appli
114	128	4.4	4604	3	US-09-830-807-22	Sequence 22, Appli
115	126	4.4	963	4	US-09-605-703B-2155	Sequence 2155, Ap
116	124.5	4.3	1786	3	US-08-956-171E-618	Sequence 618, App
117	124.5	4.3	1786	3	US-08-781-986A-618	Sequence 618, App
118	121	4.2	1266	3	US-09-602-787A-177	Sequence 177, App
119	116	4.0	540	3	US-09-221-017B-1084	Sequence 1084, Ap
120	114	3.9	1110	3	US-09-543-681A-3342	Sequence 3342, Ap
121	113.5	3.9	2049	3	US-08-481-435-5	Sequence 5, Appli
122	113	3.9	71	2	US-08-572-951-18	Sequence 18, Appli
123	111.5	3.9	1999	3	US-08-961-083-1	Sequence 1, Appli
124	111.5	3.9	1999	3	US-09-536-784-1	Sequence 1, Appli
125	111.5	3.9	1999	3	US-09-765-271-1	Sequence 1, Appli
126	111.5	3.9	1999	3	US-09-765-272A-1	Sequence 1, Appli
127	111.5	3.9	10711	3	US-08-961-527-145	Sequence 145, App
128	110.5	3.8	2260	3	US-09-583-110-1312	Sequence 1312, Ap
129	110.5	3.8	2166	3	US-09-107-433-1102	Sequence 1102, Ap
130	109.5	3.8	30244	3	US-09-949-016-12208	Sequence 12208, A
131	109.5	3.8	30245	3	US-09-949-016-13550	Sequence 13550, A
132	109	3.8	1065	3	US-09-902-540-4644	Sequence 4644, Ap
133	109	3.8	12898	3	US-09-902-540-1000	Sequence 1000, Ap
134	108.5	3.8	1534	2	US-08-588-983-1	Sequence 1, Appli
135	108.5	3.8	1534	2	US-08-588-976-1	Sequence 1, Appli
136	108.5	3.8	2481	2	US-08-290-301-1	Sequence 1, Appli
137	108.5	3.8	2481	3	US-09-013-598-1	Sequence 1, Appli
138	108.5	3.8	2484	2	US-07-841-997A-1	Sequence 1, Appli
139	108	3.7	9992	3	US-09-902-540-952	Sequence 952, App
140	106.5	3.7	2307	3	US-09-949-016-5107	Sequence 5107, Ap
141	106	3.7	1170	3	US-09-902-540-8353	Sequence 8353, Ap
142	106	3.7	6474	3	US-08-961-527-155	Sequence 155, App
143	106	3.7	8056	3	US-09-902-540-874	Sequence 874, App
144	105	3.6	1194	3	US-09-902-540-5572	Sequence 5572, Ap
145	105	3.6	41927	2	US-09-902-540-1268	Sequence 1268, Ap
146	103.5	3.6	2846	2	US-08-365-189-7	Sequence 7, Appli
147	103.5	3.6	2982	2	US-08-365-189-2	Sequence 2, Appli
148	103.5	3.6	2988	2	US-08-365-189-1	Sequence 1, Appli
149	103	3.6	7319	3	US-09-221-017B-510	Sequence 510, App
150	102.5	3.5	660	3	US-09-107-433-1123	Sequence 1123, Ap

ALIGNMENTS

US-08-941-445A-20

Sequence 20, Application US/08941445A

Patent No. 6107060

GENERAL INFORMATION:

APPLICANT: Keeling, Peter

APPLICANT: Guan, Haining

TITLE OF INVENTION: Starch Encapsulation

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/941,445A

FILING DATE: 30-SEP-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/026,855

FILING DATE: 30-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Winner, Ellen P

REGISTRATION NUMBER: 28,547

REFERENCE/DOCKET NUMBER: 89-97

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1620 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: not relevant

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1620

US-08-941-445A-20

Alignment Scores:

Pred. No.: 0

Score: 2893.00

Length: 1620

Matches: 539

Percent Similarity: 100.0%

Conservative: 0

Best Local Similarity: 100.0%

Mismatches: 0

Query Match: 100.0%

Indels: 0

DB: 3

Gaps: 0

US-10-628-525A-21 (1-539) x US-08-941-445A-20 (1-1620)

QY 1 CysValAlaGluLeuSerArgGluAspLeuGluProGluGlyTleAlaGluGly 20

|||||

DB 1 TCGCGTCGGGAGCTGAGCAGGAGGAGCCTCGGCTCTCGAAGGATTCTGAAGGT 60

|||||

QY 21 SerIleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLys 40

|||||

DB 61 TCCATCGATACACAGTAGTTGTGGCAAGTAGCAGAGATTCTGAGATTGTGGTGAAG 120

|||||

QY 41 GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerPro 60

|||||

DB 121 GAGCAAGCTCGAGCTAAAGTAACACAAAGCATTGCTTTGTTAAACCGCGGAGCTTCTCT 180

|||||

QY 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAla 80

|||||

DB 181 TATGCAAAAGTCGGGGGCTTAGGAGATGTTGTGGTTCATTGCCAGTCTCTTCTGCT 240

|||||

QY 81 ArgGlyHisArgValMetValValMetProArgTyrLeuAenGlyThrSerAspLeuAen 100  
DB 241 CGTGGTCAACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACCTCCGATAAGAAT 300  
QY 101 TyrAlaAenAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHis 120  
DB 301 TATGCAATGCATTTTACACAGAAACACACATTCGATTCGATCTTTGGCGGTGAACAT 360  
QY 121 GluValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisPro 140  
DB 361 GAAGTTACCTCTTCCATAGATAGAGATTCAGTTCAGTGGGTGTTTGTGTATCATCCC 420  
QY 141 SerTyrHisArgProGlyAenLeuTyrGlyAspLysPheGlyAlaPheGlyAspAenGln 160  
DB 421 TCATATCACAGACCTGGAAATTTATATGGAGATTAAGTTGGTGTCTTTGGGTGAATCAG 480  
QY 161 PheArgTyrThrLeuLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 180  
DB 481 TTCAGATACACACTCTTGTGCTATGCTGCATGTGAGGCTCTTTGATCCTTGAATGGGA 540  
QY 181 GlyTyrIleTyrGlyGlnAenCysMetPheValValAenAspTyrHisAlaSerLeuVal 200  
DB 541 GGATATATTTATGACAGAAATTCGATGTTGTTGTCATGATGGCATGCCAGTCTAGTG 600  
QY 201 ProValLeuLeuAlaIlySerTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
DB 601 CCAGTCTCTTCTGCTGCANAAATATAGACCATATGTTGTTTATAAAGACTCCCGCAGCAT 660  
QY 221 LeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
DB 661 CTGTGTATACATATTTAGCACATCAGGGTGTAGAGCTGCAGACCATATCTCGACCTT 720  
QY 241 GlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrPalaaArgArg 260  
DB 721 GGGTTGCCACTGAATGGTATGGAGCTCTGAGTGGGTATTCCTCGAATGGCGAGGAGG 780  
QY 261 HisAlaLeuAspLysGlyGluAlaValAenPheLeuLysGlyAlaValAlaThrAlaAsp 280  
DB 781 CATGCCCTTCAGCAAGGTGAGGAGTAAATTTTTGAAAGGTGCGAGTTGTGCACAGCAGAT 840  
QY 281 ArgIleValThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGlyGln 300  
DB 841 CGAATCGTGACTGTCAAGAGGGTTATTCGTGGAGGTCACACTGCTGAAGGTGGACAG 900  
QY 301 GlyLeuAenGluLeuLeuSerSerArgLysSerValLeuAenGlyIleValAenGlyIle 320  
DB 901 GGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACGGAATTTGAATGGAAT 960  
QY 321 AspIleAenAspTyrAenProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
DB 961 GACATTAATGATGGAAACCTGCGCACAGACAAATGTATCCCTGTCAATTTCTGTTGAT 1020  
QY 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360  
DB 1021 GACTCTCTGGAAGGCCAATGTAAAGTGCATTCGAGAGGAGCTGGGTTTACCTTATA 1080  
QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
DB 1081 AGGCGTGTATCTCTGATGGCTTTATTGGAAGGTGGATTTATCAGAAAGGCATTTAT 1140  
QY 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
DB 1141 CTCATTTCACTTATCATACAGATCTCATCGGGAAGATGTTCAATTTGTCTGCTTGA 1200  
QY 401 SerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLys 420  
DB 1201 TCTGGTGACCCAGAGCTTGAAGATTTGGATGGATCTACAGATCGCATTTCAAGGATAA 1260  
QY 421 PheArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
DB 1261 TTTTCGTGGATGGGTGGATTTAGTTTCCAGTTTCCACCGAATACTGCCGCGCTGGAT 1320  
QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAenGlnLeuTyrAlaMetGln 460

DB 1321 ATATTGTTAATGTCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTATATGCTATGCAG 1380  
QY 461 TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAenPhe 480  
DB 1381 TATGGCACAGTTCCTGTGTGTCATGCAACTGGGGGCTTAGAGATACCGTGGAGAACTTC 1440  
QY 481 AsnProPheGlyGluAenGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThr 500  
DB 1441 AACCTTTTCGGTGAGATGAGAGCAGGGTACAGGGTGGGCATTCGCACCCCTAACCCACA 1500  
QY 501 GluAenMetPheValAspIleAlaAenCysAenIleTyrIleGlnGlyThrGlnValLeu 520  
DB 1501 GAAACACATGTTTGTGGACATTTGCACTGCAATATCTACATACAGGGAACAACAAGTCTCT 1560  
QY 521 LeuGlyArgAlaAenGluAlaArgHisValLysValArgLeuHisValGlyProCysArg 539  
DB 1561 CTGGGAAGGGCTAATGAAGCAGGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 1617

## RESULT 2

US-08-941-445A-12  
; Sequence 12, Application US/08941445A  
; Patent No. 6107060  
; GENERAL INFORMATION:  
; APPLICANT: Keeling, Peter  
; APPLICANT: Guan, Hanping  
; TITLE OF INVENTION: Starch Encapsulation  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/941,445A  
FILING DATE: 30-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,855  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 89-97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1752 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: not relevant  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1752  
US-08-941-445A-12

Alignment Scores:  
Pred. No.: 0  
Score: 2861.00  
Percent Similarity: 92.5%  
Length: 1752  
Matches: 539  
Conservative: 0



## US-09-345-214-12

## Alignment Scores:

Pred. No.: 0 Length: 2008  
Score: 2832.00 Matches: 538  
Percent Similarity: 92.3% Conservative: 0  
Best Local Similarity: 92.3% Mismatches: 1  
Query Match: 97.9% Indels: 45  
DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x US-09-345-214-12 (1-2008)

Qy 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 119 TCGTCGCGGAGCTGAGCAGGAGGGCCGCCGCCGCGCTGCGCCACCGCGCTGCTG 178  
Qy 8 ----- 8  
Db 179 GCGCCCCGCTCGTNGCCCGGCTTCTCGCGCGCGCGCGCCGAGCCACGCGGTGAGCCGGCA 238  
Qy 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 239 TCGACGCGCGCGCGCGCGCGCGCGCGCGCTCGGTCTCGAACCTGAGAGGG 298  
Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 299 ATTGCTGAAGGTTCCATCGATTAACACAGTAGTTGTGGCAAGTGAAGAGATTCTGAGATT 358  
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 359 GTGGTGGAAAGGNGCAGCTCGAGCTAAGTAACACAAAGCATTGTCTTTGTAACCGGC 418  
Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 419 GAAGCTTCTCTTATGCANAGTCTGGGGTCTAGGAGATTGTGTGGTTCAATGCCAGTT 478  
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
Db 479 GCTCTGCTGCTGTCACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACC 538  
Qy 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 539 TCCGATPAGAAATATGCANATGCATTTTACACAGAAACACATTCGGATTCATGCTTT 598  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
Db 599 GCGGTGAACATGAAGTTACCTCTTCATGAGTATAGAGATTCAAGTTGAGTGGTGT 658  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
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Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
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Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196  
Db 779 CTTGAATGGGAGGATATATTTATGGACAGAAATTCGATGTTGTGTCAATGATGGCAT 838  
Qy 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 839 GCCAGTCTAGTGCAGTCCTCTTCTGCTGCAAAATATAGACCATATGCTGTTTATAAGAC 898  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 899 TCCGCGAGCATTTCTGTAAATACATATTTAGCATCAGGGGTAGAGCTTCGACAGACA 958  
Qy 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 959 TATCCTGACCTGGGTGGCCACCTGAATGATAGGAGCTCTGGAGTGGGTATTTCCCTGAA 1018  
Qy 257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276

Db 1019 TGGGCGAGGAGGCATGCCCTTGACAAGGGTGAGGCAGTTAATTTTGAAGGTCAGTT 1078  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
Db 1079 GTGACAGCAGATCGAATCGTGACTGTCTGTAAGGGTTATTTCGTGGGAGGTACAACTGCT 1138  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1139 GAAGGTGGACAGGGCCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTTATTAACCGAATT 1198  
Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1199 GTAAATGGAAATGACATTAATGATTGGAAACCTCCACACAGCAAAATGTATCCCTGTGCAT 1258  
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
Db 1259 TATCTGTTGATGATGCTCTCTGAAAGGCCAAATGTAAAGTGATTCATGAGAGAGCTG 1318  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1319 GGTTTACCTATAAGGCTGATGTTCTCTGATTGGCTTTATTGGNAGGTTGGATTATCAG 1378  
Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
Db 1379 AAAGGCATTTGATCTCAATCAACTTATCATACAGATCTCATGCGGGAAGATGTTCAATTT 1438  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
Db 1439 GTCATGCTTGGATCTGCTGACCCAGAGCTTGAAGATTGGATGAGATCTCAGAGATCGATC 1498  
Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
Db 1499 TTCAAGGATAAAATTCGTGATGGGTTGGATTTAGTGTTCAGTTTCCACCCGAATAACT 1558  
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
Db 1559 GCGGCTGGGATATATGTTAATGCCATCCAGATTCGAACTTGTGGTCTCTCAATCAGCTA 1618  
Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
Db 1619 TATGCTATGAGATATGGCAGATTCCTGTGTCATGCCAACTGGGGGCTTAGAGATACC 1678  
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGlnGlyThrGlyTyrPalaPheAla 496  
Db 1679 GTGGAGAACTTCAACCTTTCGGTGAGAAATGGAGAGCAGGGTACAGGTCGGCATTCGCA 1738  
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
Db 1739 CCCTTAACACAGAAACATGTTT-GTGGACATTTGCGAACTGCAATATCTACATACAGGA 1797  
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
Db 1798 ACAAGTCTCTCTGGGAAGGGCTAATGAAGCGGAGCATGTCAAAAGACTTTCACGTGGGA 1857  
Qy 537 ProCysArg 539  
Db 1858 CCATGCCGC 1866

## RESULT 4

US-09-743-980-12  
; Sequence 12, Application US/09743980  
; Patent No. 6570008  
; GENERAL INFORMATION:  
; APPLICANT: E. I. du Pont de Nemours and Company  
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE  
; FILE REFERENCE: BB-1147-A  
; CURRENT APPLICATION NUMBER: US/09/743,980  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 060/094,436  
; PRIOR FILING DATE: 1998-07-28  
; NUMBER OF SEQ ID NOS: 20

! SOFTWARE: Microsoft Office 97  
! SEQ ID NO 12  
! LENGTH: 2008  
! TYPE: DNA  
! ORGANISM: Zea mays  
! US-09-743-980-12

## Alignment Scores:

Pred. No.: 0 Length: 2008  
Score: 2832.00 Matches: 538  
Percent Similarity: 92.3% Conservative: 0  
Best Local Similarity: 92.3% Mismatches: 1  
Query Match: 97.9% Indels: 45  
DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x US-09-743-980-12 (1-2008)

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QY 1 CysValAlaGluLeuSerArgGlu-----8
Db 119 TCGCTCGCGAGCTGAGCAGGAGGGCCGCGCGCGCGCTGCCACCCGCGCTGCTG 178
QY 8 -----8
Db 179 GCGCCCCCGCTCGTGCCTCCCTCTCGCGCGCGCGCGCGCGCGCGCGCGCA 238
QY 9 -----AspLeuGlyLeuGluProGluGly 16
Db 239 TCGACGCCGCCCGCTGCGCGCGCGCGCGCGCTGCGGCTCGGCTCGAACTGAGGG 298
QY 17 IleAlaGluGlySerIleAspAenThrValValAlaSerGluGlnAspSerGluIle 36
Db 299 ATTGCTGAAGGTTCCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 358
QY 37 ValValGlyGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 359 GTGGTTGGAAAGGAGCAGCTCGAGTAAAGTAACACAAAGCATTTGCTTTGTAACCGGC 418
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 419 GAAGCTTCTCCTATGCAAAAGTCTGGGGCTAGGAGATGTTTGGTTTCATTGCCAGTT 478
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96
Db 479 GCTCTTGCTGCTCGTGTCCACCGTGTGATGGTTGTAATGCCCGCAGATATTTAAATGTTACC 538
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
Db 539 TCCGATAAGAAATTATGCAAAATGATTTTACACAGAAAAACACATTGGGATTCATGCTTT 598
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136
Db 599 GCGGTGAACATGAGTTACCTTCTCCATGAGTATAGAGATTTCAGTTGACTGGGTGTTT 658
QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156
Db 659 GTTGATCATCCCTCATATCACAGACCTGGAATTTATATGAGATAAAGTTTGGTCTTTT 718
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 719 GGTGATAATCAGTTCAGATACACATCTCTTGTGCTATGCTGCTATGAGGCTCCTTTGATC 778
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196
Db 779 CTTGTAATGGGAGGATATATTTATGGACAGAAATTGCATGTTTGTCTCAATGATGGCAT 838
QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 839 GCCAGTCTAGTGCCAGTCTCTTCTGCTGCAAAATATAGACCATATGTTTATATAAGAC 898
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 899 TCCCGCAGCATCTTGTGTAATACATAATTTAGCACATCAGGGGTGAGAGCTCGAAGCACA 958
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Db 959 TATCTTGACCTTGGGTGGCCACTGAATGTTATGGAGCTCTGGAGTGGGTATTCCTCGAA 1018
QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
Db 1019 TGGCGCAGGAGCATGCCCTTGACAAGGCTGAGGCAGTTAAATTTTTTGAAGGTGCAGTT 1078
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
Db 1079 GTGACAGCAGATCGAATCGTGACTGCTGAGTAAGGGTTATTCGTGGAGGTCACACTGCT 1138
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316
Db 1139 GAAGGTGGACAGGGCTCAATGAGCTTTAAGCTCCAGAAAGAGTGTATTAAACGGAATT 1198
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 1199 GTAAATGGAATTCACATTAATGATTGGAACCTGCGCACAGACAAATGTATCCCTGTCAT 1258
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 1259 TATCTGTTGATGACTCTCTGGAAGGCCAAATGTAAGGTGCATTGAGAGGAGCTG 1318
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1319 GGTTTACCTATGAAGGCTGATGTTCTCTGATGCTTTATTGGAAGTTGGATATATCAG 1378
QY 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1379 AAAGGCATTGATCTCATTCATTCATCAGATCTCATCGGGAAGATGTTCAATTT 1438
QY 397 ValMetLeuGlySerCysLysProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
Db 1439 GTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1498
QY 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
Db 1499 TTCAGGATTAATTTCTGGATGGGTGGATTGATTTAGTTTCAGTTTCCACCGAATAACT 1558
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1559 GCGCGCTCGATATATTGTTAATGTCATCCAGATCTCGAACCTTGTGCTCAATCAGCTA 1618
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1619 TATGCTATGAGTATGGCACAGTCTCTGTGTCCATGCAACTGGGGGCTTAGAGATACC 1678
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496
Db 1679 GTGGAGAACTTCAACCTTTCGTCGAGATGGAGAGCAGGGTACAGGGTGGGCATTCGCA 1738
QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
Db 1739 CCCCTAAACACAGAAAAACATGTT-GTGGACATTGGCACTGCAATATCTACATACAGGA 1797
QY 517 ThrGlnValLeuLeuGlyValArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 1798 ACACAGTCTCTCTGGGAAGGGCTAATGAAGCGAGCATGTCAAAGACATTCACGTGGGA 1857
QY 537 ProCysArg 539
Db 1858 CCATGCCGC 1866
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## RESULT 5

US-09-345-214-5  
; Sequence 5, Application US/09345214  
; Patent No. 6392120  
; GENERAL INFORMATION:  
; APPLICANT: Lightner, Jonathan E.  
; APPLICANT: Broglie, Karen E.  
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE  
; TITLE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS











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QY 337 TyrSerValAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
DB 1286 TATTCCTGTTGATGACCTCTCTGGAAGGCCAAATGTAAGTGTCATTCGAGAGGAGCTG 1345
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
DB 1346 GGTTCACCTATAAGGCGCTGATGTTCTCTGATTTGGCTTTATTGGAAGATTGGATTATCAG 1405
QY 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396
DB 1406 AAAGGCATTGATCTCAATCAACTATATACACAGATCTCATCGGGAAGATTGTTCAATTT 1465
QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416
DB 1466 GTCATGCTTGGATCTGGTACCCAGAGCTTGAGATTGGATGGATCTACAGATCGATC 1525
QY 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436
DB 1526 TTCAAGGATAAATTTCTGTGATGGGTTGGATTAGTGTTCAGTTTCCACCGAATAACT 1585
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
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QY 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
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QY 537 ProCysArg 539
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RESULT 8
US-09-931-297-1
; Sequence 1, Application US/09931297
; Patent No. 6635804
; GENERAL INFORMATION:
; APPLICANT: Jens Kossmann
; TITLE OF INVENTION: Nucleic acid molecules encoding soluble
; starch synthases from maize
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/931,297
; FILING DATE: 16-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/192,909
; FILING DATE: <Unknown>
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; APPLICATION NUMBER: DE 196 19 918.2
; FILING DATE: 17-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley, Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: GFB-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-96-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2383 base pairs
; TYPE: nucleotide
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; TISSUE TYPE: endosperm
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..1950
; OTHER INFORMATION: /function= "starch synthesis"
; /product= "soluble starch synthase"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-931-297-1

Alignment Scores:
Pred. No.: 0 Length: 2383
Score: 2818.00 Matches: 534
Percent Similarity: 92.1% Conservative: 3
Best Local Similarity: 91.6% Mismatches: 2
Query Match: 97.4% Indels: 45
DB: 3 Gaps: 1

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QY 9 ----- 9
DB 206 GCGCCCGCTCGTGCCTCGCGCTTCCTCGCGCGCGCGCGAGCGGCGAGCGCGCA 265
QY 10 -----LeuGlyLeuGluProGluGly 16
DB 266 TTGACGCGCGCGCGCTGCGCGACGCGCGCTGGGGGTCTCTCGGTGCGAACCTGAAGG 325
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36
DB 326 ATTGCTGAAGGTTCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 385
QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
DB 386 GTGGTTGGAAGAGCAGCTCGACTAAGTAACACAAACATTTGTCTTTGTAAGTGGC 445
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
DB 446 GAAGCTTCTCTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGTTTCATTCAGATT 505
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96
DB 506 GCTCTTGCTGCTCGTGGTCCACCGTGTGATGGTTGTAATGCCAGATATTTAAATGGTACC 565
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
DB 566 TCCGATAGAAATTATGCAATGTCATTTTACACAGAAACACATTCGGATTTCATGCTTT 625
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136
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Db 626 GCGCGTGAACATGATTACCTCTTCATCATGAGTATAGAGATTGAGTTCAGTGGGTGTTT 685  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 686 GTTGATCATCTCATATACAGACCTTGAATAATTTATATGAGATAGATTGGTGGCTTTT 745  
Qy 157 GlyAspGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLeu 176  
Db 746 GGTGATTAATCAGTTTCAGATACACACTCTTTTGGCTATGCTGATGAGGCTCTTTGGTC 805  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
Db 806 CTTCGAATGGGAGGATATATTATAGACAGATTGCAATTTGTTGTTGTTCAATGATTGGCAT 865  
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 866 GCCAGTCTAGTGGCAGTCTCTTGTCTGCAAAATATAGACCATATGTTGTTTATAAGAC 925  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
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Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
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Qy 277 ValThrAlaAspArgIleValThrValSerIysGlyTyrSerTrpGluValThrAla 296  
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Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
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Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1226 GTAAATGGAAATGACATTAATGATTGGAACCTGCCACAGCAAAATGTATCCCTGTGCAT 1285  
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
Db 1286 TATTCCTGTGATCACTCTCTGGAAGGCCAAATGTAAAGGTGCATTCGAGAAGGAGCTG 1345  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
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Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
Db 1406 AAAGGCAATGATCTCATTAACCTATCATACAGATCTCATGCGGGAAGATGTTCAATTT 1465  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
Db 1466 GTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1525  
Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
Db 1526 TTCAGAGATAAATTTGTTGATGGGTTGGATTAGTTGTTCCAGTTTCCACCGCAATAACT 1585  
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
Db 1586 GCGGCTGCGATATATTTGTTAATGCCATCCAGATTCGAACTTGTGTTCTCAATCAGCTA 1645  
Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
Db 1646 TATGCTATGCAATGATGCGCAGTTCCTGTTGTCTCATGCAACTGGGGGCTCTAGAGATACC 1705  
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
Db 1706 GTGGAGAACTTCAACCTTTTCGGTGAGAAATGGAGACAGGGGTACAGGGGTGGCATTCGCA 1765

Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
Db 1766 CCCCTAACCAACAGAAACATGTTTGTGACATTCGGAACCTGCAATATCTACATACAGGA 1824  
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
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Qy 537 ProCysArg 539  
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RESULT 9  
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; Sequence 1, Application US/08572951  
; Patent No. 5824790  
; GENERAL INFORMATION:  
; APPLICANT: KEELING, PETER L.  
; APPLICANT: KNIGHT, MARY E.  
; APPLICANT: GUAN, HANPING  
; TITLE OF INVENTION: MODIFICATION OF STARCH  
; TITLE OF INVENTION: SYNTHESIS IN PLANTS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN  
; ADDRESSEE: Intellectual Property Group of  
; ADDRESSEE: Pillsbury Madison & Sutro LLP  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/572,951  
; FILING DATE: 15-DEC-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/346,602  
; FILING DATE: 29-NOV-1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/263,921  
; FILING DATE: 21-JUN-1994  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul N. Kokulis  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 222957/1.02.15C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2990 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-572-951-1  
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Pred. No.: 8,45e-316 Length: 2990  
Score: 2757.00 Matches: 523  
Percent Similarity: 90.9% Conservatives: 8  
Best Local Similarity: 89.6% Mismatches: 8  
Query Match: 95.3% Indels: 45  
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QY	37 ValValGlyGlyGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
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QY	57 GluAlaSerPro-TyrAlaLysSerGlyGlyLeuGlyVAspValCysGlySerLeuProVa 76
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QY	136 eValAspHisProSerTyrHisArgProGlyAenLeuTyrGlyAspLysPheGlyAlaPh 156
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Db	1498 CTCGCGCAGCATCTTGTATATACATAATTTAGCACATCAGGGGTAGAGCCCTGCAAGCAC 1557
QY	236 rTyrProAspLeuGlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGl 256
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QY	256 uTrpAlaArgAHisAlaLeuAspLysGlyGluAlaValAenPheLeuLysGlyAlaVa 276
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QY	276 lValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThrThrAl 296
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QY	296 aGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAenGlyIl 316
Db	1738 TGAAGGTGGACAGGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACCGGAAT 1797
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Db	2338 ACCCTTAACACAGAAACATGTTTGTGGACATTGCGAACTGCAATATCTACATACAGGG 2397
QY	516 YThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHisValLysArgLeuHisValGl 536
Db	2398 AACACAGTAAATATGGGAAGGCTAATGAGCCAGGCAATGTCMAAAGAGTTCACTGGG 2457
QY	536 YProCysArg 539
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RESULT 10	
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; Sequence 6, Application US/09345214	
; Patent No. 6392120	
; GENERAL INFORMATION:	
; APPLICANT: Lightner, Jonathan E.	
; APPLICANT: Broglie, Karen E.	
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE	
; FILE REFERENCE: BB-1147	
; CURRENT APPLICATION NUMBER: US/09/345,214	
; CURRENT FILING DATE: 1999-06-30	
; EARLIER APPLICATION NUMBER: 060/094,436	
; EARLIER FILING DATE: 1998-07-28	
; NUMBER OF SEQ ID NOS: 20	
; SOFTWARE: Microsoft Office 97	
; SEQ ID NO 6	
; LENGTH: 1528	
; TYPE: DNA	
; ORGANISM: Zea mays	
US-09-345-214-6	
Alignment Scores:	

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Pred. No.: 3,44e-304 Length: 1528
Score: 2655.00 Matches: 495
Percent Similarity: 99.8% Conservative: 0
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 91.8% Indels: 1
DB: 3 Gaps: 0

US-10-628-525A-21 (1-539) x US-09-345-214-6 (1-1528)

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DB 1527 CGAGCTAAAGTAACACAAAGCATTTGCTTTGTAACCGCGGGAAGCTTCTCTATGCAAG 1468
QY 64 SerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArgGlyHis 83
DB 1467 TCTGGGGGTCTAGGAGATGTTTGGTTCATTTGCCAGTTGCTCTGTGCTGCTGCAC 1408
QY 84 ArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsn 103
DB 1407 CGTGTGATGTTGTAATGCCAGATATTTAAATGGTACCTCCGATGAAGAAATTAATGCAAT 1348
QY 104 AlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThr 123
DB 1347 GCATTTTACACAGAAAACACATTCGATTCGATGCTTTGGCGGTGNAACATGAAGTTACC 1288
QY 124 PhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSerTyrHis 143
DB 1287 TTCTTCCATGAGTATGAGATTCAGTTGATGCGGTGTTTGTGATCATCCCTCATATCAC 1228
QY 144 ArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr 163
DB 1227 AGACCTGGAAATTTATGAGATAGTATGTTGGTGTCTTTGGTGATTAATCAGTTTCAGATAC 1168
QY 164 ThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyTyrIle 183
DB 1167 ACACTCCTTTGCTATGCTGCATGTGAGGCTCCTTTGATCCTTGAATGGGAGGATATAT 1108
QY 184 TyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValProValLeu 203
DB 1107 TATGGACAGAAATGCAATGTTGTGTGTAATGATGGCATGCCAGTCTAGTGCAGTCTCT 1048
QY 204 LeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIle 223
DB 1047 CTGTGCAAAATATAGACATATGTTGTTTAAAGATCCCGCAGCATTTCTGTAATA 988
QY 224 HisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuPro 243
DB 987 CATAATTTAGCACATCAGGTTGTAGAGCTTGCAGCACATATCCTGACCTTGGTTGCCA 928
QY 244 ProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgHisAlaLeu 263
DB 927 CCTGAATGTTATGGAGCTCTGGAGTGGGTATTCCTGTAATGGCGAGGAGGCATGCCCTT 868
QY 264 AspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleVal 283
DB 867 GACAGGGGTGAGCAGTTAATTTTGAAGGTGCAGTTGTGACACAGCATCGAATCGTG 808
QY 284 ThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGlnGlyLeuAsn 303
DB 807 ACTGTCAAGTAAGGTTATTCGTGGAGGTTCACATGCTGTAAGGTGCAAGGCTCTCAAT 748
QY 304 GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323
DB 747 GAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGGAATTTGTAATGGAATTCACATTAAT 688
QY 324 AspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspLeuSer 343
DB 687 GATTGACCCCTGCCACACAAATGTATCCCTGTGTCATATTCGTGATGACCTCTCT 628
QY 344 GlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363
DB 627 GGAAGGCCCAATGTAAAGTGCATTTGCAGAGGAGCTGGGTTTACCTATTAAGGCTGAT 568
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QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383
DB 567 GTTCTCTCTGATGGCTTTATTTGGAAGGTTGGATTATCAGAAAGCATTTGATCTCATTTCAA 508
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403
DB 507 CTTATCATACCAGATCTCATGCGGAAGATGTTCAATTTGTCTGCTGGATCTGGTGAC 448
QY 404 ProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPheAspGly 423
DB 447 CCAGAGCTTGAAGATTTGGATGAGATCTACAGAGTCGATCTTCAAGGATAAATTTCTGTTGA 388
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443
DB 387 TGGTTGGATTTAGTGTTCAGTTTCCCAACCGAATAACTGCCGCTGCGATATATTGTTA 328
QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
DB 327 ATGCCATCCAGATTCGAACCTTTGTGTCTCAATCAGCTATATGCTATGCAATATGGCACA 268
QY 464 ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483
DB 267 GTTCTGTTGTCTCATGCAACTGGGGCCCTAGAGATCCGTTGAGAACTTCAACCTTTTC 208
QY 484 GlyLeuAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503
DB 207 CGTGAGATGGAGAGCAGGTTACAGGTTGGCATTCGCACCCCTAACACACAGAAACATG 148
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523
DB 147 TT-GTGGACATTTGCCAACTGCAATATCTATACACAGGGAACCAAGTCTCTCTGGGAAGG 89
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
DB 88 GCTAATGAAGCGAGCATGTCTAAAGACTTTCAGTGGGACCATGCCGC 41
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## RESULT 11

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US-09-743-980-6/c
; Sequence 6, Application US/09743980
; Patent No. 6570008
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; TITLE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS
; FILE REFERENCE: BB-1147-A
; CURRENT APPLICATION NUMBER: US/09/743,980
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 060/094,436
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1528
; TYPE: DNA
; ORGANISM: Zea mays
US-09-743-980-6
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Alignment Scores:
Pred. No.: 3,44e-304 Length: 1528
Score: 2655.00 Matches: 495
Percent Similarity: 99.8% Conservative: 0
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 91.8% Indels: 1
DB: 3 Gaps: 0
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US-10-628-525A-21 (1-539) x US-09-743-980-6 (1-1528)

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QY 44 ArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLys 63
DB 1527 CGAGCTAAAGTAACACAAAGCATTTGCTTTGTAACCGGGAAGCTTCTCTATGCAAG 1468
QY 64 SerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArgGlyHis 83
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1467 TCTGGGGCTAGGAGATGTTTGTGGTTCATTGCGCAGTTGCTCTTCTGCTCGTGGTCAC 1408  
QY 84 ArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsn 103  
Db 1407 CGTGTGATGGTTGTAATGCGCCAGATATTTAAATGGTACCTCCGATGAAGAAATATGCAAT 1348  
QY 104 AlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyClyHisGluValThr 123  
Db 1347 GCATTTTACACAGAAACACATTCGGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 1288  
QY 124 PhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSerTyrHis 143  
Db 1287 TTCTTCCATGAGTATAGAGATTGAGTTGATTCGATTCGATTCGATTCGATTCGATTCGAT 1228  
QY 144 ArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr 163  
Db 1227 AGACCTGGAAATTTATATGAGATAGATTGGTGGCTTTGGTGGTAAATCAGTTCCAGATAC 1168  
QY 164 ThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIle 183  
Db 1167 ACATCTCTTGTATGCTGCATGTGAGGCTCTTTGATCTTGAATTTGGAGGATATATT 1108  
QY 184 TyrGlyGlnAsnCysMetPheValValAsnAspTyrPheAlaSerLeuValProValLeu 203  
Db 1107 TATGGACAGAAATGCAATGTTGTGTCAATGATTGGCATGCCAGTCTAGTGCAGTCCCTT 1048  
QY 204 LeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIle 223  
Db 1047 CTTGCTGCAAAATATAGACCATATGGTGTATTAAGACTCCCGCAGCATTTCTTGAATA 988  
QY 224 HisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuPro 243  
Db 987 CATATTTAGCACATCAGGGGTAGAGCTGCAGCACATATCTGACCTTGGGTGGCA 928  
QY 244 ProGluTyrPyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeu 263  
Db 927 CTTGAATGTAATGGAGCTCTGAGTGGGTATTTCCCTGAATGGCGGAGGAGCATGCCCTT 868  
QY 264 AspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleVal 283  
Db 867 GACAGAGGTGAGGCAAGTTAAATTTTGAAGGTGCAGTTGTGACAGCATCGAATCGTG 808  
QY 284 ThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGlyGlnGlyLeuAsn 303  
Db 807 ACTGTCAGTAAGGTTATTCGTGGAGGTCAACATGCTGAAGGTGGACAGGGCTCTCAAT 748  
QY 304 GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323  
Db 747 GAGCTCTTAAAGCTCCAGAAAGAGTGTATTAACCGGAATTTGAATGGAATTCACATTAAT 688  
QY 324 AspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSer 343  
Db 687 GATTGGAACCTGCCACAGCAAAATGTATCCCTGTCTATTTCTGTGATGACCTCTCT 628  
QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363  
Db 627 GGAAGGCCAATGTAAAGTTCATTCGAGAGGAGTGGGTTTACCTATAAGGCTGTAT 568  
QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383  
Db 567 GTTCTCTGATTTGCTTTTATGGAAGTTGGATTATCAGAAAGGCATTCATCTCATTA 508  
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403  
Db 507 CTTATCATACCAAGTCTCATGCGGAAGATGTCAATTTGTCTGATCTGGATCTGGTGAC 448  
QY 404 ProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423  
Db 447 CCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCAATCTTCAGAGATAAATTTCTGGA 388  
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443  
Db 387 TGGGTTGGATTTAGTGTTCAGTTTCCCACCAATAAAGTCCCGGCTGGCATATATTGTTA 328

QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463  
Db 327 ATGCCATCCAGATTCGAACCTTGTGTCTCAATCAGCTATATGCTATGATGATGCGACA 268  
QY 464 ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483  
Db 267 GTTCTGTGTTCATGCAACTGGGGGCTTACAGATACCGTGGAGAACTTCAACCCCTTC 208  
QY 484 GlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503  
Db 207 GGTGAGATGGAGAGCAGGGTACAGGGTGGGCATTCGCACCCCTTAACACACAGAAACATG 148  
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523  
Db 147 TT-GTGGACATTCGCAACTGCAATATCTACATACAGGGAACACAAATCTCTCTGGGAAG 89  
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
Db 88 GCTAATGAAGCGAGCGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 41

## RESULT 12

US-09-508-377-11  
; Sequence 11, Application US/09508377  
; Patent No. 6916976  
; GENERAL INFORMATION:  
; APPLICANT: KALEEN, ZHONGYILI  
; APPLICANT: MORELL, MATTHEW  
; APPLICANT: RAHMAN, SADEQU  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 054270/0126  
; CURRENT APPLICATION NUMBER: US/09/508,377  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: AU PP 2509  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: PCT/AU98/00743  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: AU PP 9108  
; PRIOR FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 2662  
; TYPE: DNA  
; ORGANISM: Triticum tauschii  
US-09-508-377-11

## Alignment Scores:

Pred. No.:	1,448-281	Length:	2662
Score:	2467.50	Matches:	464
Percent Similarity:	91.8%	Conservative:	30
Best Local Similarity:	86.2%	Mismatches:	41
Query Match:	85.3%	Indels:	4
DB:	3	Gaps:	2

US-10-628-525A-21 (1-539) x US-09-508-377-11 (1-2662)

QY 2 ValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySer 21  
Db 539 GTGGGGGAACCTCGCG---CCGACCTCTGCTC-----GAAGGGATTGCTGAGGATTC 589  
QY 22 IleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGlu 41  
Db 590 ATCGACAGCAATAATGTTGGTGGTGAAGTGAAGGATTCAGATCATGATCGGAATGAG 649  
QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
Db 650 CAACCTCAAGCTAAAGTTACAGTAGCATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 709  
QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg 81  
Db 710 GCAAGTCAAGGGGCTGGGAGATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769

QY 82 GlyHisArgValMetValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
Db 770 GGTCAACGCTGGATGGTGTGAATGCCAAGTACTTGAATGGCTCTCTGTAATAAACTAT 829  
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
Db 830 GCAAGGCAATATACATCTGGNAGCACATTAAGATTTCATGCTTTGGGGGATCACATGAA 889  
QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer 141  
Db 890 GTGACCTTTTTCATGAGTATAGACACACGTCGATTGGGTGTGTGTCGATCATCCGTCA 949  
QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
Db 950 TATCATAGACAGAGATTTATATGGAGATAATTTTGGTGTCTTTGTGTGATAATCATGTTT 1009  
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGly 181  
Db 1010 AGATACACATCTCTGCTATGCTGATGCGAGGCCCATTAATCTTGAATTGGGAGGA 1069  
QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValPro 201  
Db 1070 TATATTTATGACAGAAATTCGATGTTTGTGTGAACGATTGGCATGCCAGCTTTGTGCCA 1129  
QY 202 ValLeuLeuAlaIalysTyrArgProTyrGlyValTyrIlyAspSerArgSerIleLeu 221  
Db 1130 GTCTCTTCTGCTGCAAAATATAGACCATACGGTGTTTACAGAGATTCCTCCGACGACCTT 1189  
QY 222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
Db 1190 GTTATACATATTTAGACATCAGGCTCTGGAGCTCGCATATCTCTGATCTGGGA 1249  
QY 242 LeuProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHis 261  
Db 1250 TTGCCACCTGAATGGTATGAGCTTTAGATGGGTATTTCCAGATGGGCAAGGAGCAT 1309  
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281  
Db 1310 GCCCTTGACAGGGTGAGGAGTTAACTTTTGAAGAGGACAGCTCGTGACAGCAGATCGA 1369  
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGly 301  
Db 1370 ATTGTACCGTCACTCAGGCTTATTCATGGAGGTCAACTGCTGAAGGTGACAGGGC 1429  
QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321  
Db 1430 CTCAATGAGCTCTTAAGCTCCGAAAGAGTATTTGAATGGAATTTGAATGGAATGAC 1489  
QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341  
Db 1490 ATTAATGATTTGGAAAGCCCAACACAGACAAGTGTCTCCCTCATCATTAATCTGTGATGAC 1549  
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361  
Db 1550 CTCTCTGGAAGGCCAAATGAAGCTGAATTCAGAGAGAGTGGTTTACTCTGAAGG 1609  
QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381  
Db 1610 GAGGATGTTCTCTGATGGCTTTATTTGGAAGACTGGATTACCAAGAGGCATTGATCTC 1669  
QY 382 IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
Db 1670 ATTAATAAGGCCATTCACAGCTCATGAGGAGGAGCGTGCAGTTTGTCTGCTGATCT 1729  
QY 402 GlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPhe 421  
Db 1730 GGGGATCCAAATTTTGAAGCTCGATGAGATCTACCGAGTTCGAGTACCAAGGATAAATTC 1789  
QY 422 ArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
Db 1790 CGTGGATGGTGGATTAGTGTTCAGATTTCACAGATAACTACGAGGTTCGATATA 1849  
QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461

Db 1850 TTGTTAATGCATCCAGCTTGAACCTTGTGGTCTTAATCAGCTATATGCTATGCAATAT 1909  
QY 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn 481  
Db 1910 GGTACAGTTCCTGTAGTTCATGGAACCTGGGGGGCTCCGAGACACAGTCGAGACCTTCAAC 1969  
QY 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
Db 1970 CCTTTTGGTCAAAAGGAGAGGAGGTACAGGTGGGGCTTCTCACCGCTAACCGTGGAC 2029  
QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
Db 2030 ARGATGTT-GTGGGCAATTCGAAACCGCATGTGCACATTCAGGGAGCACAGCGCTCTG 2088  
QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
Db 2089 GGAGGGCTCATGACGAGGAGCATGACGAAGACCATACGTGGGACCATGCCGC 2142

RESULT 13  
US-09-196-390-1  
; Sequence 1, Application US/09196390  
; Patent No. 6307125  
; GENERAL INFORMATION:  
; APPLICANT: Block, Martina  
; APPLICANT: Loz, Horst  
; APPLICANT: Lutticke, Stephanie  
; APPLICANT: Walter, Lennart  
; APPLICANT: Froberg, Claus  
; APPLICANT: Kosmann, Jens  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
; TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/196,390  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 196 21 588.9  
; FILING DATE: 29-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE 196 36 917.7  
; FILING DATE: 11-SEP-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP97/02793  
; FILING DATE: 28-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley, Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: AGREVO-9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2239 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA







NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 10020  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/952,677  
 FILING DATE: 14-Sep-2001  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/196,390  
 FILING DATE: 19-No. 6734339-1998  
 APPLICATION NUMBER: DE 196 21 588.9  
 FILING DATE: 29-MAY-1996  
 APPLICATION NUMBER: DE 196 36 917.7  
 FILING DATE: 11-SEP-1996  
 APPLICATION NUMBER: PCT/EP97/02793  
 FILING DATE: 28-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley, Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: AGREVO-9  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 596-9000  
 TELEFAX: (212) 596-9090  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2239 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Triticum aestivum L.  
 STRAIN: cv. Florida  
 HAPLOTYPE: ca. 21 d Caryopses  
 IMMEDIATE SOURCE:  
 LIBRARY: cDNA library in pBluescript sk (-)  
 CLONE: TaSSS  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 3..2017  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-952-677-1

Alignment Scores:  
 Pred. No.: 1,42e-281 Length: 2239  
 Score: 2466.50 Matches: 464  
 Percent Similarity: 91.8% Conservative: 29  
 Best Local Similarity: 86.4% Mismatches: 41  
 Query Match: 85.3% Indels: 4  
 DB: 3 Gaps: 2

US-10-628-525A-21 (1-539) x US-09-952-677-1 (1-2239)

QY 2 ValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyLeuAlaGluGlySer 21  
 Db 30 GTGGGGAACTCCGCG---CCCGACCTCTCGTC-----GAGGGATTGCTGAGGATCC 80  
 QY 22 IleAspAsnThrValValValAlaSerGluGlnAspSerGluIleValGlyGlySer 41  
 Db 81 ATCGACAGCATAAATTGGCTGCTCAAGTCAGCAGGATCTCGAGATCATGATCGAATGAG 140  
 QY 42 GlnAlaArgAlaGlyValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61

Db 141 CAACCTCAAGCTAAAGTTACACGTAGCATCGTGTGTGTGAGCTGCTGCTTAT 200  
 QY 62 AlAlYserGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAArg 81  
 Db 201 GCAAGTCAGGGGGTGGGAGATGTTTGGTTCGTTACCAATTCCTTGTCTGCTCGT 260  
 QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
 Db 261 GGTCAACGAGTGATGGTTGTAATGCCAAGACTATTAATGGTGGTCTCTGATAAAACTAT 320  
 QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
 Db 321 GCAAGGCATTATACACCTCGAAGCACATTAAAGATTCCATGCTTGGGGATCACATGAA 380  
 QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSer 141  
 Db 381 GTGACCTTTTTCATGAGTATAGACACAGCTCGATGGGTGTTGTTCGATCATCCGTCA 440  
 QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
 Db 441 TATCACAGACCCAGGAAAGTTTATATGAGATAAATTTGGTGTCTTTGGTGATATCATGTT 500  
 QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly 181  
 Db 501 AGATACACACTCCTTTGCTATGCTGATGCGAGGCCCACTAATCTTGAATTGGGAGGA 560  
 QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValPro 201  
 Db 561 TATATTATGGACAGAAATTCATGTTGTTGTGACGATTGGCATGCCAGCCTTGTGCCA 620  
 QY 202 ValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221  
 Db 621 GTCTTTCTTGTGCAAAATATAGACCATACGGGTGTTTACAGAGATTCCCGCAGCACCTT 680  
 QY 222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
 Db 681 GTTATACATAAATTAGCACATCAGGGGTGGAGCCCTGCAAGTACATATCCTGATCTGGGA 740  
 QY 242 LeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHis 261  
 Db 741 TTGCTCTCTGAAATGATGAGCTTTAGATGGGTATTTCCAGATGGGCGACAGGAGCAT 800  
 QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281  
 Db 801 GCCCTTGACAAGGGTGAGGAGTTAACTTTTGAAGGAGCAGCTGTGACAGCAGATCG 860  
 QY 282 IleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlnGly 301  
 Db 861 ATTTGTGACCGTCAGTCAGGGTTATTTCATGGGAGGTCACAACTGCTGAAGGTGACAGGC 920  
 QY 302 LeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321  
 Db 921 CTCATGAGCTCTTAAAGTCCCGAAAAGTATTGAATGGAAATGTAATGAATGAAATGAC 980  
 QY 322 IleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341  
 Db 981 ATTAATGATTGGAACCCACCACAGCAAGTGTCTCCCTCATCATTTATTTCTGTCGATGAC 1040  
 QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361  
 Db 1041 CTCTCTGGAAGGCCCAATGTAAGCTGAAATGTCAGAGAGAGTTGGGTTCCTCTGTAAGG 1100  
 QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381  
 Db 1101 GAGGATGTTCTCTGATTGGCTTTATTGGAAGACTGATTACCAAGAAAGCATTTGATCTC 1160  
 QY 382 IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
 Db 1161 ATTAATAATGGCCATTCACAGAGCTCATGAGGGAGGAGCTCAATTTGTCTGCTGATCT 1220  
 QY 402 GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe 421

Db 1221 GGGGATCCAAATTTTGAAGCGCTGGATGAGATCTACCGAGTCGAGTTTACAAGGATAAAATTC 1280  
QY 422 ArgGlyTyrValGlyPheSerValProValSerHisAsqIleThrAlaGlyCysAspIle 441  
Db 1281 CGTGAATGGTGGATTTAGTGTTCAGTTCCTCCACAGAATAACGAGGTTGCCGATATA 1340  
QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461  
Db 1341 TTGTTAAATGCCATCGAGATTGAACCTTCGGGTCTTAATCAGCTATATCTATGCAATAT 1400  
QY 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn 481  
Db 1401 GGTACAGTTCCCTGTAGTTTCATGAACCTGGGGGCTCCCGAGACACATCGAGACCTTCAAC 1460  
QY 482 ProPheGlyGluAsnGlyGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
Db 1461 CTTTTTGGTGCAGGAGGAGGGGTACAGGGTGGGCGTCTCACCCTAAACCGTGGAC 1520  
QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
Db 1521 AAGATGTT-GTGGGCATTCGGAACCGCGATGTCGACATTCAGGAGACACAAGCCGTCCTG 1579  
QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538  
Db 1580 GGAGGGGCTCATGAAGCGAGGCATGACGAAGACCATACGTGGGACCATGC 1630

## RESULT 15

US-09-674-824-1  
; Sequence 1, Application US/09674824  
; Patent No. 6890732  
; GENERAL INFORMATION:  
; APPLICANT: Lorz, et al  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT  
; FILE OF INVENTION: WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH  
; FILE REFERENCE: AGR 1998/M 205/ FLH514413-3848  
; CURRENT APPLICATION NUMBER: US/09/674,824  
; CURRENT FILING DATE: 2000-02-16  
; PRIOR APPLICATION NUMBER: PCT/EP99/03156  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: DE 198 20607.0  
; PRIOR FILING DATE: 1998-05-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 2771  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (280)..(2547)

## US-09-674-824-1

Alignment Scores:  
Pred. No.: 2,028-281 Length: 2771  
Score: 2466.50 Matches: 464  
Percent Similarity: 91.8% Conservative: 29  
Best Local Similarity: 86.4% Mismatches: 41  
Query Match: 85.3% Indels: 4  
DB: 3 Gaps: 2

## US-10-628-525A-21 (1-539) x US-09-674-824-1 (1-2771)

QY 2 ValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySer 21  
Db 562 GTGGGGGAACCTCGCG---CCCGACCTCTCGTCTC-----GAAGGGATTGCTGAGGATCC 612  
QY 22 IleAspAsnThrValValAlaSerGluGlnAspSerGluIleValValGlyLysGlu 41  
Db 613 ATCGACAGCATAAATTGTGCTCAAGTGAGCAGGATTCTGAGATCATGATCGCAATGAG 672  
QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
Db 673 CAACCTCAAGCTAAAGTTTACACGTAGCATCGTGTGTTGTGACTGGTGAAGCTGCTCCTTAT 732

QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAaArg 81  
Db 733 GCAAGAGTCAGGGGGTGGAGATGTTTGTGGTCTGTACCAATGCTCTTGTCTGCTCGT 792  
QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
Db 793 GGTCAACCAGTGATGTTGTTGTAATGCAAGATACTTTAAATGGGTCTCTCTGATAAAACATAT 852  
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
Db 853 GCAAAAGGCAATTATACACTCGGAAGCACATTAAGATTCCATGCTTTGGGGGATCATCATGAA 912  
QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSer 141  
Db 913 GTGACCTTTTTCATGATGATATAGACAACAGTCGATGGGTGTTGTGTCATCATCCGTCA 972  
QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
Db 973 TATCACAGACCAGGAAGTTTATATGAGATAATTTTGGTGTCTTTTGGTGATAATCAGTTTC 1032  
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 181  
Db 1033 AGATACACACTCTTGTCTATGCTCATCGAGGCCCCACTAATCTTGAATTGGGAGA 1092  
QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrPheAlaSerLeuValPro 201  
Db 1093 TATATTATGGACAGATTGCATGTTTGTGTGAACGATTGGCANTGCCAGCTTGTGCCA 1152  
QY 202 ValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221  
Db 1153 GTCCCTTCTTGTGCAAAATATAGACCATACGCGTGTTCACAGAGATTCCCGCAGCACCTT 1212  
QY 222 VallIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
Db 1213 GTTATACATAAATTTAGCACATCAGGGGTGTGGAGCCTGCAAGTACATATCTCTGATCTGGA 1272  
QY 242 LeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHis 261  
Db 1273 TTGCTCTCTGAATGTATGGAGCTTTAGAAATGGGTATTTCCAGAAATGGCAAGGAGCAT 1332  
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281  
Db 1333 GCCCTTGAACAGGCTGAGGCGAGTTAACTTTTGAAGAGGAGCAGTTGTGACACAGATCG 1392  
QY 282 IleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlnGly 301  
Db 1393 ATTGTGACCGCTCAGTCAGCGGTTAATTCATGGGAGGTCACAACTGCTGAAAGGTGACAGGC 1452  
QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321  
Db 1453 CTCATGAGCTCTTAAGCTCCGAAAAGTGTATTGAATGGAAATGTAATGGAATTGAC 1512  
QY 322 IleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341  
Db 1513 ATTAATGATTGGAACCCCAACACACAGCAAGTGTCTCCCTCATCATTAATTTCTGTCGATGAC 1572  
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuLeuProIleArg 361  
Db 1573 CTCTCTGAAAAGGCCAAATGTAAAGCTGAATTCGAAGAGGAGTGGGTTTACTGTAAAGG 1632  
QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381  
Db 1633 GAGGATGTTCTCTGATTTGGCTTTATTGGAAGACTGGATTACCAAGAGGCATTGATCTC 1692  
QY 382 IleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
Db 1693 ATTAATAATGGCCATTTCCAGAGCTCATGAGGAGGACGTGCAATTTGTCTGCTGATCT 1752  
QY 402 GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe 421  
Db 1753 GGGGATCCAAATTTTGAAGGCGCTGGATGAGATCTACCGAGTCGAGTTTACAAGGATAAATTC 1812

QY 422 ArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
Db 1813 CGTGGATGGGTGGATTTAGTTTCCAGTTTCCACAGAAATAAATCGCAGGTGGCATATA 1872  
QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461  
Db 1873 TTGTTAATGCATCGAGATTGAACCTTGGCTTGAATCAGCTATATGCTATGCAATAT 1932  
QY 462 GlyThrValProValValHisAlaThrGlyCysLeuArgAspThrValGluAsnPheAsn 481  
Db 1933 GGTACAGTTCTGTAGTTTCATGGAATCTGGGGCTCCGAGACACAGTCGAGACCTTCAAC 1992  
QY 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
Db 1993 CCTTTTGGTCAAAAGAGAGGGGTACAGGGTGGCGCTTCTCACCGCTAAACCGTGGAC 2052  
QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
Db 2053 AAGATGTT-GTGGGCAITTCGACCGGATGTCGACATTTCAGGGAGCACAGCGGTCTG 2111  
QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538  
Db 2112 GGAGGGGCTCATGAAGCGAGGCATGACGAAGACCATACGTGGGACCATGC 2162

## RESULT 16

US-09-345-214-11  
; Sequence 11, Application US/09345214  
; Patent No. 6392120  
; GENERAL INFORMATION:  
; APPLICANT: Lightner, Jonathan B.  
; APPLICANT: Broglie, Karen B.  
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE  
; FILE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS  
; FILE REFERENCE: BB-1147  
; CURRENT APPLICATION NUMBER: US/09/345,214  
; CURRENT FILING DATE: 1999-06-30  
; EARLIER APPLICATION NUMBER: 06/094,436  
; EARLIER FILING DATE: 1998-07-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 11  
; LENGTH: 1415  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-345-214-11

## Alignment Scores:

Pred. No.: 1 05e-231 Length: 1415  
Score: 2043.00 Matches: 388  
Percent Similarity: 89.8% Conservative: 0  
Best Local Similarity: 89.8% Mismatches: 0  
Query Match: 70.6% Indels: 44  
DB: 3 Gaps: 1

US-10-628-525A-21 (1-539) x US-09-345-214-11 (1-1415)

QY 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 119 TGGTCCGCGAGCTGAGCAGGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 178  
QY 8 ----- 8  
Db 179 GCGCCCGCGCTGTCGCGCGCTTCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 238  
QY 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 239 TCGACCG 298  
QY 17 IleAlaGluGlySerIleAspAnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 299 ATTGCTGAAGTTCCATCGATACACAGTAGTTGTGGCAAGTCGAGCAAGATTCTGAGATT 358  
QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56

RESULT 17

US-09-743-980-11

Db 359 GTGGTTGGAAGGAGCAAGCTCGAGCTAAAGTAACAACAAGCATTTGCTTTGTAACCGC 418  
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 419 GAAGCTTCTCTTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGGTTTCATTGCCAGTT 478  
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
Db 479 GCTCTTGTCTCTGTGTGTCTCACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACC 538  
QY 97 SerAspIleAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 539 TCCGATAAGAATATGCAATGCAATTTTACACAGAAAAACACATTCGGATTCCATGCTTT 598  
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
Db 599 GCGGTGTACATGATAGTTACCTTCTCCATGATATAGATTCAGTTGATGGTGTGTT 658  
QY 137 ValAspIleProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 659 GTTGATCATCCCTCATATCACAGACCTGGAAATTTATATGAGATAAGTTTGGTCTTTT 718  
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 719 GGTGATAATCAGTTCAGATACACATCTTTTGTCTGTATGTCATGTGAGGCTCTCTTGCATC 778  
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
Db 779 CTTGAATTTGGAGGATATATTTATGACAGATTCATGTTTGTGTCAATGATGGCAT 838  
QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 839 GCCAGTCTAGTGCAGTCTCTTCTGTCGCAAAATATAGACCATATGCTGTTTATAAGAC 898  
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 899 TCCCGCAGCATTTCTGTAATATACATAATTTAGCACATCAGGGTGTAGAGCCTGCAAGCACA 958  
QY 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 959 TATCTCGACTTGGTTGGCACCCTGAATGATGGAGCTCTGGAGTGGGTATTTCCCTGAA 1018  
QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
Db 1019 TGGCGGAGGAGCATGCCCTTGACAAGSGTGAGCGAGTTAAATTTTGAAGGTGCAGTT 1078  
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
Db 1079 GTGACAGCAGATCGAATCGTGACTGTCTAGTAAGGGTTATTTCGTGGGAGGTACAACTGCT 1138  
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1139 GAAGGTGGACGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGGAAT 1198  
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1199 GTAAATGGAATTGACATTAAATGATTGGAACCTCGCCACAGACAAATGTTATCCCTGTGCAT 1258  
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysGlyGlyAlaLeuGlnLysGluLeu 356  
Db 1259 TATTCCTGTTGATGACCTCTCTGAAAGGCCAAATGTAAAGGTGCATTTGCAAGAGGAGCTG 1318  
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1319 GGTTCACCTATTAAGGCTGATGTTCTCTGATTGGCTTTTATTGGAAGGTTGGATTATCAG 1378  
QY 377 LysGlyIleAspLeuIleGlnLeuIleIleProAsp 388  
Db 1379 AAAGGCATTGATCTCATTCACTTATCATACCAGAT 1414



APPLICATION NUMBER: PCT/EP95/04415  
 FILING DATE: 09-NOV-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 44 41 408.0  
 FILING DATE: 10-NOV-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr., James P.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: Agrevo-4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-9090  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2360 base pairs  
 TYPE: nucleotide  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Solanum tuberosum  
 STRAIN: cv. Desire  
 TISSUE TYPE: leaf tissue  
 IMMEDIATE SOURCE:  
 LIBRARY: cDNA-library in Lambda ZAPII  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 68..1990  
 US-08-836-567-9

## Alignment Scores:

Pred. No.: 1,42e-215 Length: 2360  
 Score: 1910.00 Matches: 360  
 Percent Similarity: 78.9% Conservative: 74  
 Best Local Similarity: 65.5% Mismatches: 93  
 Query Match: 66.0% Indels: 24  
 DB: 3 Gaps: 6

US-10-628-525A-21 (1-539) x US-08-836-567-9 (1-2360)

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QY 10 LeuGlyLeuGluProGluGlyIleAlaGluGlySerIle-----ValAlaSerGluGln 32
DB 290 TTGGGTGCTGAGAGATGGT-----TCGTGGCTCTGTGGTGGTTCATTTGATTGATCCA 343
QY 23 -----AspAenThrValVal-----ValAlaSerGluGln 32
DB 344 CATTCGTGTGCAGGAGATGCAACAATGGTAGAATCTCATGATATTGTAGCCAAATGATAGA 403
QY 33 Asp-----SerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGlnSer 50
DB 404 GATGACTTGAGTGAGGATCTGAGGAGATGGAGGAAACCCCAATCAAAATTAACCTTTCAAT 463
QY 51 IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspVal 70
DB 464 ATCATTTTGTACTGCTGAAGCAGCTCCCATATCTTAAGACTGGTGGATTAGGAGATGT 523
QY 71 CysGlySerLeuProValAlaLeuAlaAArgGlyHisArgValMetValMetPro 90
DB 524 TGTGGTCTTTGCCAATGCGCATAGCTGCTCGGGGTCAATCGTGTATGTGCTTCACTT 583
QY 91 ArgTyrLeuAen---GlyThrSerAspLysAsnTyrAlaAenAlaPheTyrThrGluLys 109
DB 584 AGGTATTTGAATGGAGTCTCCATGATGAAAGTAGCCCAATGCTGTGACCTTGTATGTG 643
QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPheHisGluTyrArg 129
DB 644 CGGGCCACTGTCCATTGCTTTGGTGTATGACAGAAAGTAGCCCTTCTACCATGAATACAGG 703
QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAenLeuTyr 149
DB 704 GCAGGTGTTGATGGGTATTGTTGGACCACTCTTCTTACTGACAGACTGGAAGCCCATAT 763
QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169

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DB 764 GGTGATATTATGTTGTCATTTGCTGATAAATCAGTTTGGTTCCTTCTTCTCAGCCA 823
QY 170 AlaCysGluAlaProLeuIleLeuGluGlyTyrIleTyrGlyGlnAenCysMet 189
DB 824 GCATGTGAAGCGCATTTGTTCTTCACCTGGAGGGTTCACCTATGAGAGAGTGTGTT 883
QY 190 PheValValAenAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209
DB 884 TTTCTCGCTAAATGATTGGCATGCTGCCCTGGTTCTTTACTTTTAGCGGCAAGATCGT 943
QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229
DB 944 CCTTATGGTGTTTACAAGGATGCTCGTAGTATTGTGCAATACACCAATTCACATCAG 1003
QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyVala 249
DB 1004 GGAGTGGAGCGCTGCAGTAACCTACATAATTTGGGTTTGGCTCCACATGATGTGAGCA 1063
QY 250 LeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaVal 269
DB 1064 GTTGAATGGATATTTCCACATGGGCAAGCGCATGCGCTTGACACTGGTGAACAGTG 1123
QY 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289
DB 1124 AACGTTTTGAAAGGGGCAATAGCAGTTGCTGATCGGATACTGACAGTTAGCCAGGATAC 1183
QY 290 SerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAenGluLeuLeuSerSerArg 309
DB 1184 TCATGGGAATACAACTCCTGAAGGGGGATATGGGCTACATGAGCTGTGAGCAGTAGA 1243
QY 310 LysSerValLeuAenGlyIleValAenGlyIleAspIleAsnAspTrpAenProAlaThr 329
DB 1244 CAGTCTGTTCTTAATGGAATTACTAATGGAATAGATGTTAATGATTGGAACCCGTCGACA 1303
QY 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349
DB 1304 GATGAGCATATTGCTTCGCATTAATCCATCAATGACCTCTCCGGAAGGTTTCAAGTCAAG 1363
QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369
DB 1364 ACTGATCTGCAGAAAGAAAGACTGGGCTTCATATTCGACCTGATGTCTCTGATTTGATTT 1423
QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu 389
DB 1424 ATTGGAAGGCTGCACTTACCAGAAAGGTGTGACATAATCTCTGTCAGCAATTCAGAACTT 1483
QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409
DB 1484 ATGCAGAAATGATGTCAGATTGTAATGCTTGGATCTGTGAGAGAAACAATATGAAGACTGG 1543
QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429
DB 1544 ATGAGACATACAGAAATCTTTTAAAGACAATTTTCGTGCTTGGGTTGATTTAATGTT 1603
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
DB 1604 CCAGTTTCTCATAGGATAACAGCAGGATCGGACATACATATTGATGCGCTCAAGATTCGAA 1663
QY 450 ProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
DB 1664 CGGTGTGGCTTAACCAATTTGATGCAATGAGATATGGCACCACATCTATTGTTTCATAGC 1723
QY 470 ThrGlyGlyLeuArgAspThrValGluAenPheAenProPheGlyGluAenGly---Glu 488
DB 1724 ACGGGGGGCTTAAGAGACACAGTGAAGGATTTTAATCCATATGCTCAGAGGAATAGGT 1783
QY 489 GlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAenMetPheValAspIleAla 508
DB 1784 GAAGGTACCGGTGGACCATTTTCTCTCTAACGAGTGAAGAGTGGTCTGATACACTGAAG 1843
QY 509 AsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAlaArg 528

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QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369
Db 1364 ACTGATCTGCAAAAGGAACCTGGGCTTCCCAATTCGACCTGATTGCTCTGATTGGATTT 1423
QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeu 389
Db 1424 ATTGGAGGCTGACTACCAAGAGGTTGTGATATAATCTCTGCAGCAATTCAGAACTT 1483
QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyr 409
Db 1484 ATCAGAAATGATCTCCAAAGTTGTAATGCTTGGATCTGGTGAGAAACAATAGAACTGG 1543
QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429
Db 1544 ATGAGACATACAGAAATCTTTTAAAGACAAATTTCTGCTTGGGTTGGATTAATGTT 1603
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
Db 1604 CCAGTTTCTCATAGGATAACAGCAGGATGCGACATATATTGATGCCCTCAAGATTCCGAA 1663
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
Db 1664 CCGTGTGGCTTAAACCAATTTGATGCAATGAGATATGGACCATACCTATTGTTCTATAGC 1723
QY 470 ThrGlyGlyLeuArgAspThrValGluAsnProPheGlyGluAsnGly---Glu 488
Db 1724 ACGGGGGGCTTAAGACACAGTGAAGGATTTTAAATCCATATGCTCAAGAAGGAATAGGT 1783
QY 489 GlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAla 508
Db 1784 GAAGGTACCGGGGGGACATTTCTCTCTAAACAGTGAAGTTGTTGATACACTGAAG 1843
QY 509 AsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArg 528
Db 1844 CT-GGCAATCGGACTTATACAGAACATTAAGTCATCTTGGAGGATTTGATGGAGAGG 1902
QY 529 HisValLysArgLeuHisValGlyProCys 538
Db 1903 TATGGAGGAGGACTATCTCTGGGAAAAATGC 1932

RESULT 20
US-08-836-567-3
; Sequence 3, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Springer, Franziska
; APPLICANT: Abel, Gernot
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,567
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: DE P 44 41 408.0
/ FILING DATE: 10-NOV-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haley Jr., James F.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: Agrevo-4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-596-9000
/ TELEFAX: 212-596-9090
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1758 base pairs
/ TYPE: nucleotide
/ STRANDEDNESS: unknown
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ ORGANISM: Solanum tuberosum
/ STRAIN: cv. Berolina
/ TISSUE TYPE: tuber tissue
/ IMMEDIATE SOURCE:
/ LIBRARY: cDNA-library in pBluescriptSKII+
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1377
/ OTHER INFORMATION: /function= "Polymerization of
/ OTHER INFORMATION: starch"
/ OTHER INFORMATION: /product= "Starch synthase"
US-08-836-567-3

Alignment Scores:
Pred. No.: 1,96e-184 Length: 1758
Score: 1645.50 Matches: 304
Percent Similarity: 81.7% Conservatives: 63
Best Local Similarity: 67.7% Mismatches: 70
Query Match: 56.9% Indels: 13
DB: 3 Gaps: 5

US-10-628-525A-21 (1-539) x US-08-836-567-3 (1-1758)
QY 95 GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114
Db 1 GGCACGAGC-----AATGCTGTTGACCTTGTGTCGGGCCCATGTCAT 45
QY 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyr 134
Db 46 TCGTTTGGTGATGTCACAGGAAGTAGCCTTCTACCATGAATACAGGCGAGGTGTTGATTGG 105
QY 135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154
Db 106 GTATTGTTGGACCATCTCTTACCGCAGACTGGAGCCCATATGTCGATATTATAGGT 165
QY 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174
Db 166 GCATTGTTGGATAAATCAGTTTCGCTTCACTTCTCTCACGACAGCATGTGAAGGCCCA 225
QY 175 LeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194
Db 226 TTGGTTCTTCCACTGGGAGGTTTCACTTATGAGAGAAAGTCTGTTTCTCGCTAATGAT 285
QY 195 TrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyr 214
Db 286 TCAACAGCTGCTGCTTGGTTCCTTATCTTTTAGCGGCAGATATCGTCTTATGTTGTTTAC 345
QY 215 LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234
Db 346 AAGGATGCTGCTAGTATTGTCGAATACACAACATTGCACATCAGGAGTGAGCGCTGCA 405
QY 235 SerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPhe 254
Db 406 GTAACTTCAATTAATTTGGGTTTGGCTTCCACATGTTATGGAGCAGATTGAATGGATATT 465
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QY 255 ProGluTrrAlaArgHisAlaLeuAapLysGlyGluAlaValAaenPheLeuLysGly 274  
DB 466 CCACATGGCGAAGGGCGGCTGCTGACAGCTGGTGAACAGTGAACCTTTTGAAGGG 525  
QY 275 AlaValThrAlaAapArgHisValThrValSerLysGlyTyrSerTrpGluValThr 294  
DB 526 GCAATAGCAGTTGCTGATCGGATCTAGCAGTATAGCCAGGATCTCATGGGAATAACA 585  
QY 295 ThrAlaGluGlyGlnGlyLeuAenGluLeuSerSerArgLysSerValLeuAen 314  
DB 586 ACTCTGGAAGGGGATGATGGCTACATGAGCTGTTGAGCAGTAGACAGCTGTTCTTAAT 645  
QY 315 GlyLeuValAaenGlyLeuAaenAapTrpAaenProAlaThrAaenLysCysIlePro 334  
DB 646 GGAATTAATTAATGGAATAGATGTTAATGATGGAACCGCTGACAGATGAGCATTCGCT 705  
QY 335 CysHisTyrSerValAaenAapLeuSer-----GlyLeuAlaLysCysLysGlyAlaLeu 352  
DB 706 TCGCATTAATCCATCAATGACCTCTCCCTCCCTGGGAAGTTTCAGTGCAGACTGATCTG 765  
QY 353 GlnLysGluLeuGlyLeuProLeuArgProAapValProLeuLysGlyPheIleGlyArg 372  
DB 766 CAAAAGGAATCGGCTTCCAAATTCGACCCGATGTCCTCAGTATGATGATTTATGGAAGG 825  
QY 373 LeuAapTyrGlnLysGlyLeuAaenGlnLeuLysGlyLeuAaenProAaenMetArgGlu 392  
DB 826 CTGGACTACCAAGAGGTGTGACATAATCTGTCAGCAATTCAGAACTTATGCAAGAT 885  
QY 393 AspValGlnPheValMetLeuGlySerGlyAapProGluLeuGluAaenPheMetArgSer 412  
DB 886 GATGTCGAAGTTGTAATGCTTGGATCTGTCGAGAAACAATATGAAGACTGGATGAGACAT 945  
QY 413 ThrGluSerIlePheLysAapLysPheArgGlyTrrValGlyPheSerValProValSer 432  
DB 946 ACAGAAATCTTTTAAAGACAAATTCGTGCTTGGGTTGGATTTAATGTTCCAGTTTCT 1005  
QY 433 HisArgIleThrAlaGlyCysAapIleLeuLeuMetProSerArgPheGluProCysGly 452  
DB 1006 CATAGATACAGCAGGATGCGACATATTTATGATGTCCTCAAGATTCGACCGTGTGGC 1065  
QY 453 LeuAaenGlnLeuTrrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGly 472  
DB 1066 TTAACCAATTCATGCAATGAGATATGACCACTATCTTATGTTTCATAGCAGGGGGC 1125  
QY 473 LeuArgAapThrValGluAaenPheAaenProPheGlyGluAaenGlyGlu---GlnGlyThr 491  
DB 1126 CTAAGAGACACAGTGAAGGATTTAATCCATATGCTCAAGAAAGAAAGGTGAAGGTACC 1185  
QY 492 GlyTrrAlaPheAlaProLeuThrThrGluAaenMetPhe-----ValAaenIleAlaAen 509  
DB 1186 GGGTGACATTTCTCTCTAAGAGTAAAGTGTGTTGATACATGAAGCTGGCAT- 1244  
QY 510 CysAaenIleTrrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAaenGluAlaArgHis 529  
DB 1245 CAGGACTTATAC-----AGAACATAAGTCACTTTGGGAGGATTCATGAAGAGGATAT 1298  
QY 530 ValLysArgLeuHisValGlyProCys 538  
DB 1299 GGAAGGGGACTATCTCTGGGAATGTC 1325

## RESULT 21

US-09-606-304-3  
; Sequence 3, Application US/09606304  
; Patent No. 6483010  
; GENERAL INFORMATION:  
; APPLICANT: Kossmann, Jens  
; Abel, Gernot  
; Springer, Franziska  
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES  
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC  
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES  
; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/606,304  
; FILING DATE: 28-Jun-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/836,567  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: DE P 44 41 408.0  
; FILING DATE: 10-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: Agrevo-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-596-9090  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1758 base pairs  
; TYPE: nucleotide  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Solanum tuberosum  
; STRAIN: cv. Berolina  
; TISSUE TYPE: tuber tissue  
; IMMEDIATE SOURCE:  
; LIBRARY: cDNA-library in pBluescriptSKII+  
; OTHER INFORMATION: CDS  
; FEATURE:  
; LOCATION: 1..1377  
; OTHER INFORMATION: /function= "Polymerization of  
; starch"  
; /product= "Starch synthase"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-606-304-3  
  
Alignment Scores:  
Pred. No.: 1,966-184 Length: 1758  
Score: 1645.50 Matches: 304  
Percent Similarity: 81.7% Conservative: 63  
Best Local Similarity: 67.7% Mismatches: 70  
Query Match: 56.9% Indels: 13  
DB: 3 Gaps: 5  
  
US-10-628-525A-21 (1-539) x US-09-606-304-3 (1-1758)  
  
QY 95 GlyThrSerAapLysAaenTrrAlaAaenAlaPheTrrThrGluLysHisIleArgIlePro 114  
DB 1 GGCACGAGC-----AATGCTGTTGACCTTGTGTCGGGCGCACTGTGCCAT 45  
QY 115 CysPheGlyGlyGluHisGluValThrPheHisGlyTrrArgAaenPheValAaenTrp 134  
DB 46 TCGTTTGGTGTGCACAGGAGTAGCTTCTACCATGATACAGGCGCAGGTGTGTGTTGG 105  
QY 135 ValPheValAaenPheSerTrrHisArgProGlyAaenLeuTrrGlyAaenLysPheGly 154  
DB 106 GTATTGTGGACCACTCTTCTTACCGCAGACCTGGAAACGCAATATGTTATGTTGTT 165



QY 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174  
DB 166 GCATTTGGTGAATAATCAGTTTCGCTTCTCCTCAGCAGCATGTCGAAGGCCA 225  
QY 175 LeuLeuLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194  
DB 226 TTGGTTCCTTCACATGGAGAGGTTCACTTATGGAGAGTGTCTGTTCCTCGCTAATGAT 285  
QY 195 TrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyr 214  
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QY 255 ProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
DB 466 CCCACATGGCGCAAGGCGCATGCGCTTGACACTGGTGAACACTGAACGTTTGAAGGG 525  
QY 275 AlaValValThrAlaPheArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294  
DB 526 GCATAGCAGTTGCTGATCGATACACTGACAGTAGTGGCAGGATCTCATGGGAATAACA 585  
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DB 646 GGAATTACTAATGGAATAGATTTAATGATGGACCCGTCGACAGATGAGCATTCGCT 705  
QY 335 CysHisTyrSerValAspLeuSer-----GlyLysAlaLysCysLysGlyAlaLeu 352  
DB 706 TCGCATTTACTCCATCAATGACCTCTCCCGCCCTGGAAAGGTTTCAGTGCAGACTGATCTG 765  
QY 353 GlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArg 372  
DB 766 CAANAAGAACTGGGCTTCCAAATCCACCGGATGTGCCACTGAATGGATTTATTTGAAGG 825  
QY 373 LeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGlu 392  
DB 826 CTGGACTACCAGAAAGGTGTGACATAATCTCTGACGAATTCAGAACTTATGCAGAT 885  
QY 393 AspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSer 412  
DB 886 GATGTCCTCAAGTTGTAATGCTTGGATCTGGTGAGAAACAATATGAAGACTGGATGACAT 945  
QY 413 ThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSer 432  
DB 946 ACAGAAATCTTTTAAAGACAAATTCGGTGTGGTGGTGGATTTAATGTTCAGTTTCT 1005  
QY 433 HisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGly 452  
DB 1006 CATAGATTAACAGCAGATGCGACATCTATTGATGCCCTCAAGATTCGAACTGTGGC 1065  
QY 453 LeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGly 472  
DB 1066 TTAACCAATTTGATGCAATGAGATATGGCACCATACCTATTGTTTCATAGCAGCGGGGC 1125  
QY 473 LeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlu-----GlnGlyThr 491  
DB 1126 CTAAGAGACACAGTGAAGGATTTAATTCATATGCTCAAGAAAGAAAGGTGAAGTACC 1185  
QY 492 GlyTyrAlaPheAlaProLeuThrThrGluAsnMetPhe-----ValAspIleAlaAsn 509  
DB 1186 GGGTGGACATTTCTCTCTAAGCAGTGAAGGTTGTTGATACACTGAAGCTGGCGAT- 1244

QY 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
DB 1245 CAGGACTTATAC-----AGAACATAAGTCACTCTGGAGGAGTTGATGAAGAGGTAT 1298  
QY 530 ValLysArgLysHisValGlyProCys 538  
DB 1299 GGGAGAGGACTATTCTCTGGGAAATATGC 1325

## RESULT 22

US-09-508-377-13  
; Sequence 13, Application US/09508377  
; Patent No. 6916976  
; GENERAL INFORMATION:  
; APPLICANT: KALEEN, ZHONGYILI  
; APPLICANT: MORELL, MATTHEW  
; APPLICANT: RAHMAN, SADROUR  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 054270/0126  
; CURRENT APPLICATION NUMBER: US/09/508,377  
; CURRENT FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: AU PP 2509  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: PCT/AU98/00743  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: AU PP 9108  
; PRIOR FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 10337  
; TYPE: DNA  
; ORGANISM: Triticum tauschii  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (10232)  
; OTHER INFORMATION: a, t, c, g, other or unknown  
US-09-508-377-13

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Pred. No.: 1,72e-139 Length: 10337  
Score: 1277.00 Matches: 345  
Percent Similarity: 29.2% Conservative: 19  
Best Local Similarity: 27.6% Mismatches: 21  
Query Match: 44.1% Indels: 865  
DB: 3 Gaps: 9

US-10-628-525A-21 (1-539) x US-09-508-377-13 (1-10337)

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QY 32 GlnAspSerGluIleValValGlyLysGlnAlaArgAlaLysValThrGlnSerIle 51  
DB 1520 CAGGATTCGAGATCATGATGCGAATGAGCAACCTCAAGCTAAAGTTACACGTAGCATC 1579  
QY 52 ValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCys 71  
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QY 72 GlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValValMetProArg 91  
DB 1640 GGTTCGTTACCAATGCTCTTCTGCTCGTGGTCCCGTGTGATGTTGTTATGCCAAGA 1699  
QY 92 TyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIle 111  
DB 1700 TACTTGAATGGGTCTCTCTGATAAAACTATGCAAGGCCATTATACACTCGAAGCACTT 1759  
QY 112 ArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSer 131  
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QY 132 ValAspTrpVal----- 135

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Db 1820 GTCCATGGGT-GGGTACACAATCACCTTCTTATTCTCTGTTGAATTGTAGCACTGTTT 1878  
QY 135 ----- 135  
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QY 135 ----- 135  
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QY 135 ----- 135  
Db 1999 ATGTGCTAGTATTTTTTGGTGTGGTGCCTTTAACTTTCAGGGAATTAATACGTGGAATTT 2058  
QY 135 ----- 135  
Db 2059 GATACTAAAGTTTATTTTATTGAAAAAAATTTGTAGTTGGCTGAGCCCAAGCCACGCA 2118  
QY 135 ----- 135  
Db 2119 GTGGACCACTGCTTGCACATGATTTTGGCAATTTCTGTTTGGCCAGAGCACTTCATGTGAA 2178  
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Db 2239 ATTTATCTTGGCTCAATCATGGAGTACTGTGCATTCAGTGACCATCATTTGTTCTAAG 2298  
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QY 160 -----GlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuG1 178  
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Db 2899 CGTGCAGTTCAGATACACACTCCTTTGCTATGCTGCATCGAGGCCCACTAATCCTTGA 2958  
QY 178 uLeuGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSe 198  
Db 2959 ATTGGAGGATATATTATGGACAGAAATGTCATGTTTGTGTGAACGATGGCATGCCAG 3018  
QY 198 PheValProVal----- 202  
Db 3019 CCTTGTGCCAGT-GTACGTTGTTTGTGGATCTGAAAGTCCAATCCTTTATTCATTCTCTG 3077  
QY 202 ----- 202  
Db 3078 CTTTGCAGTGTGCCCATGTCACATTTCTTTTATGCTTTTTCATGCTCTGTTCTTATATT 3137  
QY 202 ----- 202  
Db 3138 GCATATATGCTTATGAGTCTAAAGTTTACCGGAGGAAATAACTCTTAAGGATTTCTCTCA 3197  
QY 202 ----- 202  
Db 3198 ATCAATTATCTTTAGCTTTTAGTTAACTTTACTGTGGCAACAATAATGTGTTTGAGATT 3257  
QY 202 ----- 202  
Db 3258 TACAAGTTTCAGAGATTGCACTTTCACCTAGTTCGTAGCTAATCTGATGTTTTTCCCGAGAAA 3317  
QY 202 ----- 202  
Db 3318 ATGCCTAAAGCTTTGTGCTCTTGATGCAATGTAGTAAAGAAAGATTTTATGTACACTCCCAA 3377  
QY 202 ----- 202  
Db 3378 GAGGGGACCCAAAATTACAACACCAACCCCTGAGAACTAGGGGCTGCCGGAAGAACGA 3437  
QY 202 ----- 202  
Db 3438 TGCAAGCCCACTGCCCTGCTGCTTAGCTCAAGCCGGGCGTCAGCTTGATGTGTCAAGT 3497  
QY 202 ----- 202  
Db 3498 AAGCTAGCAGTGTAGATTGCGCAAGTGCATTCGTGCGAAGATGACAGTGTTCGCGTGTCT 3557  
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Db 3558 TCCAAATCCACCAAACTATGACCATGATCACTGGAGAGTACCTTTTCTCGCGGCTGAGG 3617  
QY 202 ----- 202  
Db 3618 GGGTGGACTGGTGGTCTGCTGCTGCCAGTTTTTCAGATAATCTGAAAAAATGCATGTTTTGA 3677  
QY 202 ----- 202  
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Db 3738 TACACCTATAAAGTAACGGTCAATGATGATGATGTTTGGGTAGATCATGCTGCATGC 3797  
QY 202 ----- 202  
Db 3798 ATTTTAGGAAATPAGGACATGCCAGAACCCAGCGTAGGCTTTATGGGGCAATTCATTGTTCC 3857  
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Db 3858 ATTATACGAGTCATGAATAATGTTTCAGCATGTTTGGACGCTACTTGTGTTGGGGCAATTTTC 3917  
QY 202 ----- 202  
Db 3918 AGATGGTAATGTAGTCTGCTTGTATGTTGGCTAGCTGGCTTATTTTGTACAAAGTATCGAT 3977  
QY 202 ----- 202  
Db 3978 GTTAGATGCATATTTCTTTTGTCTTGTGCTGTTTGGCATGTTGTATTTCCCTTTTCTG 4037





TELEPHONE: 212-596-9000			
TELEFAX: 212-596-9090			
INFORMATION FOR SEQ ID NO: 7:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 2793 base pairs			
TYPE: nucleotide			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: cDNA to mRNA			
ORIGINAL SOURCE:			
LIBRARY: CDNA-library in Lambda ZAPII			
FEATURE:			
NAME/KEY: CDS			
LOCATION: 242..2542			
US-08-836-567-7			

  

Alignment Scores:			
Pred. No.:	1.43e-120	Length:	2793
Score:	1109.50	Matches:	240
Percent Similarity:	61.2%	Conservative:	65
Best Local Similarity:	48.2%	Mismatches:	162
Query Match:	38.4%	Indels:	32
DB:	3	Gaps:	9

  

US-10-628-525A-21 (1-539) x US-08-836-567-7 (1-2793)			
QY 50 SerileValPheValThrGlyGluAlaSerProTyrAlaIysSerGlyGlyLeuGlyAsp 69			
Db 1070 AACATTATTTTGGTGGCTTCAGAATGCGCTCCATGGTCTAAACACAGCTGGCTTGGAGAT 1129			
QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89			
Db 1130 GTTGCTGGAGCATTTACCAAGCTTTTGGCTCGACGTGGCCACAGATTATGGTTGTGGCA 1189			
QY 90 ProArgTyrLeuAsn-----GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThr 107			
Db 1190 CCTCGTTATGACAACTATCTCGAACCTCAGATTCTGGTGTAGAAAAATTTATAAGTT 1249			
QY 108 GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127			
Db 1250 GAT-----GGTCAGATGTGGAAGTGACTTACTTCCAGCT 1285			
QY 128 TyrArgAspSerValAspTrpValPheValAsp---HisProSerTyrHisArgProGly 146			
Db 1286 TTTATTGATGGTGTGATTTTTTTTTTTTTCATTGACAGTCATATGTTAGACACATTTGGGAAC 1345			
QY 147 AsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeu 166			
Db 1346 AACATTACGGA-----GGAAACCGTGTGATATTTTAAACCGCATGGTTTATTT 1396			
QY 167 CysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln 186			
Db 1397 TGCAAAGCAGCATTCAGGTTCTTGGCANGTTCCATGGTGGGGTCTGCTATGGAGAT 1456			
QY 187 ---AsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAla 205			
Db 1457 GGAAATTTAGTTGTTTATGCTAATGATTGGCATACTGCTTTATTGGCAGTATATCTGAAA 1516			
QY 206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn 225			
Db 1517 GCTTATTTCGTGACAAATGGAATTTATGAACATAACAAGATCTGCTCTGGTGATTCATAAC 1576			
QY 226 LeuAlaHisGlnGlyValGluProAlaAsnThrTyrProAspLeuGlyLeuProProGlu 245			
Db 1577 ATCGCTCATCAGGTCGTGTCTCTTTGGAGGATTTTTCATATGTAGATCTTCACACACAC 1636			
QY 246 TrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLys 265			
Db 1637 TATATGGACCCCTTCAAGTTGTATGATGACCCAGTA-----GGA 1672			

STATE: New York  
 COUNTRY: USA  
 ZIP: 10020

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/606,304  
 APPLICATION NUMBER: US/09/606,304  
 FILING DATE: 28-Jun-2000  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/836,567  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: DE P 44 41 408.0  
 FILING DATE: 10-NOV-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Haley Jr., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: Agrevo-4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-596-9000  
 TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2793 base pairs  
 TYPE: nucleotide  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 ORIGINAL SOURCE:  
 ORGANISM: Solanum tuberosum  
 STRAIN: cv D, sir, e  
 TISSUE TYPE: leaf tissue  
 IMMEDIATE SOURCE:  
 LIBRARY: cDNA-library in Lambda ZAPII  
 OTHER INFORMATION: CDS

FEATURE:  
 LOCATION: 242..2542  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 US-09-606-304-7

## Alignment Scores:

Pred. No.: 1 43e-120 Length: 2793  
 Score: 1109.50 Matches: 240  
 Percent Similarity: 61.2% Conservative: 65  
 Best Local Similarity: 48.2% Mismatches: 162  
 Query Match: 38.4% Indels: 32  
 DB: 3 Gaps: 9

US-10-628-525A-21 (1-539) x US-09-606-304-7 (1-2793)

Qy 50 SerileValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69  
 Db 1070 AACATTATTTGGTGGCTTCAGAAATCGCTCCATGCTCTAAAACAGGTGGGCTGGAGAT 1129  
 Qy 70 ValCysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValMet 89  
 Db 1130 GTTGTGGAGCAATTACCCAAAGCTTTGGCTCGACGTGGCCACAGAGTTATGTTGGCA 1189  
 Qy 90 ProArgTyrLeuAsn-----GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThr 107  
 Db 1190 CTCGTATGACACTATCTGACCTCAAGATCTGGTGAAGAAAATTTATAAAGTT 1249  
 Qy 108 GluLysHisileArgileProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127  
 Db 1250 GAT-----GGTCAGGATGTGGAAGTGACTTACTTCCAAAGCT 1285  
 Qy 128 TyrArgAspSerValAspTrpValPheValAsp---HisProSerTyrHisArgProGly 146  
 Db 1286 TTATTATGATGGTGGATTTTGTTCATTGACAGTCATGATGTTTAGACACATGGGAAC 1345

Qy 147 AsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeu 166  
 Db 1346 AACATTITACGA-----GGAAACCGTGGGATATTTTAAACGCATGGTTTATTT 1396  
 Qy 167 CystYrAlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyGlyTyrileTyrGlyGln 186  
 Db 1397 TGCAAAAGCAGCGATTGAGGTTCTTGGCATGTGTCCATGTGGTGGGTCTGCTATGGAGAT 1456  
 Qy 187 ---AsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAla 205  
 Db 1457 GGAATTTTATGTTTCATTGCTAATGATTGGCATCTGCTTATTCGCATATATCTGAAA 1516  
 Qy 206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerileLeuValileHisAsn 225  
 Db 1517 GCTTATTATCGTGACAAATGGAATTATGAATATCAAGATCTGTCTGGTGTATTATAC 1576  
 Qy 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu 245  
 Db 1577 ATCGCTCATAGGTCGTGGTCTTTGGAGGATTTTTCATATGTAGATCTTCCACCACAC 1636  
 Qy 246 TrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLys 265  
 Db 1637 TATATGGACCCCTTCAAGTTGTATGACCAGTA-----GGA 1672  
 Qy 266 GlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgileValThrVal 285  
 Db 1673 GGTGAGCATTTCAACATTTTTCGGCTGGTCTAAAGACACGACAGTCGTGTAGTTACAGTT 1732  
 Qy 286 SerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeu 305  
 Db 1733 AGTCATGGATATTTCATGGAACTTAAAGACTTCCCAAGGTGGTGGGAGTGCATCAGATA 1792  
 Qy 306 LeuSerSerArgLysSerValLeuAsnGlyLeuValAsnGlyLeuAspLeuAspTrp 325  
 Db 1793 ATTAATGAGAACGATTGGAAATTACAGGATTTGTGAATGGGATGATGATCAAAAAGAGTGG 1852  
 Qy 326 AsnProAlaThrAspLysCysilePro-----CysHisTyrSerValAspAsp 341  
 Db 1853 AACCTTGATGGAGCTTCACTTACAGTCAGATGGTGTACATGACTCTCTTGGACAG 1912  
 Qy 342 Leu---SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProfile 360  
 Db 1913 CTACAGACTGGCAAGCCTCAATGTAAAGCTGCTTGCAGAGAACTTGGTTTACAGTT 1972  
 Qy 361 ArgProAspValProLeuileGlyPheileGlyArgLeuAspTyrGlnLysGlyLeuAsp 380  
 Db 1973 CGTGATGATGTCCCACTGATCGGTTTCATTGGAGGCTTGACCCACAAAGGGTGTGAT 2032  
 Qy 381 LeuileGlnLeuileProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 Db 2033 CTGATTCGTGAGCCAGTCGTGGATGATGGGTGAGGATGTACAACTGCTCATGTTGGGG 2092  
 Qy 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerilePheLysAspLys 420  
 Db 2093 ACGGGGAGCGGTGACCTTGAACAGATGCTAAGGCAATTTAGTGTCAACACACATGATAA 2152  
 Qy 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgileThrAlaGlyCysAsp 440  
 Db 2153 ATTAGAGGATGGTGGTGTCTCTGTGAAGACTTCTCATCGTATTAACGTCTGGTCAGAC 2212  
 Qy 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
 Db 2213 ATTCGTCTCATGCTTCTAGATTGAGCCTTGGGAGCTGAACAGCTTATGCAATGAA 2272  
 Qy 461 TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe 480  
 Db 2273 TATGGGACTATTCTCTGTGTTTCATGAGTAGGAGACTCAGAGATACCTGTGAGCCCTTT 2332  
 Qy 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThr 500  
 Db 2333 GATCCTTTTAAATGATCA-----GGACTGGGGGTGACCTTCAGTAGGCGCTGAGCT 2383  
 Qy 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520

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Db 2384 AGCCAGCTGATCCACGCAATTAGGAATAATGCTTACTGAC-TTATCGTGAAGTACAAAAAGAG 2442
Qy 521 LeuGlyArgAlaAsnGluAlaArgHisVallysArgLeuHisValGlyProCys 538
Db 2443 TTGGAGGGGATTACAGACACCTTGTATGACACACAGACTTAAGTTGGGATAATGC 2496

RESULT 26
US-09-388-743-25
; Sequence 25, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
; FILE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 2418
; TYPE: DNA
; ORGANISM: Typha latifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2418)
US-09-388-743-25

Alignment Scores:
Pred. No.: 6.63e-120 Length: 2418
Score: 1103.00 Matches: 243
Percent Similarity: 59.7% Conservative: 78
Best Local Similarity: 45.2% Mismatches: 176
Query Match: 38.1% Indels: 42
DB: 3 Gaps: 12

US-10-628-525A-21 (1-539) x US-09-388-743-25 (1-2418)
Qy 15 GluGlyLeuAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSer 34
Db 574 GAAGATCTTGAGAGCAAAATGGATAGTGTACATGTC-----AAAGAT 618
Qy 35 GluIleValValGlyLysGluGln-----AlaArgAlaLysValThr 48
Db 619 GATTTGAATCTCTGGGAAGAAATAGGTTCTCTTCTTCTTGGCTGGGCAATGTC--- 675
Qy 49 GlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGly 68
Db 676 ATGAACATCATATAGTAGTGTCTGCAGAAATGTGCTCTTGGTCCAAAACAGGTGGGCTTGA 735
Qy 69 AspValCysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValVal 88
Db 736 GATGTTGCAGAGCATTGCCAAGGCTTTGGCCAGAAAGAGGACATAGGTTGATGGTGTG 795
Qy 89 MetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGlu 108
Db 796 GCACCAAGGTATGCAAACTATGCTGAACCCCAAGATATAGGAGTCCGCAAAATACACAG 855
Qy 109 LysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlyTyr 128
Db 856 GTTCAT-----GGCCAGGATATGGAAGTAACCTATTATTCATGCTTAT 897
Qy 129 ArgAspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsn 147
Db 898 ATCCAGGTGTGGATTTGTTTATGATAGTCCAGACTTCGCTCACCAGGGGGGAATCGT 957
Qy 148 LeuTyr---GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeu 166
Db 958 ATTTATGAGGGAACCGAGTG-----GATATCTTAAACGATGATGTTTGTTC 1005
Qy 167 CysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln 186
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Db 1006 TGCAGGCGAGCTGTAGAGGTTCTTGGCATGTTCCATGTTGGTCTCTGTATGGAGAT 1065
Qy 187 ---AsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAla 205
Db 1066 GGTAAATTTGGCTTTTCATCAGCAATGATTGGCATACTGCTCTCTTGGCTGTTTATCTGAAG 1125
Qy 206 AlalysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn 225
Db 1126 GCATATTATCGTCAATGCTTGATGATGATATGCTCGGCTGTTCTGGTAAATACACAC 1185
Qy 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGlu 245
Db 1186 ATAGCCCAACCCAGGCTCGTGGCTCTGTAGATGACTTCAAAATTTGGGGCTTGGCCGATCAC 1245
Qy 246 TrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLys 265
Db 1246 TACTTGGACCTTTTTCAGATTGTATGACCCCGTC-----GGA 1281
Qy 266 GlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrVal 285
Db 1282 GGTGAACACCTCAATATTTTGTCTGCTGGCTGAAGACTGCTGACCGAGTGGTTACTGTT 1341
Qy 286 SerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeu 305
Db 1342 AGCCATGTTTATGCTGAGGAGCTGAAAAACATCAGAAGGTGTTGGGGCTTACATGAAT 1401
Qy 306 LeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrp 325
Db 1402 ATAAATGAAGATTAACCTGAAGTTTCAAGTATTGTAATGGCATTTGATGCAAGAGAGTGG 1461
Qy 326 AsnProAlaThrAspLysCysIlePro-----CysHisTyrSerValAspAsp 341
Db 1462 AGCCCGAATTTGATGTGCACCTTAATCCGATGGATACACAATTTATTTCTAGATACT 1521
Qy 342 LeuSer---GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluGlyLeuProIle 360
Db 1522 TTAGAGATGGTAAAGCCAGTATGTAAGGCTGCTTTCAGCGAGAGTGGCTGCTGCTGTT 1581
Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380
Db 1582 CGTGATATATGTTACCCCATTTGCAATTCATTGGAAGGTTAGACCACCAAGAGCGCTCGAT 1641
Qy 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400
Db 1642 CTCAATTCGCGAGGCCATGCTTGGATGTGTCATGATGTTCAAGTAGTCACTGTTAGGC 1701
Qy 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420
Db 1702 ACGGGAGGCAAGACCTTGAGAATTTTACTGAGGAACCTTTGAGGGTCAACACAGGGACAA 1761
Qy 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440
Db 1762 GTTAGAGATGGGTGTCATTTTCAGTAAAGATGGCGCATAGAAATTCACAGCGTGGCGAC 1821
Qy 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460
Db 1822 ATCTCATGATGCTTCGAGGTTTGAGCCATGCGGATGACCCAGCTTTACGCATGATG 1881
Qy 461 TyrGlyThrValProValValHisAlaThrGlyLysLeuArgAspThrValGluAsnPhe 480
Db 1882 TATGGAACCATTTCCAGTGGTGCATGCTGTGGGGGCTTTAGAGATACAGTCACTCAATTT 1941
Qy 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThr 500
Db 1942 GATCTCTTCAACAGAGTCT-----GGTCTTGGTTGACCTTCACAGGGCAGAGGCA 1992
Qy 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520
Db 1993 GGAAGAGCTCATTCATGCTTGAATGACTGCTT-GAATACATCTACTGGAATTCAGAGCAG 2051
Qy 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538
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Db 2052 TTGGAAGGCTCTTCAACACAGAGGATGATCCAGATCTTAGCTGGGATAATGC 2105

RESULT 27

US-10-044-543-25

; Sequence 25, Application US/10044543

; Patent No. 6734341

; GENERAL INFORMATION:

; APPLICANT: Singletary, George

; APPLICANT: Zhou, Lan

; TITLE OF INVENTION: No. 6734341el Starch Synthase Polynucleotides

; TITLE OF INVENTION: and Their Use in the Production of New Starches

; FILE REFERENCE: 1144D

; CURRENT APPLICATION NUMBER: US/10/044,543

; CURRENT FILING DATE: 2002-01-11

; PRIOR APPLICATION NUMBER: 09/388,743

; PRIOR FILING DATE: 1999-09-02

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 25

; LENGTH: 2418

; TYPE: DNA

; ORGANISM: Typha latifolia

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2418)

US-10-044-543-25

Alignment Scores:

Pred. No.:	6.63e-120	Length:	2418
Score:	1103.00	Matches:	243
Percent Similarity:	59.7%	Conservative:	78
Best Local Similarity:	45.2%	Mismatches:	176
Query Match:	38.1%	Indels:	42
DB:	3	Gaps:	12

US-10-628-525A-21 (1-539) x US-10-044-543-25 (1-2418)

QY	15	GluclytlealaGluGlySerIleAspAsnThrValValValAlaSerGluGlnAspSer	34
Db	574	GAAGATCTTGTAGAAGCAAAATTGGATAGTGATCATGTC	618
QY	35	GlutleValValGlyLysGluGln	48
Db	619	GATTTGAATCTGGGGAAGAAATAGAGTGCTCTCTTGGCTGGGGCAATGTC	675
QY	49	GlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGly	68
Db	676	ATGAACATCATAGTAGTTGCTGCAGAAATGTCTCTTGGTCCAAAACAGGTGGGCTTGA	735
QY	69	AspValCysGlySerLeuProValAlaLeuAlaIleArgGlyHisArgValMetValVal	88
Db	736	GATGTTCCAGGAGCATTTGCCAAGGCTTTGGCCAGAAGACATAGGGTCATGGTTGTG	795
QY	89	MetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAlaPheTyrThrGlu	108
Db	796	GCACCAAGGTATGGAACATATGCTGAACCCAGATATAGAGTGCCCAAAATCTACAG	855
QY	109	LysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlyTyr	128
Db	856	GTTCAT	897
QY	129	ArgAspSerValAspTrpValPheValAspHisProSerTyr	147
Db	898	ATCGACGGTGTGGATTTTGTATGGATAGTCCAGACTTCGGTCCACCGGGGAATCGT	957
QY	148	LeuTyr	166
Db	958	ATTATGAGGGAACCGAGTG	1005
QY	167	CysTyrAlaAlaCysGluAlaProLeuIleLeuGlyGlyTyrIleTyrGlyGln	186
Db	1006	TGCAAGCAGCTGTAGAGGTTCTTGGCATGTTCCATGTGGTGGCTCTCTGTATGGAGAT	1065

RESULT 28



US-09-345-214-16/c  
; Sequence 16, Application US/09345214  
; Patent No. 6392120  
; GENERAL INFORMATION:  
; APPLICANT: Lightner, Jonathan E.  
; APPLICANT: Broglie, Karen E.  
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE  
; TITLE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS  
; FILE REFERENCE: BB-1147  
; CURRENT APPLICATION NUMBER: US/09/345,214  
; CURRENT FILING DATE: 1999-06-30  
; EARLIER APPLICATION NUMBER: 060/094,436  
; EARLIER FILING DATE: 1998-07-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 16  
; LENGTH: 1798  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-345-214-16

Alignment Scores:  
Pred. No.: 6.24e-119 Length: 1798  
Score: 1093.00 Matches: 244  
Percent Similarity: 58.2% Conservative: 73  
Best Local Similarity: 44.8% Mismatches: 167  
Query Match: 37.8% Indels: 62  
DB: 3 Gaps: 12

US-10-628-525A-21 (1-539) x US-09-345-214-16 (1-1798)

```
QY 10 LeuGlyLeuGluProGluGlyLeuAlaGluGlySerLeuAspLeuThrValValAla 29
Db : : : : :
QY 1601 GTTGGTCGATGATGCTGCTGCTTTTGAACATTTATGGGACAAAT----- 1557
Db : : : : :

QY 30 SerGluGlnAspSerGluLeuValValGlyGluGlnAlaArgAlaLysValThrGln 49
Db : : : : :
QY 1556 -----GATTCGGGCTTTGGCCGGGAGAAAT-----GTTATG 1524
Db : : : : :

QY 50 SerLeuValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69
Db : : : : :
QY 1523 AACGTGATCGTGTGGTGTCTGTAATGTTCTCCATGGTGGTGAACAGGTGCTTGGAGAT 1464
Db : : : : :

QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89
Db : : : : :
QY 1463 GTTGTGGGAGCTTTACCAAGGCTTTAGCGGAGAGAGACATCGTGTATGTTGGTA 1404
Db : : : : :

QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109
Db : : : : :
QY 1403 CCAGGGTAT-----GGGACATATGTTGGAAACCTTTGATATGGGAATC 1362
Db : : : : :

QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
Db : : : : :
QY 1361 CGGAATACTACAAAGCTGCAGCAGGACCTAGAGTGAATATTTCCATGATTTATTT 1302
Db : : : : :

QY 130 AspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeu 148
Db : : : : :
QY 1301 GATGGAGTCGACTTGTGTTGTTCAATGATGCCCTCTTTTCGGGACCGTCAAGATGACATA 1242
Db : : : : :

QY 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGluPheArgTyrThrLeuLeuCysTyr 168
Db : : : : :
QY 1241 TATGGG-----GGAGTAGCGAGGAATCATGAAAGCGCATGATTTGTTTCAAG 1191
Db : : : : :

QY 169 AlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyCysTyrIleTyrGlyGln---Asn 187
Db : : : : :
QY 1190 GTTGTGTTGAGGTTCCTTGGCAGCTTCATCGGTGGTGTGTGCTACGGAGATGGAAT 1131
Db : : : : :

QY 188 CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLys 207
Db : : : : :
QY 1130 TTGGTGTTCATTCCTCCAAATGATTGGCAGCTCTGCTGCTTTATCTGAAGGCATAT 1071
Db : : : : :

QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227
Db : : : : :
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RESULT 29

US-09-743-980-16/c

; Sequence 16, Application US/09743980

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Db 1070 TACAGAGACCATGGTTAAATGCAGTACACTCGCTCCGTCTCATACATACATACATCGCC 1011
QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247
Db : : : : :
QY 1010 CACCGGGCGGTGGTCTCTGTAGTAGTAATTCCTGATGACTTGCCTTGAACACTACTCTT 951
Db : : : : :
QY 248 GlyAlaLeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGlyGlu 267
Db : : : : :
QY 950 CAACATTTTCGAGCTGTACGATCCGTC-----GGTGGCGAG 915
QY 268 AlavalAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287
Db : : : : :
QY 914 CACGCCAACATCTTTGCCGCGGTCTGAAGATCGACACCGGGTGTGTGACTGTTCAGCGC 855
QY 288 GlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuSer 307
Db : : : : :
QY 854 GGCTACTGTGGAGCTGAAGACAGTGGAGGGGGCTGGGGCTCCACGACATCTCCGT 795
QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327
Db : : : : :
QY 794 TCTAACGACTGGAAGATCAATGCGATCGTGAACCGCATCGACACCGAGGAGTGAACCCC 735
QY 328 AlaThrAspLysCysIlePro-----CysHisTyrSerValAspAspLeu--- 342
Db : : : : :
QY 734 AAGGTGACGTGACCTGCGGTGCGGACGCGTACACCAACTACTCTCCGAGACACTCGAC 675
QY 343 SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGlyLeuGlyLeuProIleArgPro 362
Db : : : : :
QY 674 GCTGGAAGCGGCGAGTGAAGGGCGCTGCGACGGGAGCTGGGCTTGGAAAGTGGCGAC 615
QY 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIle 382
Db : : : : :
QY 614 GACGTGCGCTGCTCGGCTTCATCGGGCGTCTGATGGAAGAGCGCGTGGACATCATC 555
QY 383 GlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402
Db : : : : :
QY 554 GGGGACGCGATGCGTGGATTCGGGGGCGAGCGTGCAGCTGTGTATGCTGGGACACCGG 495
QY 403 AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422
Db : : : : :
QY 494 CGCGCGGACTTGAACGAATGCTGCGAGCACTTGGAGGGGAGCATCCCAACAGGTGGCG 435
QY 423 GlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442
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QY 434 GGGTGGTGGTCTCTCGGTGCTATGCGGCATCGCATCAGCGCGGCGCGCGAGTGTG 375
QY 443 LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGly 462
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QY 374 GTGATGCTTCCGCTTCGAGCGCTCGGGCTGAACGAGCTCTACGCGATGGCATACGC 315
QY 463 ThrValProValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnPro 482
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QY 314 ACCGTCCCTGTGGTGCACCGCGTGGCGGGCTCAGGGACACCGGTGGCGCGTTCGACCCG 255
QY 483 PheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsn 502
Db : : : : :
QY 254 TTC-----AGCGACGCGGCTCGGGTGGACTTTT----- 225
QY 503 MetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu----- 520
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QY 224 -----GACCGYCCGAGGCCAACAGCTGATCGA--GGCGCTCAGGACACTCGCTCGA 175
QY 521 -----LeuGlyArgAlaAsnGluAlaArgHisValLysArg 532
Db : : : : :
QY 174 CAGGTACCGGAACACTAGCAGGAGCTGGAAAGTCTCCAGGCGCGCGCATGTCCGAGGA 115
QY 533 LeuHisValGlyPro 537
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QY 114 CCTCAGCTGGGACCA 100
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; Patent No. 6570008
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; FILE REFERENCE: BB-1147-A
; CURRENT APPLICATION NUMBER: US/09/743,980
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 060/094,436
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-743-980-16

Alignment Scores:
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Score: 1093.00 Matches: 244
Percent Similarity: 58.2% Conservative: 73
Best Local Similarity: 44.8% Mismatches: 167
Query Match: 37.8% Indels: 62
DB: 3 Gaps: 12

US-10-628-525A-21 (1-539) x US-09-743-980-16 (1-1798)

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QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69
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QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMet 89
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QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109
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QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
   :::::
Db 1361 CGGAATACTACAAGCTGCAGGACAGGACCTAGAGTGAATTTTCCATGCAATTATT 1302

QY 130 AspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeu 148
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QY 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168
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Db 1241 TATGGG-----GGAAGTAGGAGGAGAAATCATGAAGCGCATGATTTTGTGTCAG 1191

QY 169 AlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyTyrIleTyrGlyGln---Asn 187
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Db 1190 GTTGTCTGTTGAGTTCCTTGGCAGCTTCCATGCGGTGGTGTGTCTACGGAGATGGA 1131

QY 188 CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLys 207
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QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227
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Db 1070 TACAGAGACATGGGTGTTATGATGATACACTCGCTCGCTGCTGATACATACATCGCC 1011

QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyr 247

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## RESULT 30

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US-09-345-214-15
; Sequence 15, Application US/09345214
; Patent No. 6392120
; GENERAL INFORMATION:
; APPLICANT: Lightner, Jonathan E.

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QY 268 AlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287
   :::::
Db 914 CACGCCAACATCTTTGCGCGGTCTGAAGATGGCAGACCGGTGGTGTGATGTGTCAGCCG 855

QY 288 GlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307
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Db 854 GGCTACCTGTGGAGCTGAAGACAGTGGNAGCGGCTGGGGCTCCACACATCATCCGT 795

QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327
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QY 343 SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362
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QY 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuLeu 382
   :::::
Db 614 GACGTGCGCTCTCGGCTTCATCGGGCTCTGGATGGACAGAGGGCTGGACATCATC 555

QY 383 GlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402
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Db 554 GGGGACCGGATCCCTGGATCGGGGCGAGGACGTGACGTGATGCTGGGACCCGG 495

QY 403 AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422
   :::::
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QY 423 GlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442
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Db 434 GGTGGTGGCTGCTGCTGCTGCTATGGCGCATCGCATCACGGCGGCGGCCGACGTGTG 375

QY 443 LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGly 462
   :::::
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QY 463 ThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnPro 482
   :::::
Db 314 ACCGTCCCTGTGTGTCACCGCGTGGCGGGCTCAGGACACCGTGGCGCGCTTCGACCCG 255

QY 483 PheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsn 502
   :::::
Db 254 TTC-----AGCGACCGCGGCTCGGGTGGACTTTT----- 225

QY 503 MetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu----- 520
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Db 224 -----GACCGTGGCGGCGGCGGAGCTGGAAGTGTGA-----GGCGCTCAGGAC 175

QY 521 -----LeuGlyArgAlaAsnGluAlaArgHisValLysArg 532
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Db 174 CACGTACCGGAACACTACGAGGAGAGCTGGAAGAGTCTCCAGGCGCGCGCATGTCCG 115

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RESULT 30
US-09-345-214-15
; Sequence 15, Application US/09345214
; Patent No. 6392120
; GENERAL INFORMATION:
; APPLICANT: Lightner, Jonathan E.

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; APPLICANT: Broglie, Karen E.
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; FILE REFERENCE: BB-1147
; CURRENT APPLICATION NUMBER: US/09/345,214
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 060/094,436
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-345-214-15

Alignment Scores:
Pred. No.: 7,55e-119 Length: 2019
Score: 1093.00 Matches: 244
Percent Similarity: 58.2% Conservative: 73
Best Local Similarity: 44.8% Mismatches: 167
Query Match: 37.8% Indels: 62
DB: 3 Gaps: 12

US-10-628-525a-21 (1-539) x US-09-345-214-15 (1-2019)

Qy 10 LeuGlyLeuGluProGluGlyLeuAlaGluGlySerileAspAthrValValAla 29
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204 GTTGGTCAGATGATGCTGTTCTTTTGAACATTATGGGACAAAT----- 248

Qy 30 SerGluGlnAspSerGluLeuValValGlyGluGlnAlaArgAlaLysValThrGln 49
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249 -----GATTCCTGGGCTTTGGCCGGGGAGAAAT-----GTTATG 281

Qy 50 SerileValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69
Db : : : : :
282 AACGTGATGCTGGTGGCTGCTGATGTTCTCCATGTCGAACAGGTGCTTGGAGAT 341

Qy 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89
Db : : : : :
342 GTTGTGGGAGCTTTACCAAGGCTTTAGCGAAGAGGACATCGTGTATGTTGGTA 401

Qy 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109
Db : : : : :
402 CCAAGGTAT-----GGGAGCTATGTGGAAGCCTTTGATATGGGAATC 443

Qy 110 HisileArgileProCysPheGlyGlyGluHisGluValThrPheHisGluTyrArg 129
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444 CGGAATACTACAAGCTGCAGACAGGACCTAGAGTGAACATATTTCCATGCAATTATT 503

Qy 130 AspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeu 148
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Qy 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLysTyr 168
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Qy 169 AlaAlaCysGluAlaProLeuLeuGluLeuGlyTyrileTyrGlyGln---Asn 187
Db : : : : :
615 GTTGCTGTTGAGGTTCTTGGCAGCTTCATGCGGTGGTGTGTGCTACGGAGATGGAAT 674

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Db : : : : :
675 TTGGTGTTCATTGCAATGATTGGCACACTGCTGCTGCTGTTTATCTGAAGGCATAT 734

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Qy 288 GlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLysSer 307
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Db : : : : :
1251 GGGGACGCGATGCGTGGATCGCGGGGCGAGCGTGTGATGCTGGGCGACCGGG 1310

Qy 403 AspProGluLeuGluAspTrpMetArgSerThrGluSerilePheLysAspLysPheArg 422
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1311 CGCGCGACTGGAACGAATGCTGCGAGCTTGGAGCGGAGCATCCCAACAGGTGCGC 1370

Qy 423 GlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442
Db : : : : :
1371 GGGTGGTGGTCTCTCGTGGCTATGCGGCATCGCATCAGCGGGCGCGCGACGTGTG 1430

Qy 443 LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGly 462
Db : : : : :
1431 GTGATGCCCTCCGCTTCGAGCCCTCGGGCTGACACGCTCTACGCGATGGCATACGGC 1490

Qy 463 ThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnPro 482
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86	718.5	24.8	1427	3	US-09-974-300-757	Sequence 757, App
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124	587	20.3	1830121	9	US-10-981-687-1	Sequence 1, Appli
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131	574	19.8	1386	6	US-10-369-493-39259	Sequence 39259, A
132	574	19.8	1386	6	US-10-369-493-39632	Sequence 39632, A
133	570	19.7	1380	6	US-10-369-493-40000	Sequence 40000, A
134	569.5	19.7	1462	6	US-10-369-493-43581	Sequence 43581, A
135	567	19.6	1443	6	US-10-369-493-31662	Sequence 31662, A
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139	549.5	19.0	992	7	US-10-628-525-4	GENERAL INFORMA
140	547.5	18.9	4470	8	US-10-425-114-15417	Sequence 15417, A
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142	533.5	18.4	1464	6	US-10-369-493-37806	Sequence 37806, A
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144	528	18.3	3434	6	US-10-369-493-42704	Sequence 42704, A
145	526.5	18.2	1476	6	US-10-044-543-9	Sequence 9, Appli
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147	521	18.0	1286	7	US-10-369-493-47119	Sequence 47119, A
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					US-10-424-799-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1		US-10-628-525-20	
		; Sequence 20, Application US/10628525	
		; Publication No. US20040185114A1	
		; GENERAL INFORMATION:	
		APPLICANT: Keeling, Peter	
		Guan, Hanning	
		TITLE OF INVENTION: Starch Encapsulation	
		NUMBER OF SEQUENCES: 37	
		CORRESPONDENCE ADDRESS:	
		ADDRESSER: Greenlee, Winner and Sullivan, P.C.	
		STREET: 5370 Manhattan Circle	
		CITY: Boulder	
		STATE: CO	
		COUNTRY: US	
		ZIP: 80303	
		COMPUTER READABLE FORM:	
		MEDIUM TYPE: Floppy disk	
		COMPUTER: IBM PC compatible	
		OPERATING SYSTEM: PC-DOS/MS-DOS	
		SOFTWARE: Patentin Release #1.0, Version #1.30	
		CURRENT APPLICATION DATA:	
		APPLICATION NUMBER: US/10/628,525	
		FILING DATE: 28-Jul-2003	
		CLASSIFICATION: 800	
		PRIOR APPLICATION DATA:	
		APPLICATION NUMBER: US/08/941,445	
		FILING DATE: 30-SEP-1997	
		APPLICATION NUMBER: US 60/026,855	
		FILING DATE: 30-SEP-1996	
		ATTORNEY/AGENT INFORMATION:	
		NAME: Winner, Ellen P	
		REGISTRATION NUMBER: 28,547	
		REFERENCE/DOCKET NUMBER: 89-97	
		TELECOMMUNICATION INFORMATION:	
		TELEPHONE: (303) 499-8080	
		TELEFAX: (303) 499-8089	
		INFORMATION FOR SEQ ID NO: 20:	
		SEQUENCE CHARACTERISTICS:	
		LENGTH: 1620 base pairs	
		TYPE: nucleic acid	
		STRANDEDNESS: double	
		TOPOLOGY: Not Relevant	
		MOLECULE TYPE: cDNA to mRNA	
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		NAME/KEY: CDS	
		LOCATION: 1..1620	
		SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
		US-10-628-525-20	
		Alignment Scores:	
		Pred. No.: 0	
		Score: 2893.00	
		Length: 1620	
		Matches: 539	
		Conservative: 0	
		Mismatch: 0	
		Best local Similarity: 100.0%	
		Query Match: 100.0%	
		Indels: 0	
		DB: 8	
		US-10-628-525-21 (1-539) x US-10-628-525-20 (1-1620)	
QY	1	CysValAlaGluLeuSerArgGluAspLeuGluProGluGluGluGluGluGly	20
DB	1	TGCGTCGGCGAGCTGAGCAGGAGGACCTCGGTCCTCGAACCTGGAAGGATTCTGAAGGT	60
QY	21	SerIleAspAsnThrValValAlaSerGluGlnAspSerGluIleValValGlyLys	40
DB	61	TCCATCGATACACAGTAGTTGTGGCAAGTAGGATTCGAGATTGTGGTTGGAAG	120
QY	41	GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyLysAlaSerPro	60
DB	121	GAGCAAGCTCGAGCTAAAGATTAACACAAAGCATTTGTTTGTAAACCGGCGAGCTTCTCCT	180

Qy	61	TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAla 80
Db	181	TATGCAAAAGTCTGGGGGCTCTAGGAGATGTTTGTGGTTCATTGCCAGTTGCTCTTGCTGCT 240
Qy	81	ArgGlyHisArgValMetValValMetProArgTyrLeuAenGlyThrSerAspLysAen 100
Db	241	CGTGGTCACCGCTGTGATGGTTGTAATGCCAGATATTAAATGGTGTACCTCCGATAAAGAA 300
Qy	101	TyrAlaAenAlaPheTyrThrGluLysHisLeArgLleProCysPheGlyGlyGluHis 120
Db	301	TATGCAAAATGCAATTTTACACAGNAAAACACATTCGGATTCATGCTTTGGCGGGTGAACAT 360
Qy	121	GluValThrPhePheHisGluTyrArgAspSerValAspTTPValPheValAspHisPro 140
Db	361	GAAGTTACCTCTCCATGAGTATAGAGATTCAGTTGACTGGGTGTTTGTGTGATCATCCC 420
Qy	141	SerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAenGln 160
Db	421	TCATATCACAGACCTGGAAATTTATATGCAGATAAGTTTGGTGTCTTTGGTGATAAATCAG 480
Qy	161	PheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLleLeuGluLeuGly 180
Db	481	TTCCAGATACACACCTCTTGTCTATGTGTCATGTAGGCTCTTTGATGCTTTGAATTCGGGA 540
Qy	181	GlyTyrIleTyrGlyGlnAsnCysMetPheValValAenAspTTPHisAlaSerLeuVal 200
Db	541	GGATATATTATGACAGAAATTCATGTTGTGTCTCAATGATTTGGCATGGCATGCTTAGTG 600
Qy	201	ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220
Db	601	CCAGTCTCTTCTGCTGCAAAATATAGACCATATGGTGTGTTTATAAAGACTCCCGCAGCAT 660
Qy	221	LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240
Db	661	CTTGTAATACATAATTTAGCACATCAGGGGTAGAGCCTGCAAGCACATATCTCGACCTT 720
Qy	241	GlyLeuProGluTTPTrpTyrGlyAlaLeuGluTTPValPheProGluTTPAlaArgArg 260
Db	721	GGGTGGCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTTCCCTGTAATGGGCGAGGAGG 780
Qy	261	HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280
Db	781	CATGCCCTTGACAAGGGTGAGGCAGTTAAATTTTTGAAAGGTGCAGTTGTGACAGCAGAT 840
Qy	281	ArgIleValThrValSerLysGlyTyrSerTTPGluValThrThrAlaGluGlyGlyGln 300
Db	841	CGAATCTGATCTGTCACTAAAGGGTTATTCGGGGAGGTCACAACTGCTGAAGGTGGACAG 900
Qy	301	GlyLeuAenGluLeuLeuSerSerArgLysSerValLeuAenGlyLleValAenGlyLle 320
Db	901	GGCCTCAATGAGCTCTTAAGCTCCAGAAAGNGTGTATTAAACGGAAATTTGAATGGAAAT 960
Qy	321	AspIleAenAspTTPAenProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340
Db	961	GACATTAATGATTGGAAACCTTCCACACAGACAAATGTATCCCTGTCTATTCTCTGTTGAT 1020
Qy	341	AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLysProIle 360
Db	1021	GACCTCTCTGAAAGGCCAAATGTAAAGGTGCATTCAGAAAGGAGCTGGGGTTTACCTATA 1080
Qy	361	ArgProAspValProLeuLleGlyPheIleGlyArgLeuAspTyrGlnLysGlyLleAsp 380
Db	1081	AGGCCTGATGTTCTCTGATTGGCTTTATTGGAAGTTGGATATACAGAAAGGCATTTGAT 1140
Qy	381	LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400
Db	1141	CTCATTCAACTTATCATACACAGATCTCATGGCGGAAGATGTTCAATTTGTCTGCTTTGGA 1200
Qy	401	SerGlyAspProGluLeuGluAspTTPMetArgSerThrGluSerIlePheLysAspLys 420
Db	1201	TCTGGTGACCCAGAGCTTGAAGATTGATGAGATCTACAGAGTGCATCTTCACAGGATATAA 1260

Qy	421	PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp	440
Db	1361	TTTCGTGGATGGGTGGATTAGTGTTCAGTTTCCACCAGATAACTGCCGGCTGCGAT	1320
Qy	441	IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrrAlaMetGln	460
Db	1321	ATATTGTTAATGCCATCCAGATTTCGAACCTTGTGGTCTCAATCAGCTATATGCTATGTCAG	1380
Qy	461	TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe	480
Db	1381	TATGGCACAGTTCCTGTTGTCCATGCNACTGGGGGCCCTTAGAGATACCGTGGAGAAGCTTC	1440
Qy	481	AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrPalaPheAlaProLeuThrThr	500
Db	1441	AACCTTTCCTGGTGGAGATGGAGACGAGGGTACAGGGTGGGCATTTCGCACCCCTAACCCACA	1500
Qy	501	GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu	520
Db	1501	GAATAACATGTTTGTGGACATTGGGNACTGGCAATATCTACATACAGGGACACAAAGTCTCTC	1560
Qy	521	LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg	539
Db	1561	CTGGGAAGGCGCTAATGAAGCGAGCGATGTCAAAAGACTTCACGTGGGACCATCGCCG	1617

## RESULT 2

US-10-336-753-52

; Sequence 52, Application US/10336753

; Publication No. US20030226176A1

; GENERAL INFORMATION:

; APPLICANT: Guan, Hanping

; APPLICANT: Keeling, Peter L.

; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN

; TITLE OF INVENTION: HOSTS

; FILE REFERENCE: 2461-52

; CURRENT APPLICATION NUMBER: US/10/336,753

; CURRENT FILING DATE: 2003-01-06

; PRIOR APPLICATION NUMBER: US/09/402,254

; PRIOR FILING DATE: 1998-10-01

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 52

; LENGTH: 1749

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1) .. (1749)

US-10-336-753-52

Alignment Scores:				
Pred. No.:	0	Length:		1749
Score:	2861.00	Matches:		539
Percent Similarity:	92.5%	Conservative:		0
Best Local Similarity:	92.5%	Mismatches:		0
Query Match:	98.9%	Indels:		44
DB:	6	Gaps:		1

US-10-628-525A-21 (1-539) x US-10-336-753-52 (1-1749)

1 CyeValAlaGluLeuSerArgGlu-----8  
 Qy |||||  
 1 TGGTTCGCGAGCTGACGAGGAGGGCCGCGCGCGCTGCCACCGCGCTGCTG 60  
 Db |||||  
 8 -----8  
 Qy  
 61 GGCGCCCGCTGTCGCCCGCTTCTCGGCGCGCGCGAGACCCACGGGTGAGCCGGCA 12  
 Db |||||  
 9 -----AspLeuGlyLeuGluProGluGly 16  
 Qy |||||

Db 121 TCACGCCGCCGCCCTGGCCGACGCCGCTGGGGACCTCGGTCTCGAACCTGAAGG 180  
Qy 17 IleAlaGluGlySerIleAspThrValValAlaSerGluGlnAspSerGluIle 36  
Db 181 ATTGCTGAAGGTTCCATCATCAACAGTAGTGTGGCAAGTGGAGCAAGATTCAGATT 240  
Qy 37 ValValGlyGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 241 GTGGTTGGAAGGAGCAGCTCGAGCTAAGTAACACAAAGCATTCCTTTGTAAACCGC 300  
Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 301 GAAGCTTCCTTATCAAAAGTCTGGGGCTAGGAGATGTTTGTGGTTCATTGCCAGTT 360  
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrIleuAsnGlyThr 96  
Db 361 GCTCTTGGCTGCTGGTGCACCGTGGATGGTGTGTAATCCCAAGATATTTAAATGGTACC 420  
Qy 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 421 TCCGATAAGATTAATGCAATGCAATTTACACAGAAACACATTCGGATTCATGCTTT 480  
Qy 117 GlyGlyGluGlnValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
Db 481 GCGCGTGAACATCAAGTTACCTTCTCCATGAGTATAGAGATTCAGTTGACTGGGTGTTT 540  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 541 GTTGATCATCCCTCATATCACAGACTCGGAATTTATATGGAGATAAGTTTGGTGTCTTT 600  
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 601 GGTGATAAATCAGTTACAGATACACACTCTTTCATGCTGCATGTGAGGCTCTCTTGATC 660  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
Db 661 CTTGAATGGGAGGATATATTTATGACAGAAATTCATGTTGTTGTCATGATGGCAT 720  
Qy 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 721 GCCAGTCTAGTGCCAGTCTCTTCTGTCGCAAAATATAGACCATATGTTGTTATAAAGAC 780  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 781 TCCCGCAGCATCTCTGTAATACATAATTTAGCACATCAGGGGTAGAGCTCGACACACA 840  
Qy 237 TyrProAspLeuGlyLeuProGluTyrPyrGlyAlaLeuGluTyrPyrValPheProGlu 256  
Db 841 TATCCTGACCTTGGGTGGCCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTCCTGAA 900  
Qy 257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
Db 901 TGGCGGAGGAGGATGCCCTTGACAGGGGTAGGCGAGTTAAATTTTGAAGGTCGAGTT 960  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrPyrGluValThrAla 296  
Db 961 GTGACAGCAGATCGAATCTGACTGTCTAGTAAAGGTTATTCGTGGAGGTCACTGCT 1020  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1021 GAAGGTGAGCAGGGCCTCAATGAGCTCTTAAAGTCCAGAAAGAGTGATTTAAACCGAAT 1080  
Qy 317 ValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1081 GTAATGGAAATTTGACATTAATGATTGGAACCTCGCCACACAGAAATGATCCCTGTGAT 1140  
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyValAlaLeuGlnLysGluLeu 356  
Db 1141 TATTCCTGTTGATGACCTCTCTGMAAGGCCAAATGTAAGGTGATTCAGAAAGGAGCTG 1200  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1201 GGTTTTACCTATAAGGCCCTGATGTTCTCTGATGGCTTTTATTGGAAGGTTGGATTATCAG 1260

Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
Db 1261 AAAGGCAATGATCTCATTCACATTTATPACACAGATCTCATCGGGAAGATGTTCAATTT 1320  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416  
Db 1321 GTCATGCTTGGATCTGGTGCACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1380  
Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
Db 1381 TTCAAGGATAAAATTTCTGGATGGGTGGATTAGTGTTCAGTTCCTCCACCGAATAACT 1440  
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
Db 1441 GCCGGCTGGATATATTTGTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 1500  
Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
Db 1501 TATGCTATGCAGTATGGCACAGTCTCTGTGTCCATGCAACTGGGGGCTTAGAGATACC 1560  
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496  
Db 1561 GTGGAGAACTTCAACCTTTTCGGTGCAGATGGAGATGGAGAGCAGGTACAGGGTGGCATTCGCA 1620  
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
Db 1621 CCCCTAACACAGAAACATGTTTGGACATTCGCACTTCGCAATCTACATACAGGGA 1680  
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
Db 1681 ACACAAGTCTCTCTGGGAAGGCTAATGAAGCGAGGCATGTCAAAAGACTTCACGTGGGA 1740  
Qy 537 ProCysArg 539  
Db 1741 CCATGCCGC 1749  
RESULT 3  
US-10-628-525-12  
; Sequence 12, Application US/10628525  
; Publication NO. US20040185114A1  
; GENERAL INFORMATION:  
; APPLICANT: Keeling, Peter  
; Guan, Haining  
; TITLE OF INVENTION: Starch Encapsulation  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESSES:  
; ADDRESS: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/628,525  
; FILING DATE: 28-Jul-2003  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/941,445  
; FILING DATE: 30-SEP-1997  
; APPLICATION NUMBER: US 60/026,855  
; FILING DATE: 30-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winner, Ellen P  
; REGISTRATION NUMBER: 28,547  
; REFERENCE/DOCKET NUMBER: 89-97  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080



**TELEFAX: (303) 499-8089**

\*\*\*\*\* (303) 499-6085  
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1752 base pairs

TYPE: nucleic acid

TYPE: NUCLEIC ACID  
STRANDEDNESS: double

TOPOLOGY: Not Relevant

TOPOLOGY: NOT RELEVANT  
MOLECULAR TYPE: cDNA FOR mRNA

MOLECULE TYPE: CDNA TO mRNA  
HYPOTHETICAL: NO

**HYPOTHETICAL: NO  
ORIGINAL SOURCE:**

ORIGINAL SOURCE:  
ORGANISM. 703 11110

ORGANISM: *Zea mays*  
FRUITING.

FEATURE:

NAME/KEY:	CDS
LOCATION:	1. 1000

LOCATION: 1.1752

SEQUENCE	DESCRIPTION	SEQ ID
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99	...	...
100	...	...

**Alignment Scores:**

Pred. No.:	0	Length:	1752
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1234: NO.:	9	length:	1752
score:	2861.00	Matches:	539

SCORE:	2861.00	MATCHED:	539
Percent similarity:	92.5%	Conservative:	0

Percent Similarity:	92.3%	Conservative:	0
Best Local Similarity:	92.5%	Mismatches:	0

Best Local Similarity:	92.5%	Mismatches:	0
Query Match:	98.9%	Indels:	44

Query Match:	98.9%	Indels:	44
DB:	0	Cont:	1

US-10-628-525A-21 (1-539) x US-10-628-525-12 (1-1752)

1	CysValAlaGluLeuSerArgGlu	8
1	TGCGTCGGAGCTGAGCAGGGGCGCGCGCGCGCTGCCACCGCGCTGCTG	60
8	-----	8
61	GGCGCCCCGCTCGTCCCGGCTTCTCGCGCGCGCGCGCGCGCGCGCGCGCA	120
9	-----AspLeuGlyLeuGluProGluGly	16
121	TCGACGCGCGCGCGTCCCGACGCGCGGCTGGGGGACCTCGGTCTCGAACCTGAGGG	180
17	IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle	36
181	ATTGCTGAGGTTCCATGCATAACACAGTAGTTGTGGCAAGTGAAGCAAGATTCTGAGATT	240
37	ValValGlyLyseGluGlnAlaArgAlaIysValThrGlnSerIleValPheValThrGly	56
241	GTGGTTGGNAGGACCAAGCTCGAGCTAAGTAACTAACAAAGCATGTGTTTGTAAACCGGC	300
57	GluAlaSerProTyrAlaIysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal	76
301	GAAGCTTCTCTTATGCAAAGCTCTGGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT	360
77	AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr	96
361	GCTCTTGCTGCTCGTGGTCAACGCTGATGTTGTAATGCCAGATATTTAAATGGTACC	420
97	SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe	116
421	TCCGATAGAAATTATGCANAATGCATTTTACACAGAAAACACATTCGATTCATGCTTT	480
117	GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe	136
481	GGCGGTGAACATGAAGTTTACCTCTCTCCATGAGTATAGAGATTCAGTTCGGTGT	540
137	ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe	156
541	GTGTGATCATCCCTCATATCACAGACCTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT	600
157	GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle	176
601	GGTGATAATCAGTTCAGATACACACTCTTTGCTATGCTGCATGTGAGGCTCCTTTGATC	660
177	LeuGluLeuGlyGlyTyrIleTyrGlyClnAsnCysMetPheValValAsnAspTyrHis	196



Db 2279 GTGAGAACTTCAACCCCTTTTCGTGAGAAATGGAGAGCAGGGTACAGGGTGGGCATTTCGCA 2338  
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
Db 2339 CCCCTAACCA CAGAAACATGTTTGTGGACATTGCGAACTGCAATATCTACATACAGGA 2398  
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValIysArgLeuHisValGly 536  
Db 2399 ACACAAGTCTCTCTGGGAAGGGCTAAATGAACGAGGCAATGTCAAAGACTTCAAGTGGGA 2458  
Qy 537 ProCysArg 539  
Db 2459 CCATGCCGC 2467

RESULT 5  
US-10-425-115-54073/c  
; Sequence 54073, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 54073  
; LENGTH: 3123  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(3123)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_149315C.1  
US-10-425-115-54073

Alignment Scores:  
Pred. No.: 0 Length: 3123  
Score: 2861.00 Matches: 539  
Percent Similarity: 92.5% Conservative: 0  
Best Local Similarity: 92.5% Mismatches: 0  
Query Match: 98.9% Indels: 44  
DB: 8 Gaps: 1

US-10-628-525A-21 (1-539) x US-10-425-115-54073 (1-3123)

Qy 1 CysValAlaGluLeuSerArgGlu-----8  
Db 2273 TGGTTCGGAGCTGAGCAGGAGGGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTG 2214  
Qy 8 -----8  
Db 2213 GCGCCCGCGCTCGTGGCGCGCTTCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 2154  
Qy 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 2153 TCAGCGGG 2094  
Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 2093 ATTGCTGAAGTTCATCGATACACAGTAGTGTGGCAAGTAGGCAAGATTCTGAGATT 2034  
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 2033 GTGGTTGGAAAGGAGCAAGCTCGAGCTAAAGTAAACAAAGCATTTGTCTTTTAAACCGGC 1974  
Qy 57 GluAlaSerProTyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProVal 76

Db 1973 GAAGCTTCTCTTATNGCAAGTCTGGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT 1914  
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
Db 1913 GCTCTTGTCTCTGTGTGTACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACC 1854  
Qy 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 1853 TCCGATAAAGAAATATGCAAAATGCAATTTTACACAGAAAAACACATTTCGATTCATGCTTT 1794  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
Db 1793 GCGCGTGAACATGAAGTTACCTTCTTCCATGAGTATAGAGATTTCAGTTGATGCGGTGTTT 1734  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 1733 GTTGATCATCCCTCATATACAGACCTGGAAATTTATATGGAGATAAGTTTGGTGCCTTTT 1674  
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 1673 GGTGATAAATCAGTTTCAGATACACACTCTTTCGTATGCTGCAATGTAGGCTCTCTTCATC 1614  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrPhe 196  
Db 1613 CTTGAATTTGGAGAGATATATTTATGACAGAAATTCATGTTTGTTCATGATTGGCAT 1554  
Qy 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 1553 GCCAGTCTAGTGCAGTCTCTTCTGTGCAAAATATAGACCATATGGTGTGTTATAAGAC 1494  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 1493 TCCCGCAGCATCTCTGTAATACATAATTTAGCACATCAGGGTGTAGAGCTCGCAAGCACA 1434  
Qy 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 1433 TATCCTGACCTTGGGTTCGCACCTGAATGGTATGAGAGCTCTGAGTGGGTATTCCCTGAA 1374  
Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyValAlaVal 276  
Db 1373 TGGCGCGAGGAGCATGCCCCCTTGACAGGGTGTAGCGAGTTAATTTTGAAGGTGCAGTT 1314  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
Db 1313 GTGACAGCAGATCGAATCGTGAATCGTGAAGGGTATTTCGTGGAGGAGTGCACAACTGCT 1254  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1253 GAAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAAAT 1194  
Qy 317 ValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1193 GTAAATGGAAATTGACATTAATGATTGGAACTCTGCCACAGCAAAATGATATCCCTGTGAT 1134  
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysGlyGlyAlaLeuGlnLysGluLeu 356  
Db 1133 TATTCCTGTGTGATGACCTCTCTGAAAGGCCAAATGTAAGGTGCAATTGCAGAGGAGCTG 1074  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1073 GGTATTACCTATTAAGGCTCATGTTCTCTGATTTGGCTTTTATTGGAAGGTGGGATATTCAG 1014  
Qy 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396  
Db 1013 AAAGCATTTGATCTCATTTCACTTATCATCCAGATCTCATGCGGAGAGATGTTCAATTT 954  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416  
Db 953 GTCATCTCTGGATCTCGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTGCATC 894  
Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
Db 893 TTCAGAGATAAAATTTTCGTGGATGGGTGGATTTAGTGTTCAGTTTCCAGTTTCCCAACCAACT 834

QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAanGlnLeu 456  
Db 833 GCGGGTGGATATATTGTAATGCCATCCAGATTCGAACCTTGTTGTTCTCATCAGCTA 774  
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
Db 773 TATGCTATGAGTATGCCACAGTTCCTGTTGTCATGCAACTGGGGCCCTTAGAGATACC 714  
QY 477 ValGluAanPheAanProPheGlyGluAanGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
Db 713 GTGGAGAACTTCAACCTTTCGGTGAGATGGAGACGCGGTACAGGGTGGGCATTCGCA 654  
QY 497 ProLeuThrThrGluAanMetPheValAspIleAlaAanCysAanIleTyrIleGlnGly 516  
Db 653 CCCCTAACACAGAAACATGTTTGGACATTCGCACTGCAATATCTACATACAGGA 594  
QY 517 ThrGlnValLeuLeuGlyArgAlaAanGluAlaArgHisValLysArgLeuHisValGly 536  
Db 593 ACACAAGTCTCTCTGGGAAGGCTAATGAAGCGAGGCATGTCAAAGACTTTCACGTGGGA 534  
QY 537 ProCysArg 539  
Db 533 CCATGCCGC 525

## RESULT 6

US-09-931-297-1  
; Sequence 1, Application US/09931297  
; Publication No. US2002008023A1  
; GENERAL INFORMATION:  
; APPLICANT: Jens Rosemann  
; Claus Froberg  
; TITLE OF INVENTION: Nucleic acid molecules encoding soluble  
; starch synthases from maize  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: James F. Haley, Jr., c/o FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPA)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/931,297  
; FILING DATE: 16-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/192,909  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: DE 196 19 918.2  
; FILING DATE: 17-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley, Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: GFB-9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-96-9090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2383 base pairs  
; TYPE: nucleotide  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:

ORGANISM: Zea mays  
TISSUE TYPE: endosperm  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..1950  
OTHER INFORMATION: /function= "starch synthesis"  
/product= "soluble starch synthase"  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-931-297-1  
Alignment Scores:  
Pred. No.: 0 Length: 2383  
Score: 2818.00 Matches: 534  
Percent Similarity: 92.1% Conservative: 3  
Best Local Similarity: 91.6% Mismatches: 2  
Query Match: 97.4% Indels: 45  
DB: 3 Gaps: 1  
US-10-628-525A-21 (1-539) x US-09-931-297-1 (1-2383)  
QY 1 CysValAlaGluLeuSerArgGluAsp-----9  
Db 146 TCGTGGCGGAGCTGAGCAGGAGGCGCCCGCGCGCGCGATGCCACCCGCGTGTG 205  
QY 9 -----9  
Db 206 GCGCCCCGCTCGTGGCCGGCTTCCTCGCGCGCGCGCGCGAGCCACCGGGTGAGCCGGCA 265  
QY 10 -----LeuGlyLeuGluProGluGly 16  
Db 266 TTGACGCGCGCCCGCTGCCGCGCGCGCTGGGGGTCTCGGTGTGCAACCTGAAGGG 325  
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 326 ATTGCTGAAGTTCCATCGATAACACAGTAGTGTGGCAAGTAGGAGCAAGATTCTGAGATT 385  
QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 386 GTGGTTGGNAAGGAGCAGCTGAGCTAAAGTAAACAAACATTTGCTTTGTAACGGC 445  
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 446 GAAGCTTCTCTTATGCAAAAGTCTGGGGTCTAGGAGATGTTTGTGGTTCAITGCCAGTT 505  
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrIleuAsnGlyThr 96  
Db 506 GCTCTGTGCTCGTGGTCCCGTGTGATGGTGTGTAATATCCAGATATTTAAATGTATCC 565  
QY 97 SerAspLysAsnTyrAlaAanAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 566 TCCGATAGAATTATGCAAAATGCAATTTACACAGAAAAACACATTCGGATTCCATGCTTT 625  
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
Db 626 GCGCGTGAACATGAAGTTACCTTCTCCATGATAGTAGAGATTTCAGTTCAGTGGGTGTTT 685  
QY 137 ValAspHisProSerTyrHisArgProGlyAanLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 686 GTTGATCATCCCTCATATCACAGACTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT 745  
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAaCysGluAlaProLeuIle 176  
Db 746 GGTGATATCAGTTCAAGATACACACTCCTTTGCTATGCTGATGTGAGGCTCCTTTGGTC 805  
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAanCysMetPheValValAanAspTrpHis 196  
Db 806 CTTGAATTGGGAGGATATATTTATGGACAGAAATTCATGTTGTTGTTGTTCAATGATGCGCAT 865  
QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 866 GCCAGTGTAGTCCAGTCTCTTCTGTCGAAATATAGACCATATGTTGTTTATTAAGAC 925  
QY 217 SerArgSerIleLeuValIleHisAanLeuAlaHisGlnGlyValGluProAlaSerThr 236

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Db 926 TCCGCGAGCATCTTGTAAATACATAAATTTACACATCAGGTGTAGAGCCTGCAAGCACA 985
Qy 237 TyrProAspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGlu 256
Db 986 TATCTCGACCTTGGTGGCCACCTGAATGGTATGAGCTCTGGAGTGGGTATTCCTGAA 1045
Qy 257 TrpAlaArgArgHisAlaLeuAspGlyGlyAlaValIleAsnPheLeuLysGlyAlaVal 276
Db 1046 TGGCGAGGAGGCGATGCCCTTGACAGGGTGAGCGAGTGAATTTTGAAGGTGCAGTT 1105
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
Db 1106 GTGACACAGATCGAATCGTACTGTCTAGTAAGGTTATTCATGGGAGGTACAACTGCT 1165
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316
Db 1166 GAAGGTGCAGAGGCGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAAAT 1225
Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 1226 GTAAATGGAAATGACATTAATGATTTGAACCTGCCACAGACAAATGTATCCCTGTCAT 1285
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 1286 TATTCGTGTGATGACCTCTCTGGAAGGCCAAATGTAAAGTGCATTTGCAAGAGGAGCTG 1345
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1346 GGTATTACCTATAGGCGCTGATGTCCTCTGATTTGGCTTTATTTGAAGATTTGATATCAG 1405
Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1406 AAAGGCAATGATCTCAATTCATCACTATCATCCAGATCTCATGCGGGAAGATGTTCAATTT 1465
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
Db 1466 GTCATGCTTGATCTGTGTGACCCAGAGCTTTGAAGATTTGGATGAGATCTACAGAGTCGATC 1525
Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436
Db 1526 TTCAAGGATAAATTTGTGTGATGGTGGTGGATTTAGTGTCCAGTTTCCACCGCAATAACT 1585
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1586 GCGCGCTCGCATATATTTGTAATGCCATCCAGATTCGAACCTTTGTGTCTCAATCAGCTA 1645
Qy 457 TyrAlaMetGlnTyrGlyThrValProValIleAlaThrGlyGlyLeuArgAspThr 476
Db 1646 TATGCTATGCAATGATGCAAGTTCCTGTTGTCCATGCAACTGGGGGCTTTAGAGATACC 1705
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496
Db 1706 GTGGAGAACTTCAACCTTTCCGTGAGATGGAGAGCAGGGGTACAGGGTGGGCAATTCGCA 1765
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
Db 1766 CCCCTAACCCACAGAAACATGTTTGTGACATTCGCAACTGCAATATATACATACAGGGA 1824
Qy 517 ThrGluValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 1825 ACACAAGTCTCTCTGGGAAGGGCTAATGAAGCGAGGATGTCAAAAGAGACTTTCACGTGGGA 1884
Qy 537 ProCysArg 539
Db 1885 CCATGCGC 1893
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## RESULT 7

US-10-767-701-13043  
; Sequence 13043, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 13043  
; LENGTH: 2670  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS52\_1  
US-10-767-701-13043

Alignment Scores:  
Pred. No.: 0 Length: 2670  
Score: 2753.00 Matches: 522  
Percent Similarity: 90.3% Conservative: 6  
Best Local Similarity: 89.2% Mismatches: 11  
Query Match: 95.2% Indels: 47  
DB: 7 Gaps: 1

US-10-628-525A-21 (1-539) x US-10-767-701-13043 (1-2670)

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Qy 8 -----8
Db 330 CTGCTGGCGCGCGCGCTCGTGGCGCGCTTCTCGCGCGCGCTCGAGCCCGAGGGTGAG 389
Qy 9 -----AspLeuGlyLeuGluPro 14
Db 390 CCGCGCTGCACACCGCGCGCGCTGCGCGCAGCGCGCTCTCGCGCACCTCGGTCTCCAACCT 449
Qy 15 GluGlyIleAlaGluGlySerIleAspAsnThrValValAlaIleAspGluGlnAspSer 34
Db 450 GAAGGATTTGCTGAGGGTTCATCGATGAGCAGTAGTGTGGCAAGTAGCAGATTTCT 509
Qy 35 GluIleValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheVal 54
Db 510 GAGATCGTGGTTGGAAGGAGCAAGCTCGAGCTAAAGTAACAACAAGCATTTGTTTGTGA 569
Qy 55 ThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeu 74
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Qy 75 ProValAlaLeuAlaAlaArgGlyHisArgValMetValMetValMetProArgTyrLeuAsn 94
Db 630 CCAGTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689
Qy 95 GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114
Db 690 GGTACCTCTGATAAGAAATTCGCAATGCAATTTTACACAGAAAGCACATTCGGATTCCA 749
Qy 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrThrArgAspSerValAspTrp 134
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Qy 135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154
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Qy 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174
Db 870 GCTTTTGGTGAATAATCAGTTTCAGATCAGCTCCTTTGCTGCTGCTGCTGCTGCTGCT 929
Qy 175 LeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194
Db 930 TTGGTCTCTTGAATTTGGGAGGATATATTTATGACAGAGATTTGTCATTTGTTGTGAATGAT 989
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QY 215 LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234  
Db 1050 AAAGACTCCGCGAGCATCTTGTAATACATATTTAGACATCAGGGTGTAGAGCCTGCA 1109  
QY 235 SerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPhe 254  
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QY 255 ProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
Db 1170 CTTGAATGGCAAGGAGGATGCCCTTGACAGGGTGAGCGAGTTAAATTTTGAAGGT 1229  
QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThr 294  
Db 1230 GCAGTTGTGACAGCAGATCGAATTTGTGACTGTCTAGTAAGGTTATTCATGGGAGGTCA 1289  
QY 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314  
Db 1290 ACTGCTGAAGGTGGACAGGGTCTCAATGAGCTCTTAAGCTCCGAAAGAGTGTATTAAC 1349  
QY 315 GlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro 334  
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QY 335 CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354  
Db 1410 TGTCAATATCTGTTGATGACCTCTCTGGAAAGCCAAATGTAAAGTGCATTCGAGAG 1469  
QY 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374  
Db 1470 GAGCTGGGTTTACCTATAAGGCTGAAGTCTCTCTGATGGTTTATTTGGAAGATTGGAT 1529  
QY 375 TyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspVal 394  
Db 1530 TATCAGAAAGGCAATGATCTCAATCAACTTATCATACCACTCTCATGCGGAGCAGCGTT 1589  
QY 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGlu 414  
Db 1590 CAATTTGTCTATGCTTGGATCTGGTGACCCAGAGCTCGAAGCTGGATGAGATCTACAGAG 1649  
QY 415 SerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArg 434  
Db 1650 TCGGACTTCAAGGATAAAATTTCTGGATGGGTGGATTTAGTGTTCAGTTTCCACCCGA 1709  
QY 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454  
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Db 1770 CAGCTATATGCTATGCAATATGCAAGTTCCTGTTGTCATGCAACTCGGGGCGCTTAGA 1829  
QY 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlnGlyThrGlyTyrAla 494  
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QY 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514  
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QY 515 GlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHis 534  
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QY 535 ValGlyProCysArg 539  
Db 2009 GTGGGACCATGCCG 2023

## RESULT 8

US-10-425-115-184334  
; Sequence 184334, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 184334  
; LENGTH: 1988  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_996C.1  
US-10-425-115-184334

## Alignment Scores:

Pred. No.:	7,01e-314	Length:	1988
Score:	2681.00	Matches:	499
Percent Similarity:	99.8%	Conservative:	3
Best Local Similarity:	99.2%	Mismatches:	1
Query Match:	92.7%	Indels:	1
DB:	8	Gaps:	0

US-10-628-525A-21 (1-539) x US-10-425-115-184334 (1-1988)

QY	37	ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly	56
Db	2	ATGGTGGAAAGGAGCAGCTCGAGCTAAAGTAACACAAAACATTCCTCTTTGTAACGTGC	61
QY	57	GluAlaSerProTyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProVal	76
Db	62	GAAAGCTTCCTTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGGTTTCATTTGCCAGTT	121
QY	77	AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr	96
Db	122	GCTCTGTCTGCTCGTGGTCACCGTGTGATGGTTGTAATGCCAGATATTTAAATGGTACC	181
QY	97	SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe	116
Db	182	TCCGATAAGAAATTATGCAAAATGCAATTTTACACAGAAAAACACATTCGGATTCATGCTTT	241
QY	117	GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe	136
Db	242	GCGGTGAACATGAAGTTACCTTCTTCATGATATAGAGATTCAGTTGACCTGGGTGTTT	301
QY	137	ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe	156
Db	302	GTTGATCATCCCTCATATACAGACCTCGAAATTTATATGGAGATAAGTTTGGTCTTTT	361
QY	157	GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle	176
Db	362	GGTGATAATCAGTTTCAGATACACACTCTCTTCTATGCTATGCTGTCATGTGAGGCTCTCTTTGGTC	421
QY	177	LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis	196
Db	422	CTTGAATTTGGGAGGATATATTTATGACAGAAATTCATGCTGTTGTTGTCATGATGGCAT	481
QY	197	AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp	216
Db	482	GCCAGTCTAGTCCAGTCTCTTCTGTCGCAAAATATAGACCATATGCTGTTTATTAAGAC	541
QY	217	SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr	236
Db	542	TCCCCGAGCATTTCTGTAATACATAATTTAGCACATCAGGGGTAGAGCCTGCAGCAC	601

QY 237 TyrProaspLeuGlyLeuProGluTyrPheGlyAlaLeuGluTyrValPheProGlu 256  
 Db 602 TATCTGACCTTGGTTCACCACTGGAATGGTATGGAGCTCTGGAGTGGTATCCCTGAA 661  
 QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValaAsnPheLeuLysGlyAlaVal 276  
 Db 662 TGGCGAGGAGCATGCCCTTGACAGGGTGAGCAGTTAATTTTGAAGGTGGAGTT 721  
 QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
 Db 722 GTGACAGCAGATCGAATCGTGACTGTCTAGTAAGGGTTATTCATGGGAGGTCCACAACGTCT 781  
 QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyLe 316  
 Db 782 GAAGGTGGACAGGCGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACCGAATT 841  
 QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
 Db 842 GTAAATGGAATTGACATTAATGATGGAACTGCGCCACAGCAAAATGATCCCTGTGCAT 901  
 QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
 Db 902 TATTCCTGATGACCTCTCTGGAAGGCCAAATGTAAAGGTGCATTCAGAGGAGCTG 961  
 QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
 Db 962 GGTTCATTAAGGCTGATGTTCCCTCTGATGGCTTTATTTGAAGATTGGATTATCAG 1021  
 QY 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
 Db 1022 AAGGCATTCATCTCACTTATCATACCAATCTCATGCGGAGAGATGTTCAATTT 1081  
 QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
 Db 1082 GTCATGCTTGCATCTGGTACCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1141  
 QY 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
 Db 1142 TTCAGGATTAATTTTCGTGGATGGTGGATTTAGTGTTCAGGTTCCCAACCGAATAACT 1201  
 QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
 Db 1202 GCCGGCTGCATATATTTTAATGCCATCCAGATTCGAACTTGTGTCTCAATCAGCTA 1261  
 QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
 Db 1262 TATGCTATGCAGTATGCACAGTTCCTGTGTTCATGCCAATCTGGGGCTTAGAGATACC 1321  
 QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGlnGlyThrGlyTyrAlaPheAla 496  
 Db 1322 GTGGAGAACTTCAACCTTTTCGGTGAGATGGAGAGCAGGGTACAGGGTGGGCATTCGCA 1381  
 QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
 Db 1382 CCCTTAACCAACAGAAACATGTT- GTGGACATTCGCACTGCAATATCTACATACAGGGA 1440  
 QY 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
 Db 1441 ACACAAGTCTCTCGGAGGGCTAATGAAGCGAGGCATGTCAAAAGACTTTCACGTGGGA 1500  
 QY 537 ProCysArg 539  
 Db 1501 CCATGCCGC 1509

## RESULT 9

US-10-425-114-19497

; Sequence 19497, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; NUMBER FILING DATE: 2003-04-28

; SEQ ID NO 19497

; LENGTH: 1855

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3150-035-F10\_FLI

US-10-425-114-19497

## Alignment Scores:

Pred. No.: 1,41e-296 Length: 1855  
 Score: 2538.00 Matches: 471  
 Percent Similarity: 99.8% Conservative: 0  
 Best Local Similarity: 99.8% Mismatches: 1  
 Query Match: 87.7% Indels: 1  
 DB: 7 Gaps: 0

US-10-628-525A-21 (1-539) x US-10-425-114-19497 (1-1855)

QY 68 GlyAspValCysGlySerLeuProValAlaLeuAlaAaArgGlyHisArgValMetVal 87  
 Db 1 GGAGATGTTTGTGGTTCATTCGACGTTGCTCTTGTCTGCTGCTGCTACCGTGTGATGGTT 60  
 QY 88 ValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThr 107  
 Db 61 GTAATGCCAGATATTTAAATGGTCTCCGATGAAGAAATATGCAATGCAATTTACACA 120  
 QY 108 GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127  
 Db 121 GAAAAACACATTCGGATTCATGCTTTGGCGGTGAACATGAAGTTACCTTTCTTCATGAG 180  
 QY 128 TyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsn 147  
 Db 181 TATAGAGATTCAGTTCAGCTGGGTGTTGTGATCATCCCTCATATCAAGACCTGGAAAT 240  
 QY 148 LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys 167  
 Db 241 TTATATGGAGATAAGTTTGTGTCTTTTGTGATAAATCAGTTTCAGATACACACTCTTTC 300  
 QY 168 TyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn 187  
 Db 301 TATGCTGCATGTGAGGCTCTTTTGATCTTGAATTGGAGGATATATTTATGGACAGAA 360  
 QY 188 CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuAlaAlaLys 207  
 Db 361 TGCATGTTTGTGTCAATGATTTGGCATGCCAGTCTAGTGCCAGTCTCTTCTTGTGCAAAA 420  
 QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227  
 Db 421 TATAGACCATATGTTTATAAAGACTCCCGCAGCATCTTCTGTAATACATAATTTAGCA 480  
 QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247  
 Db 481 CATCAGGGGTGAGAGCTCAAGACACATATCTCCAGCTTTGGGTGGCCATCGAATGAT 540  
 QY 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGlu 267  
 Db 541 GGAGCTCTGGAGTGGGTATTTCCCTGAATGGCGAGGAGGATGCCCTTTGACAAAGGTGAG 600  
 QY 268 AlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287  
 Db 601 GCAGTTAAATTTTGAAGGTGCAGTTGTGACAGCAGATCGAATCGTACTGTCAGTAAG 660  
 QY 288 GlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307  
 Db 661 GGTATTCGTGGAGGTCAAACTGCTGAAGGTGGACAGGGCCTCAATGAGCTCTTAAGC 720



QY 308 SerArgLysSerValLeuAenGlyIleValAenGlyIleAspIleAenAspTrpAenPro 327  
 Db 721 TCAGAAAGAGTGATTAACGGAATGTAAATGGAAATGACATTAATGATGGAAACCC 780  
 QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyIysAlaLys 347  
 Db 781 GCCACAGACAAATGTATCCCTGTCTATTCTCTGTTGATGACCTCTCTGGAAGGCCAA 840  
 QY 348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIle 367  
 Db 841 TGTAAAGGTGCATTCAGAGGAGCTGGGTATACCTATAGGCTCATGTTCCTCTGATT 900  
 QY 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIlePro 387  
 Db 901 GCGTTTATTGGAAAGTTGATATACAGAAAGCATGATCTCATTCACCTTATCATACCA 960  
 QY 388 AspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGlu 407  
 Db 961 GATCTCATCGGGAGAGATGTCATTTGTCATGCTTGGATCTGGTGACCCAGAGCTTGAA 1020  
 QY 408 AspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPhe 427  
 Db 1021 GATTGATGAGATCTACAGAGTCGATCTTCAAGGATAAAATTTTCGTGGATGGTTCGATT 1080  
 QY 428 SerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArg 447  
 Db 1081 AGTTTCCAGTTTCCACCGAATACTCGCGGCTGCGATATATTTGTTAATGCCATCCAGA 1140  
 QY 448 PheGluProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValVal 467  
 Db 1141 TTCGAACCTTGTGTCCTCAATCAGCTATATGCTATGCTGACGATGGCACAGTTCTCTGTTGTC 1200  
 QY 468 HisAlaThrGlyGlyLeuArgAspThrValGluAenPheAsnProPheGlyGluAenGly 487  
 Db 1201 CATGCAACTGGGGGCTTAGAGATACCGTGGAGAACTTCAACCCCTTCGTGGATGGA 1260  
 QY 488 GluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAenMetPheValAspIle 507  
 Db 1261 GAGCAGGGTACAGGGTGGGCAATTCGACCCCTTAACACAGAAACATGTT-GTGGACATT 1319  
 QY 508 AlaAenCysAenIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAla 527  
 Db 1320 CGGAACGTCAATATCTACATACAGGGAACACAAAGTCTCTCTGGGAAGGCTTAATGAAGCG 1379  
 QY 528 ArgHisValLysArgLeuHisValGlyProCysArg 539  
 Db 1380 AGGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 1415

RESULT 10

US-10-437-963-51322  
 ; Sequence 51322, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 51322  
 ; LENGTH: 2812  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_53725C.1  
 US-10-437-963-51322

Alignment Scores:  
 Pred. No.: 4,36e-293 Length: 2812  
 Score: 2511.50 Matches: 476  
 Percent Similarity: 85.9% Conservative: 31  
 Best Local Similarity: 80.7% Mismatches: 32  
 Query Match: 86.8% Indels: 52  
 DB: 7 Gaps: 3  
 US-10-628-525A-21 (1-539) x US-10-437-963-51322 (1-2812)

QY 1 CysValAlaGluLeuSerArgGlu-----8  
 Db 238 TCGTGGCGGAGCTGAGCAGGACGGTGGTCCGGCGCAGCGCCGCTGGCACCGCGCGCG 297  
 QY 8 -----8  
 Db 298 CTGGTGAAGCAGCGGCTCTGCGGACCTTCTCTGTCGCCAGCTCGAGGCCACCGCGCGCC 357  
 QY 9 -----AspLeuGly-----11  
 Db 358 ACGCAGTCCGCCGCGCGCGCGCGCGCGCGCGCGCTTCCGCGACTCCGCGCGTGGGGAG 417  
 QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
 Db 418 ATCGACCGCGATCTAGAGGTCTTCCAGAAAGTTCATCAGCAAAACAATTTTGTGGCT 477  
 QY 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49  
 Db 478 AGTGACGAGGAGCTCGAGATCATGGATGTGAAGGAGCAAGCTCAAGCTAAAGTAAACAGC 537  
 QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69  
 Db 538 AGCGTGTCTTTGTAACCGGTGAAGCTTCTCTTATGCAAGTCAAGTGGACTAGGAGAT 597  
 QY 70 ValCysGlySerLeuProValAlaLeuAlaAargGlyHisArgValMetValMet 89  
 Db 598 GTTGTGGTTCTACTGCCAATCTCTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 657  
 QY 90 ProArgTyrLeuAenGlyThrSerAspLysAenTyrAlaAenAlaPheTyrThrGluLys 109  
 Db 658 CCGAGATACATGACCGGGCTTTGAACAAAATTTTGCAACGCATTTTACACTGAGAAG 717  
 QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
 Db 718 CACATTAAAGATTCCATGCTTTCGCGGAGAAACATGAAGTTACTTTTTTTCACGAGTATAG 777  
 QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGluValAenLeuTyr 149  
 Db 778 GATTCTGTGATTGGGTGTTTGTGATCATCTCTCATATCATAGACTCGAAATTTGTAT 837  
 QY 150 GlyAspLysPheGlyAlaPheGlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAla 169  
 Db 838 GGAGATAATTTTGGTGTCTTTTCGCGATAATCAGTTTCAGATACACACTCTCTGCTATGCG 897  
 QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAenCysMet 189  
 Db 898 GCGTGTGAAGCCCATTAATCTTGAATCGGAGGATATATCTATGAGACAGAAATGCATG 957  
 QY 190 PheValValAenAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArg 209  
 Db 958 TTGTGTGAATGATTGGATCCAGTCTTGTGCCAGTCTTGTGCCAATCTCTTCTGCTCAAAATATAGA 1017  
 QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229  
 Db 1018 CCATATGGTGTATACAGGAGTCCCGCAGTGTCTTGTTCATACATAATCTAGCACATCAG 1077  
 QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyrGlyAla 249  
 Db 1078 GGTGTGGAGCCTGCCAGTACATATCTGACCTGGGATGTCACCTGAATGGTATGGAGCA 1137







QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
DB 261 GGTCAACGAGTGATGGTTGTAATCCCAAGATACCTTAAATGGGTCTCTGTGATAAAACCTAT 320  
QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
DB 321 GCAAAGGCATATATACACTCGCAAGCACATTAAGATTCCATGCTTTGGGGGATCATGAA 380  
QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer 141  
DB 381 GTGACCTTTTTCATGAGTATAGAGACAACTGATTGGGTGGTTGTTCGATCATCCGTC 440  
QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
DB 441 TATCACAGACGAGGATATATATGGAGATAATTTTGGTGTCTTTGGTGATTAATCAGTTTC 500  
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGly 181  
DB 501 AGATACACACTCTTTGCTATGCTGCTGATGCGAGGCCCACTAATCTTGAATTGGAGGA 560  
QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValPro 201  
DB 561 TATATTTATGACAGAATTGCTATGTTGTGTGAACGATTGGCATGCCAGCTTGTGCCA 620  
QY 202 ValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221  
DB 621 GTCTCTTCTGCTGCAAAATATAGACCATACGGTGTTCACAGAGATTCCCGCAGCACCTTT 680  
QY 222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
DB 681 GTTATACATAATTAGCACATCAGGGTGTGGAGCTGCAGTACATATCTGTATCTGGGA 740  
QY 242 LeuProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgHis 261  
DB 741 TTGCCTCTGAATGGTATGAGCTTTAGATGGGTATTTCCAGAAATGGCAAGGAGCAT 800  
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArg 281  
DB 801 GCCCTTGACAGGGGTGAGGAGTTAACTTTTGAAGGAGCAGTGTGTGACAGCAGATCGG 860  
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGly 301  
DB 861 ATTGTGACCTCAGTCAGGGTTATTCATGGAGGTCAACTCTGAGGTGACAGGGC 920  
QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsp 321  
DB 921 CTCATAGCTCTTAAAGCTCCCGAAAGAGTGTATTGAATGGAATTGTAAATGGAATTGAC 980  
QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 341  
DB 981 ATTAATGATTGGAACCCCAACACAGACAAAGTGTCTCCCTCATCATTTATTTCTGCGATGAC 1040  
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361  
DB 1041 CTCTCTGGAAGGCCAAATGTAAGCTGAATTCAGAGAGAGTGGTTTACTCTGTAAGG 1100  
QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381  
DB 1101 GAGGATGTTCTCTGATTGGCTTTATTTGGAAGACTGGATTACCAGAAAGGCATTGATCTC 1160  
QY 382 IleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
DB 1161 ATTAATGATGGCCATTTTGAAGCTGGATGAGATCTACCGAGTGGAGGAGCGTCAATTTGTCTGCTGGATCT 1220  
QY 402 GlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPhe 421  
DB 1221 GGGGATCCCAATTTTGAAGCTGGATGAGATCTACCGAGTGGAGGAGCGTCAATTTGTCTGCTGGATCT 1280  
QY 422 ArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
DB 1281 CGTGGATGGTGGATTGATTAGTGTCCAGTTTCCACAGATAACTGCAGGTGGGATATA 1340  
QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461

DB 1341 TTGTTAATGCCATCGAGATTGAACCTTGGGCTTAAATCAGCTATATGCTATGCAATAT 1400  
QY 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn 481  
DB 1401 GGTACAGTTCTCTGTAGTTTCATGGAACTGGGGGCCCTCCGAGACACACAGTCGAGACCTTCAAC 1460  
QY 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
DB 1461 CCTTTTGGTCAAAAGAGAGAGGGGTACAGGGTGGGGCGTTCTCCCGCTTAACCGTGAC 1520  
QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
DB 1521 AAGATGTT-GTGGCATTCGAAACCGCATGTGCACATTTCAGGGAGCACAAAGCGCTCTG 1579  
QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538  
DB 1580 GGAGGGCTCATGAAGCGAGCATGACGAAAGACCATACGTGGGACCATGC 1630  
RESULT 13  
US-10-818-624-1  
; Sequence 1, Application US/10818624  
; Publication No. US20040204579A1  
; GENERAL INFORMATION:  
; APPLICANT: Block, Martina  
; Lorz, Horst  
; Lutticke, Stephanie  
; Walter, Lennart  
; Proberg, Claus  
; Kossmann, Jens  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES  
; FROM WHEAT WHICH ARE INVOLVED IN STARCH  
; SYNTHESIS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: James F. Haley, Jr., c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/818,624  
; FILING DATE: 05-Apr-2004  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/952,677  
; FILING DATE: 14-Sep-2001  
; APPLICATION NUMBER: 09/196,390  
; FILING DATE: 19-Nov-1998  
; APPLICATION NUMBER: DE 196 21 588.9  
; FILING DATE: 29-MAY-1996  
; APPLICATION NUMBER: DE 196 36 917.7  
; FILING DATE: 11-SEP-1996  
; APPLICATION NUMBER: PCT/EP97/02793  
; FILING DATE: 28-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley, Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: AGREVO-9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2239 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Triticum aestivum L.  
 ; STRAIN: cv. Florida  
 ; HAPLOTYPE: ca. 21 d Caryopses  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: cDNA library in pBluescript sk (-)  
 ; CLONE: TaSSS  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 3..2017  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-10-818-624-1

Alignment Scores:  
 Pred. No.: 8,87e-288 Length: 2239  
 Score: 2466.50 Matches: 464  
 Percent Similarity: 91.8% Conservative: 29  
 Best Local Similarity: 86.4% Mismatches: 41  
 Query Match: 85.3% Indels: 4  
 DB: 8 Gaps: 2

US-10-628-525A-21 (1-539) x US-10-818-624-1 (1-2239)

QY 2 ValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyLeuAlaGluGlySer 21  
 DB 30 GTGGGGAACTCGCG---CCCAGCTCTCGTCTC-----GAAGGGATTCTGAGGATTC 80  
 QY 22 IleAspAsnThrValValAlaSerGluGlnAspSerGluIleValValGlyLysGlu 41  
 DB 81 ATCGACAGCATTAATTGGCTGCAGTGCAGGAGTCTGAGATCATGATCGCATGAG 140  
 QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
 DB 141 CAACCTCAAGCTAAAGTTACAGTCAGTACGTCGTGTTGTGACTGGTGAAGCTGCTCTTAT 200  
 QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArg 81  
 DB 201 GCAAGTACAGGGGGTGGGAGATGTTGTGTTGTTGTTTACCAATTGCTCTGCTGCT 260  
 QY 82 GlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyr 101  
 DB 261 GGTCCAGGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 320  
 QY 102 AlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu 121  
 DB 321 GCAAGGCAATTATACACTCGAAGCACATTAAGATTCCATGCTTTGGGGGATCATCATGAA 380  
 QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSer 141  
 DB 381 GTGACCTTTTTCATGAGTATAGACAAACGTCGATTGGGTGTTGTGTCATCATCGTCA 440  
 QY 142 TyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161  
 DB 441 TATCAGACACCGAGGATTTATATGAGATATTTGGTCTTTGGTATATATCAGTTC 500  
 QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLeuLeuGlyGly 181  
 DB 501 AGATACACACTCTTTGCTATGCTGATCGAGGGCCCACTAATCTTGAATTGGGAGGA 560  
 QY 182 TyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValPro 201  
 DB 561 TATATTATGGACAGAAATTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 620  
 QY 202 ValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeu 221  
 DB 621 GTCTCTTCTGCTGCAAAATATAGACCATCAGGTGTTTACAGAGATTCCTCCGAGCACCTT 680  
 QY 222 ValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGly 241  
 DB 681 GTTATACATAATTTAGCACATCAGGTGTGGAGCTTGCAGATGATATCTGATCTGGA 740

QY 242 LeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHis 261  
 DB 741 TTGCTCTCTGTAATGATGATGAGCTTTAGAAATGGGTATTTCCAGAAATGGCAGGAGGCAT 800  
 QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyValAlaValThrAlaAspArg 281  
 DB 801 GCCCTTGACAAGGGTGAGGCACTTAACCTTTTGAAGGAGGAGCAGTTGTGACAGCAGATCG 860  
 QY 282 IleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGlnGly 301  
 DB 861 ATTGTGACCGTCACTCAGGCTTATTCATGCGAGGTCAACAACCTGCTGAAGGTGACAGGCG 920  
 QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321  
 DB 921 CTCATAGAGCTCTTAAGCTCCCGAAAAAGTGATTGAATGGAATTTGTAATGGAATTGAC 980  
 QY 322 IleAsnAspTyrAsnProAlaThrAspLysCysIlePheProCysHisTyrSerValAspAsp 341  
 DB 981 ATTATGATTGGAACCCACACACACAGTCTCTCCCTCATCATTTATCTGTGATGAC 1040  
 QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361  
 DB 1041 CTCCTCGAAAGGCCAAATGTAAAGCTGAATTCGAGAAGAGTGTGGTGTACCTGTAAAG 1100  
 QY 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381  
 DB 1101 GAGGATGTTCTCTGATTGGCTTTATTGGAAGCTGGATTACCAAGAGGCATTGATCTC 1160  
 QY 382 IleGlnLeuIlePheProAspLeuMetArgGluAspValGlnPheValMetLeuGlySer 401  
 DB 1161 ATTAAATGGCCATTCACAGAGCTCATGAGGAGGAGCGTCAATTTGTCATGCTTGGATCT 1220  
 QY 402 GlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPhe 421  
 DB 1221 GGGGATCCAAATTTTGAAGGCTGGATGATCTACCGAGTCGAGTTTACAAGGATAAATTC 1280  
 QY 422 ArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIle 441  
 DB 1281 CTTGATGTTGGTGGATTTAGTGTCTCCAGTTTCCCACAGAAATTAACGAGTTGCGATATA 1340  
 QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461  
 DB 1341 TTGTTAATGCCATCGAGATTGAACTTGGCTTCTTAATCAGCTATATCTATGCAATAT 1400  
 QY 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsn 481  
 DB 1401 GGTACAGTTCCTGTAGTTTCATGGAACCTGGGGGCTCCGAGACACAGTCGAGACCTTCAAC 1460  
 QY 482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
 DB 1461 CTTTTTGTGCAAGGAGGAGGAGGTACAGGGTGGCGTCTTCCCGCTAACCGTGGAC 1520  
 QY 502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
 DB 1521 AAGATGTT-GTGGCATTTGCGAACCCGATGTCGATTCGAGCATTCAGGGAGACAACGCGCTTG 1579  
 QY 522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538  
 DB 1580 GGAGGGGCTCATGAAGCGGAGCATGACAAAGACCATAGCTGGGACCATGC 1630

## RESULT 14

US-10-284-668-9  
 ; Sequence 9, Application US/10284668  
 ; Publication NO. US20030106100A1

; GENERAL INFORMATION:  
 ; APPLICANT: Kossmann, Jens

; Springer, Franziska  
 ; Abel, Gernot

; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES

; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC  
 ; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES

; NUMBER OF SEQUENCES: 17



QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
DB 1604 CCAGTTTCTCAGGATACAGCAGGATCGCATACTATTGATGCCCTCAAGATTCGAA 1663  
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
DB 1664 CCGTGTGGCTTAAACCAATTGTATGATCAATGAGATATGGCACCACCTATTGTTTATAGC 1723  
QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGly---Glu 488  
DB 1724 ACGGGGGGCTTAAGAGACACAGTGAAGGATTTAATCCATATGCTCAAGAAGGAATAGGT 1783  
QY 489 GlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAla 508  
DB 1784 GAAGGTACCGGTGGACATTTCTCTCTTAAAGAGTGAAGTGGTGGTGGTGGTGGTGGT 1843  
QY 509 AsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArg 528  
DB 1844 CT-GGCAATCGGACCTATACAGAACATAAGTCATCTTGGGAGGGATTGATGAGGAGAGG 1902  
QY 529 HisValValArgLeuHisValGlyProCys 538  
DB 1903 TATGGAAGGAGCTATTCTCTGGGAAATGTC 1932

## RESULT 15

US-10-284-668-3  
; Sequence 3, Application US/10284668  
; Publication No. US20030106100A1  
; GENERAL INFORMATION:  
; APPLICANT: Kossmann, Jens  
; ; Springer, Franziska  
; ; Abel, Gernot  
; ;  
; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES  
; INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC  
; PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES  
; ;  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/284,668  
; FILING DATE: 29-Oct-2002  
; CLASSIFICATION: <Unknown>  
; PRIORITY INFORMATION:  
; APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,567  
; FILING DATE: 24-JUL-1997  
; APPLICATION NUMBER: PCT/EP95/04415  
; FILING DATE: 09-NOV-1995  
; APPLICATION NUMBER: DE P 44 41 408.0  
; FILING DATE: 10-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: Agrevo-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-596-9090  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1758 base pairs  
; TYPE: nucleotide  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Solanum tuberosum  
; STRAIN: cv. Berolina  
; TISSUE TYPE: tuber tissue  
; IMMEDIATE SOURCE:  
; LIBRARY: cDNA-library in pBluescriptSKII+  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1377  
; OTHER INFORMATION: /function= "Polymerization of  
; starch"  
; /product= "Starch synthase"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-284-668-3  
Alignment Scores:  
Pred. No.: 2,48e-188 Length: 1758  
Score: 1645.50 Matches: 304  
Percent Similarity: 81.7% Conservatives: 63  
Best local Similarity: 67.7% Mismatches: 70  
Query Match: 56.9% Indels: 13  
DB: 5 Gaps: 5  
US-10-628-525A-21 (1-539) x US-10-284-668-3 (1-1758)  
QY 95 GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114  
DB 1 GGCACGAGC-----AATGCTGTGACCTTGATGCGGGCCACTGTCCAT 45  
QY 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrp 134  
DB 46 TCGTTTGTGTGATGCACAGAAAGTAGCCTTCTACCAATGAATACAGGCGAGGTGTTGATTGG 105  
QY 135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154  
DB 106 GTATTTGTGGACCACTCTTCTTACCGCAGACCTGGAACGCCATATGGTGATATTATGGT 165  
QY 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174  
DB 166 GCATTTGGTGATATACAGTTTCGCTTCTTCTCAGCGCAGCATGTGAAGCGCCA 225  
QY 175 LeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194  
DB 226 TTGGTTCTCCACTGGGAGGGTTCACTTATGAGAGAGAGTGTCTTCTTCCTAATGAT 285  
QY 195 TrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyr 214  
DB 286 TGCAACGCTGCTTGGTTCTTACTTTTAGCGCCAAAGTATCGTCTTATGTTGTATTAC 345  
QY 215 LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234  
DB 346 AAGGATGCTCGTAGTATTGTGCAATACACAACTTGCACATCAGGAGTGGAGCTGCA 405  
QY 235 SerThrTyrProAspLeuLeuProGluTyrTyrGlyAlaLeuGluTrpValPhe 254  
DB 406 GTAACCTACAATAATTGGGTTTGGCTCCACATGTTATGGAGCAGTGAATGGATATT 465  
QY 255 ProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
DB 466 CCCACATGGGCAAGGGCGCATGCGCTGCACACTGGTGAACAGTGAACGTTTGAAGGG 525  
QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294  
DB 526 GCATAGCAGTGTGCTGATCGGATCTGACAGTTAGCCAGGAGTACTCATGGGAAATAACA 585  
QY 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314  
DB 586 ACTCCTGAAGGGGGATATGGGCTACATGAGCTGTTGAGCAGTAGACAGCTGTTCTTAT 645  
QY 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIlePro 334

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Db 646 GGAATTACTAATGAAATAGATGTTAAATGATGGAAACCGTCGACAGATGACATATCGCT 705
Qy 335 CyehisTyrSerValaspAspLeuSer-----GlyLysAlaLysCysLysGlyAlaLeu 352
Db 706 TCGCATTAATCCATCAATGACCTCCCGCCCTGGAAAGGTTTCAGTCGACAGATGATCTG 765
Qy 353 GlnLysGlnLeuGlyLeuProIleArgProaspValProLeuLeuGlyPheIleGlyArg 372
Db 766 CAAGAAGNAATCGGCCCTTCCAAATTCGACCGCATGTCACATGATGATTTATTTGGAAGG 825
Qy 373 LeuaspTyrGlnLysGlyIleaspLeuLeuGlnLeuLeuIleProaspLeuMetArgGlu 392
Db 826 CTGACATACCAAGAAGGTGTGACATAATCTGTGACCAATTCAGAACTTATGCGAAT 885
Qy 393 AspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSer 412
Db 886 GATGTCCAACTGTGAATGCTTGGATCTGGTGAGNAACAATAGAGACTGGATGAGACAT 945
Qy 413 ThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSer 432
Db 946 ACAGAAATCTTTTAAAGACAAATTTTCGTCTGGTTCGATTTAATGTTCCAGTTTCT 1005
Qy 433 HieArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGly 452
Db 1006 CATAGGATAACAGCAGATGCGACATACATATGATGCCCTCAAGATTTCGAACCGTGTGGC 1065
Qy 453 LeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGly 472
Db 1066 TTAACCAATGTATGCAATGAGATATGGACCATACCTATTGTTCTATAGCAGCGGGGC 1125
Qy 473 LeuArgaspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlu---GlnGlyThr 491
Db 1126 CTAAGAGACACAGTGAAGGATTTAATCCATATGCTCAAGAAGGAAAGGTGAAGGTACC 1185
Qy 492 GlyTyrAlaPheAlaProLeuThrThrGluAsnMetPhe-----ValAspIleAlaAsn 509
Db 1186 GGGTGACATTTTCTCTCTAACGAGTGAAGGATGTTGATACACTGAAGCTGGCGAT- 1244
Qy 510 CysAsnIleTyrIleGlnGlnThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529
Db 1245 CAGGACTTATAC-----AGAACATAAGTATCTCTGGAGGGGATTTGATGAGAGAGGTAT 1298
Qy 530 ValLysArgLeuHisValGlyProCys 538
Db 1299 GCGAAGGGACTATTCTCGGGAAAAATGC 1325

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RESULT 16

```

US-10-425-114-30782
; Sequence 30782, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 30782
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-2MFLB73078D02_FLI
US-10-425-114-30782

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Alignment Scores:

```

Pred. No.: 2,14e-170 Length: 1294
Score: 1496.00 Matches: 284
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 51.7% Indels: 1
DB: Gaps: 0

US-10-628-525A-21 (1-539) x US-10-425-114-30782 (1-1294)

Qy 255 ProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValaAsnPheLeuLysGly 274
Db 2 CTTGAATGGCGAGGAGGATGCCCTTGCAAGGGTGAGCAGTTAATTTTTTGAAGGT 61
Qy 275 AlaValValThrAlaaspArgIleValThrValSerLysGlyTyrSerTyrGluValThr 294
Db 62 GCAGTTGTGACAGCAGATCGATCGTACTGTCTCAGTAAGGGTTATTCATCGGAGGTGACA 121
Qy 295 ThrAlaGlnGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314
Db 122 ACTGCTGAAGGTGGACAGGGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAC 181
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro 334
Db 182 GGAATTTGTAATGGAATTGACATTAATGATTTGGAACCTGCCACACAAATGATATCCCC 281
Qy 335 CysHisTyrSerValaspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354
Db 242 TGTCAATTAATCTGTTGATGACCTCTCTGGAAAGGCCAAATGTAAGGTGCTATTCAGAG 301
Qy 355 GluLeuGlyLeuProIleArgProaspValProaspValProLeuIleGlyPheIleGlyArgLeuAsp 374
Db 302 GAGCTGGGTTTACCTATAAGGCTGATGTTCTCTGATTTGGCTTTATTTGGAAGTTGGAT 361
Qy 375 TyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProaspLeuMetArgGluAspVal 394
Db 362 TATCAGAAAGGCATTTGATCTCAATTCATACCAATCTCATGCCAGATCTCATGGGGAAGATGT 421
Qy 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGlu 414
Db 422 CAATTTGTCATGCTTGGATCTGTCAGCCAGAGCTTGAAGATTGGATGAGATCTACAGAG 481
Qy 415 SerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArg 434
Db 482 TCGATCTTCAAGGATAAATTTCTGTTGATGGTTGGATTTAGTGTTCAGTTTCCACCGA 541
Qy 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454
Db 542 ATAACCTGCGGCTGCGATATATTGTTAATGCCATCCAGATTCGAACCTTGTGTGCTCAAT 601
Qy 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474
Db 602 CAGCTATATGCTATGTCAGTATGTCAGATTCCTGTTGTCATGCACTGGGGGCTTAGA 661
Qy 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlnGlnGlyThrGlyTyrAla 494
Db 662 GATACCGTGGAGAACTTCAACCTTTTCGGTGAGAAATGGAGAGCAGGGTACAGGGTGGCA 721
Qy 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514
Db 722 TTCGACACCTTACCAAGAAACATGTT-TGGACATTCGCACTGCAATATCTACATA 780
Qy 515 GlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHis 534
Db 781 CAGGGAACACAAGTCTCTCTGGGAGGGCTAATGAAGCGAGGATGTCATGTCACAAAGACTTAC 840
Qy 535 ValGlyProCysArg 539
Db 841 GTGGGACCATGCCGC 855

```

RESULT 17

```

US-10-425-114-3524
; Sequence 3524, Application US/10425114
; Publication No. US20040034888A1

```

```
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 3524
; LENGTH: 1300
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700268092_FLI
US-10-425-114-3524

Alignment Scores:
Pred. No.: 6,64e-166 Length: 1300
Score: 1459.00 Matches: 278
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 50.4% Indels: 1
DB: 7 Gaps: 0

US-10-628-525A-21 (1-539) x US-10-425-114-3524 (1-1300)
QY 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyValValThrAlaAsp 280
DB 3 CATGCCCTTGACAAAGGTGAGCGAGTTAAATTTTGAAGGTGCAGTTGTGACAGCAT 62
QY 281 ArgIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGln 300
DB 63 CGAATCGTGACTGTCAAGTAAAGGTATTTCATGGAGGTCAAACTGCTGAAGGTGACAG 122
QY 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320
DB 123 GGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGGTATTAAACGGAATTTGTAATGGAATT 182
QY 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340
DB 183 GACATTAAATGATTGGAAACCTGCCACAGACAATGTATCCCTGTCTATTCTGTGTAT 242
QY 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360
DB 243 GACCTCTCTGGAAGGCCAAATGTAAGGTGCATTGCAAGAGAGCTGGGTTTACCTATA 302
QY 361 ArgProAspValProIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380
DB 303 AGGCTCGATGTTCCTCTGATTGGCTTTATTGGAAGATTGGATTATCAGAAAGGCATTGAT 362
QY 381 LeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400
DB 363 CTCATTCAACTTATCATACAGATCTCATGCGGAGAGATTTCATTTGTCTATGCTTGA 422
QY 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420
DB 423 TCTGGTGACCCAGAGCTTCAAGATTGGATGAGATCTACAGATCGCATCTTCAAGGATAA 482
QY 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440
DB 483 TTTCGTGGATGGGTGGATTTAGTTAGTTTCAGTTTCCACCGAATAACTCCCGGCTGCGAT 542
QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460
DB 543 ATATTGTTAATGCCATCCAGATTCGAACTTTGGTCTCAATCAGCTATATGCTATGCGAG 602
QY 461 TyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPhe 480
```

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DB 603 TATGGCACAGTTCTCTGTTCATGCACACTGGGGCCTTAGAGATACCGTGGAGAACTTC 662
QY 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThr 500
DB 663 AACCCCTTTTCGGTGAGAAATGGAGACGAGGTAACAGGTTGGGCATTCGCACCCCTTAACACA 722
QY 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520
DB 723 GAAACATGTTTGTGGACATTCGGAACCTGCATATCTACATACAGGGAACACAGTCTCTC 781
QY 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
DB 782 CTGGGAAGGCTTAATGAAGCGAGGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 838

RESULT 18
US-10-424-599-73305
; Sequence 73305, Application US/10424599
; Publication NO. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5323)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 73305
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3720C.1
US-10-424-599-73305

Alignment Scores:
Pred. No.: 2,01e-153 Length: 1158
Score: 1355.50 Matches: 251
Percent Similarity: 86.0% Conservative: 44
Best Local Similarity: 73.2% Mismatches: 47
Query Match: 46.9% Indels: 2
DB: 7 Gaps: 1

US-10-628-525A-21 (1-539) x US-10-424-599-73305 (1-1158)
QY 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216
DB 2 GCCAGCCTAGTTTCCAAATACTTTTGGCAGCGAAGTATCGTCCACATGGGGGTATATAAGGAT 61
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
DB 62 GCACGTAGTATTTTGGTGATACATAATATACACACACCGAGGAGTGGAACTGCAATTACA 121
QY 237 TyrProAspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGlu 256
DB 122 TATACCAATTTGGGCTACTCTCCAGATGGTATGAGACACTGGGATGGGTGTTCCCTACG 181
QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
DB 182 TGGGCAAGGACACATGCTCTTGACACGGGAGAAGCTGTCAACTTTCTAAAGGTGCTGTT 241
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
DB 242 GTTACATCTGACCGGATTTGTACAGTAAGCAAGGCTATTCTCGGAGATAACGACTAGT 301
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316
DB 302 GAAGGTGATGGTCTACATGATTTTAAAGCATCGAAAAGTATTCTCAGTGGGATC 361
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
```







```
Db 1896 AAGCGTCAGTCAAAAGCGCCTTGCAAAAGGAGCTCGGTTTGCCTGTCCGTGAGGATGTT 1955
Qy 365 ProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeu 384
Db 1956 CCGTTACTTGGATTCAITGGAGGCTGGATCAACAGAAAGGCAITGATCTCATAGCCGAA 2015
Qy 385 IleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspPro 404
Db 2016 GCAATTCCTTGGATAGTGGCCGAGGATGTGCAGCTAGTCAITGTTGGAACTGGGAAGCCG 2075
Qy 405 GluLeuGluAspTyrMetArgSerThrGlnSerIlePheLysAspLysPheArgGlyTyr 424
Db 2076 GACTTAGAGATATGCTTAGGCAGCTTTGAGTCCCAACCGTGACAAAGTCAGAGGATGG 2135
Qy 425 ValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMet 444
Db 2136 GTTGGCTTTTGGTCAAGATGGCTCACCGGATACAGCGGTGCAGACATATTGCTGATG 2195
Qy 445 ProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrVal 464
Db 2196 CCATCAAGATTGAGCCATGTTGGATTTGAATCAACTATGCCATGAATTAACGGAACAATT 2255
Qy 465 ProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGly 484
Db 2256 CCAGTTGTACATGCTGTGCGTGGATTGAGGATACAGTGAAGCCTTTTATCCATTGAA 2315
Qy 485 GluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPhe 504
Db 2316 GAGTCG-----GGCCTTGGTGGACATTTTGACAGTGCAGAAACTAAACAGTTAATA 2366
Qy 505 ValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAla 524
Db 2367 AATGCATTAGGAACTGCTT-GTTCACCTTCAGGCAGTATAAGCAGAGCTGGGAAGGGCT 2425
Qy 525 AsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 2426 CCAACCGCGAGGGATGA-CGCAGGATCTTAGTTGGG 2460

RESULT 21
US-10-628-525-10
; Sequence 10, Application US/10628525
; Publication No. US20040185114A1
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/628,525
; FILING DATE: 28-Jul-2003
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445
; FILING DATE: 30-SEP-1997
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2097 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: Not Relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURES:
; NAME/KEY: CDS
; LOCATION: 1..2097
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-628-525-10

Alignment Scores:
Pred. No.: 9.82e-126 Length: 2097
Score: 1130.50 Matches: 254
Percent Similarity: 57.2% Conserves: 64
Best Local Similarity: 45.7% Mismatches: 159
Query Match: 39.1% Indels: 80
DB: Gaps: 11

US-10-628-525A-21 (1-539) x US-10-628-525-10 (1-2097)
Qy 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySerIle 22
Db 565 GCTCCTTATGACAGGAGGAT-----AATGAACCTTGGCCCTTTGGTGGGCCCTAATGTG 618
Qy 23 AspAsnThrValValAlaLaserGluGlnAspSerGluIleValValGlyLysGluGln 42
Db 619 ATGAAGCTGCTGCTGTGGCTTCT----- 642
Qy 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluLaserProTyrAla 62
Db 643 -----GAATGTGCTCTTCTTCGC 660
Qy 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAAsrGly 82
Db 661 AAGACAGGTGGCCCTTGAGATGTCTGGGTGCTTTTGCCTAAGGCTCTGGCGAGAGGA 720
Qy 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102
Db 721 CACCGTGTATGCTGTGTATACACAGATAT-----GGAGAGTATGCT 762
Qy 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122
Db 763 GAAGCCCGGATTTAGGTGTAAAGGACGTTACAGGTAGCTGCAGAGGATTCAGAGATT 822
Qy 123 ThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisProSerTyr 142
Db 823 ACTTATTTTCACTCTTACATTTGATGAGTGTGATTTTGTATTCGTAGAGCCCTCCCTTC 882
Qy 143 ---HisArgProGlyAsnLysTyrGlyAspLysPheValAlaPheGlyAspAsnGlnPhe 161
Db 883 CGGCACCGGCACAAATATATTTATGG-----GGAGAAAGATTGATATTTTGAAG 933
Qy 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGlyGly 181
Db 934 CGCATGATTTTCTTCTGCAAGCGCTGTGAGTTCCATGTTGATGCTCCATGTCGCGGT 993
Qy 182 TyrIleTyrGlyGln---AsnCysMetPheValValAsnAspTyrHisAlaserLeuVal 200
Db 994 ACTGCTATGTTGATGGCAACTTAGTTTTCATTTGATTAATGATGGCATACCGCACTTCTG 1053
Qy 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220
Db 1054 CTGTCTATCTAAAGCCCTATTACCGGGCAATGTTTGCATGATGCTGCTCTGTG 1113
Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaserThrTyrProAspLeu 240
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Db 1114 CTGTGATACACACATTCTCATCAGGCTCGTGGCCCTGTAGACGACTTCGCTCAATTTT 1173
QY 241 GlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArg 260
Db 1174 GACTTGCCT-----GAA 1185
QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272
Db 1186 CACTACATCGACACTTCAACTGTATGACACATTGGTGGGATCACAGCACTGTTTTT 1245
QY 273 LysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292
Db 1246 GCTGCGGGCTGAAGACGCGACACCGGCTGACCGTTAGCAATGGCTACATGTGGAG 1305
QY 293 ValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312
Db 1306 CTGAAGACTTCGGAAGCGGCTGGGCTCCACGACATCATAAACCCAGAACGACTGGAAG 1365
QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332
Db 1366 CTGACGGGCTCGTGAACGGCATCGACATGAGCGAGTGAACCCCGCTGTGGAC----- 1419
QY 333 IleProCysHisTyrSerValAspAspLeu-----Ser 343
Db 1420 -----GTGCACCTCCACTCCGACGACTACACCACTACACGCTTCGAGACGCTGGACACC 1473
QY 344 GlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363
Db 1474 GGCNAGCGCGAGTGCNAGCGCGCTTCGACGCGAGCTGGGCTGCAGCTCGCGACGAC 1533
QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383
Db 1534 GTGCCACTATCGGGTTTCATCGGCGCGCTGGACCCACGACGAGCGCTGACATCATCGCC 1593
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403
Db 1594 GAGCGCATCACTGATCGCGGGCAGAGCTGCAGCTCGTATGCTGGCACCAGCGGCGG 1653
QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423
Db 1654 GCGGACCTGGAGGACATGCTGCGCGCGTTCGAGTCGGAGCACAGCACGAGTGCAGCG 1713
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 443
Db 1714 TGGTGGGCTTCCTCGTGCCTCGCGGCACCGCATCACGCGGCGCGCGACATCTCTGCG 1773
QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
Db 1774 ATGCCGTCGGGTTTCAGCGCGTGGGCTGTAACGACCTACGCCATGGCGTACGGGAC 1833
QY 464 ValProValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483
Db 1834 GTGCCGCTGTCACCGCTGGGGGCTCCGGGACACGCTGCGCGCTTCGACCGCGTTC 1893
QY 484 GlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503
Db 1894 AACGACACC-----GGGCTCGGGTGGACGTTTCGACCGCGCGAGCGCAACCGGATG 1944
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523
Db 1945 ATCGACCGCTCTCGCACTGCCT-CACACGCTACCGGAACTACAGGAGCTGGCGCGC 2003
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db 2004 CTGACGGCGCGGGCATGGCGGACGCTCAGCTGGGACCGCGC 2051

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RESULT 22

US-10-336-753-48

; Sequence 48, Application US/10336753

; Publication No. US20030226176A1

; GENERAL INFORMATION:

; APPLICANT: Guan, Hauping

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; APPLICANT: Keeling, Peter L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; FILE OF INVENTION: HOSTS
; FILE REFERENCE: 2461-52
; CURRENT APPLICATION NUMBER: US/10/336,753
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/09/402,254
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 2423
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (join(1..2094, 2098..2103, 2107..2304, 2308..2421))
US-10-336-753-48

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Alignment Scores:

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Pred. No.: 1,22e-125 Length: 2423
Score: 1130.50 Matches: 254
Percent Similarity: 57.2% Conservative: 64
Best local Similarity: 45.7% Mismatches: 159
Query Match: 39.1% Indels: 80
DB: 6 Gaps: 11

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US-10-628-525A-21 (1-539) x US-10-336-753-48 (1-2423)

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QY 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySerIle 22
Db 565 GCTCCTTATGACAGGAGGAT-----AATGAACCTGGCCCTTGGCTGGGCTTAATGTG 618
QY 23 AspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGluGln 42
Db 619 ATGAACGTCGTCGTGGTGGCTTTCT-----642
QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62
Db 643 -----GAATGTGCTCCTTTCTGC 660
QY 63 LysSerGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGly 82
Db 661 AAGACAGGTGGCTTGGAGATGCTGGGTGCTTTGGCTTAAGGCTCTGGCGAGGAGGA 720
QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102
Db 721 CACCGTGTATGTCGTGATACCAAGATAT-----GGAGAGTATGCC 762
QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122
Db 763 GAAGCCCGGATTTAGGTGTAAGGAGACGTTACAAGGTAGCTGGACAGGATTCAGAAGTT 822
QY 123 ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyr 142
Db 823 ACTTATTTTCACTCTTACATGATGAGTGTGATTTGTATGTTATGTTAGTAAACCCCTCCCTTC 882
QY 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPheGlyValaPheGlyAspAsnGlnPhe 161
Db 883 CGGCACCGGCACAATAATATTTATGGG-----GGAGAAAGATTGATATTTTGAAG 933
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly 181
Db 934 CGCATGATTTTCTCTGCAAGCGCGCTGTGGTTCATGTTGATGTTCCATGTTGCTCCATGTTGGCGT 993
QY 182 TyrIleTyrGlyGln---AsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200
Db 994 ACTGTCTATGTTGATGCGCAACTAGTTTTCATTTGCTTAATGATTGGCATACCGCACTTCTG 1053

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QY 201 ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerile 220
Db 1054 CCTGCTATCTAAAGGGCTATTACCGGACAATGTTGATGCAGATATGCTCGCTCTGTG 1113
QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240
Db 1114 CTTGTGATACACAACTTCTCATCAGGTCGTGGCCCTGTAGACGACTTCGTCATTTT 1173
QY 241 GlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260
Db 1174 GACTTGCT-----GAA 1185
QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272
Db 1186 CACTATCATGACCCCTTCAACTCTATGACAACATTCGTGGGGATCATACAGACGTTT 1245
QY 273 LysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292
Db 1246 GCTGGGGCTGAAGACGCGAGCCGGTGTGACCTTAGCAATGGCTACATGCGGAG 1305
QY 293 ValThrAlaGluGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerVal 312
Db 1306 CTGAAGACTTCGAAGCGGCTGGGCTCCACGACATATAAACACGACGACTGGAAG 1365
QY 313 LeuAsnGlyIleValAlaGlnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332
Db 1366 CTGAGGGCATCGTGAACGGCATCGACATGAGCGAGTGAACCCCGCTGTGGAC----- 1419
QY 333 IleProCysHisTyrSerValAspAspLeu-----Ser 343
Db 1420 -----GTGCACCTCCACTCCGACGACTACACCACTACAGCTTCGAGCGCTGGACACC 1473
QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363
Db 1474 GGCAAGCGGAGTGAAGCGCCCTGTCAGCGCAGCTGGGCTCGAGGTCGCGGACGAC 1533
QY 364 ValProIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 393
Db 1534 GTCCCACTGATCGGGTTTCATCGCGCGCTGACACACGAGGCGGTGGACATCATCGCC 1593
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403
Db 1594 GACCGCATCCACTGGATCGCGGGCGAGGCTGACGCTGTGATGCTGGCACCGGGCGG 1653
QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423
Db 1654 GCGGACCTGGAGGACATGCTGCGCGGCTTCGAGTCGAGGCACACGACGACGAGGTCGCG 1713
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443
Db 1714 TGGGTGGGGTTCTCGGTGCCCCCTGGCGGCACCGCATCACGCGCGCGCGGACATCTCTG 1773
QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
Db 1774 ATGCCCTCGGGTTCGAGCGCTCGGGCTGAACCACTCTACCCATGGCGTACGGGACC 1833
QY 464 ValProValHisAlaThrGlyLeuArgAspThrValGluAsnPheAsnProPhe 483
Db 1834 GTGCCCGGTGTGCACCGCGTGGGGGCTCCGGGACACGCTGGCGCGCTTCGACCGCTTC 1893
QY 484 GlyGluAsnGlyGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503
Db 1894 AACGACACC-----GGGCTCGGGTGGACGCTTCGACCGCGCGGAGCGAACCGGATG 1944
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523
Db 1945 ATCGACGCGCTCTCGCACTGCTCT-CAACGAGTACCGGAACCTACAGGAGCTGGCGGC 2003
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db 2004 CTGACGGCGCGCGGATGCGCGAGGACCTCAGCTGGGACCGACCGCGC 2051
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RESULT 23

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US-10-109-048-1144
; Sequence 1144, Application US/10109048
; Publication No. US20040107461A1
; GENERAL INFORMATION:
; APPLICANT: COMMURI, PADMA
; APPLICANT: KEELING, PETER L.
; APPLICANT: RAMIREZ, NONA
; APPLICANT: MCKEAN, ANGELA
; APPLICANT: GAO, ZHONG
; APPLICANT: GUAN, HANPING
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS
; FILE REFERENCE: 2461-76
; CURRENT APPLICATION NUMBER: US/10/109, 048
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/279, 720
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 1154
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1144
; LENGTH: 2480
; TYPE: DNA
; ORGANISM: Zea mays
US-10-109-048-1144
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Alignment Scores:
Pred. No.: 1,27e-125 Length: 2480
Score: 1130.50 Matches: 254
Percent Similarity: 57.2% Conservative: 64
Best Local Similarity: 45.7% Mismatches: 159
Query Match: 39.1% Indels: 80
DB: Gaps: 11
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US-10-628-525A-21 (1-539) x US-10-109-048-1144 (1-2480)

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QY 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySerile 22
Db 622 GCTCTTATGACAGGGAGGAT-----AATGAACCTTGGCCCTTGGCTGGCCCAATGTG 675
QY 23 AspAsnThrValValAlaAlaSerGluGlnAspSerGluIleValValGlyLysGluGln 42
Db 676 ATGAAGCTGCTGCTGGTGGCTTCT----- 699
QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62
Db 700 -----GAATGTGCTCTCTTCTGCG 717
QY 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGly 82
Db 718 AAGACAGGTGGCTTGGAGATGCTGGGTGCTTTTGCCTAAGGCTCTGCGGAGGAGGA 777
QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102
Db 778 CACCGTGTATGCTGTGTATACCAAGATAT-----GGAGAGTATGCC 819
QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122
Db 820 GAAGCCCGGATTTAGGTGTAAGGAGACCTTACAAGGTAGCTGGACAGGATTCAGAGTT 879
QY 123 ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyr 142
Db 880 ACTTATTTTCACTCTTACATTCGATGAGTGTGATTTTGTATTCGTAGAACCCCTCCCTTC 939
QY 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161
Db 940 CGGACCGGACCAATATTTATGCG-----GGAGAAAGATTGGATATTTTGAAG 990
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGly 181
Db 991 CGCATGATTTTCTTCTGCAAGCGCGCTGTGAGGTTCATGCTGCTCCATGTCGCGGT 1050
QY 182 TyrIleTyrGlyGln-----AsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200
Db 1051 ACTGTCTATGGTGATGGCAACTTAGTTTTCATGCTAATGATGGCATACCGCACTTCTG 1110
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QY 201 ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220
Db 1111 CCTGCTATCTAAAGCCCTATTACCGGCAATGTTTATGTCAGTATGCTCGCTCTG 1170
QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240
Db 1171 CTTGTGATACACACATTGCTCATCAGGTCGTGGCCCTGTAGACACTTCGTCAATTT 1230
QY 241 GlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArg 260
Db 1231 GACTTGCCT-----GAA 1242
QY 261 HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu 272
Db 1243 CACTACTGACGACTTCAAACTGTATGACAACTGTTGGGGATCACAGCAGCTTTT 1302
QY 273 LysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292
Db 1303 GCTGGGGCTGAAGACGGCAGACCGGGTGTGACCGTTAGCAATGGCTACATGTGGAG 1362
QY 293 ValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312
Db 1363 CTGAAGACTTCGAAGCGGCTGGGGCTCCACGACATCATAAACCAAGACGACTGGAAG 1422
QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProIaThrAspLysCys 332
Db 1423 CTGCAGGGATCGTGAACGGCATCGACATGAGCGAGTGAACCCCGCTGTGAC----- 1476
QY 333 IleProCysHisTyrSerValAspAspLeu-----Ser 343
Db 1477 -----GTGCACCTCCACTCCGACGACTACACCACTACACGTTTCGACGCGTGGACAC 1530
QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363
Db 1531 GGCAGCGCGAGTGCAGGCGCGCTTCGACGCGCAGCTGGGCTGCAGGTCCGCGACGAC 1590
QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383
Db 1591 GTGCCACTGATCGGGTTTCATCGGGCGGCTGGACACCAAGCGCGGTGCACATCATCGCC 1650
QY 384 LeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403
Db 1651 GACCGGATCCACTGGATCGCGGGCAGGAGCTGACGCTGATGCTGGCGCACCGGCGG 1710
QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423
Db 1711 GCCGACCTCGAGGACATGCTGCGGGCGGTTTCGAGTCGAGGCACAGCGACAGGTGCGCG 1770
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443
Db 1771 TGGGTGGGGTCTTCGGTGGCCCTTGGCGCACCGGATCACGGCGGCGCGACATCTCGTGG 1830
QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
Db 1831 ATGCGGTTCGGTTCGAGCGGTTCGGGCTGAACAGCTCTACGCCATGCGGTACGGGACC 1890
QY 464 ValProValIleHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483
Db 1891 GTGCCCGTGTGCACCGCTGGGGGGGCTCCGGGACACGCGTGGCGCGCTTCACCGCGTTC 1950
QY 484 GlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503
Db 1951 AACGACACC-----GGGCTCGGGTGGAGCTTCACCGCGGAGCGGACCGGATG 2001
QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523
Db 2002 ATCGAGCGGCTCTCGCACTGCCT-CACACAGTACCGGAACACTACAGGAGAGCTGGCGCG 2060
QY 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db 2061 CTGCAGGGCGCGCGCATCGCCGAGGACCTAGCTGGGACCACTCGCGC 2108

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RESULT 24

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US-10-425-115-149880
; Sequence 149880, Application US/10425115
; Publication NO. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 149880
; LENGTH: 2813
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_68215C.1
US-10-425-115-149880

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Alignment Scores:
Pred. No.: 6,21e-125 Length: 2813
Score: 1125.50 Matches: 254
Percent Similarity: 57.0% Conservative: 63
Best Local Similarity: 45.7% Mismatches: 160
Query Match: 38.9% Indels:
DB: 8 Gaps: 11

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US-10-628-525A-21 (1-539) x US-10-425-115-149880 (1-2813)

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QY 3 AlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGlySerIle 22
Db 692 GCTCCTTATGATCAGCGAGGAT-----AATGAACCTGGCCCTTGGCTGGCCCTAATGTG 745
QY 23 AspAsnThrValValValAlaSerGluGlnAspSerGluIleValValGlyLysGluGln 42
Db 746 ATGAACGTCGTCGTGGTGGCTTCT----- 769
QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62
Db 770 -----GAATGTCCTCTTCTGC 787
QY 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGly 82
Db 788 AAGACAGGTGGCTTGGAGATGTCGTGGGTGCTTTGCCCTAAGGCTCTGCGGAGGAGGA 847
QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAla 102
Db 848 CACCGTGTATGTCGTGATACCAAGATAT-----GGAGAGTATGCC 889
QY 103 AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal 122
Db 890 GAAGCCCGGATTTAGGTGTAGGAGACGTTACAGGTAGCTGGACAGATTTCAGAAGTT 949
QY 123 ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyr 142
Db 950 ACTTATTTTCACTCTTACATTGATGAGTTGATTTTGTATTGCTAGAACCCCTCCCTTC 1009
QY 143 ---HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe 161
Db 1010 CGGCACCGGCACAAATAATTTATGGG-----GGAGAAAGATTGATATTTTGAAG 1060
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGly 181
Db 1061 CGCATGATTTTGTCTGCAAGGCCGCTGTTGAGTTCCATGTTATGCTCCATGTTGGCGGT 1120
QY 182 TyrIleTyrGlyGln---AsnCysMetPheValAsnAspTrpHisAlaSerLeuVal 200
Db 1121 ACTGTCATGTTGATGGCAACTTAGTTTTCATTGCTTAATGATTGGCATACCGCACTTCTG 1180

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QY 50 SerIleValPheValThrGlyLeuAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69  
Db 1070 AACATTATTGGTGGCTTCAGATGCGCTCCATGGTCTAAACACAGGTGGCTTGGAGAT 1129  
QY 70 ValCysGlySerLeuProValAlaLeuAlaAargGlyHisArgValMetValValMet 89  
Db 1130 GTTCTGGAGCAATTACCAAGCTTTGGCTCGAGTGGCCACAGAGTTATGGTTGGCA 1189  
QY 90 ProArgTyrLeuLeu-----GlyThrSerAspLysAsnTyrAlaAlaAlaPheTyrThr 107  
Db 1190 CCTGTTATGACCACTATCTGGAACCTCAAGATCTCGTGTGAAGAAAAATTATAAAGTT 1249  
QY 108 GluLysHisIleArgIleProCysPheGlyGlyLeuHisGluValThrPhePheHisGlu 127  
Db 1250 GAT-----GGTCAGAGTGTGAAGTACTTACTTACCAAGCT 1285  
QY 128 TyrArgAspSerValAspTrpValPheValAsp---HisProSerTyrHisArgProGly 146  
Db 1286 TTTATTGATGGTGGATTTGTTTTCATTGACAGTCATATGTTTACACATTTGGGAC 1345  
QY 147 AsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeu 166  
Db 1346 AACATTTTACCGA-----GGCAACCGTGTGATATTTTAAACCGCATGGTTTATTT 1396  
QY 167 CysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln 186  
Db 1397 TGCAAGACCGCATGAGGTTCCTTGGCATGTTCCATGTGGTGGGTCTGCTATGGAGAT 1456  
QY 187 ---AsnCysMetPheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAla 205  
Db 1457 GGAATTTAGTGTTCATTGATGATGGCATCTGCTTTATGGCAGTATATCTGAAA 1516  
QY 206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn 225  
Db 1517 GCTTATTATGTCACATGAATTAATGAACTATACAAAGATCTGCTGGTGGTATTCATAAC 1576  
QY 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu 245  
Db 1577 ATCGCTCATCAGGTGCGTGTCTCTTGGAGGATTTTTCATATGATAGATCTTCCACCACAC 1636  
QY 246 TrpTyrGlyAlaLeuGluTyrPhePheProGluTyrAlaArgArgHisAlaLeuAspLys 265  
Db 1637 TATATGACCTTTCAAGTTGTATGACCCAGTA-----GGA 1672  
QY 266 GlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrVal 285  
Db 1673 GGTGAGCATTTCAACATTTTGGCGCTGGTCTAAAGACACACAGATCGTGTAGTTACAGTT 1732  
QY 286 SerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeu 305  
Db 1733 AGTCATGGATATTTCATGGGAACCTAAAGACTTCCCAAGGTGGTTGGGGATTGCATCAGATA 1792  
QY 306 LeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrp 325  
Db 1793 ATTAAATGAGAACATTTGGAATTTACAGGGTATTTGTAATGGGATTTGATACAAAGAGTGG 1852  
QY 326 AsnProAlaThrAspLysCysIlePro-----CysHisTyrSerValAspAsp 341  
Db 1853 AACCTGAGTTGGACGCTTCACTACAGTCAGATGGTTTACATGAATCTCTCTTGGACAGC 1912  
QY 342 Leu---SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360  
Db 1913 CTACAGACTGGCAAGCTCAATGTAAGCTGCATTCAGAGGAACTTGGTTTACAGATT 1972  
QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380  
Db 1973 CGTGATGATGCTCCACTGATCGTGTTCATGGAGGCTTGACCCACAAAGGGTGTGTAT 2032  
QY 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
Db 2033 CTGATTGCTGAGGCCAGTCTGGATGATGGGTGAGATGTACACTGTGCTATGTTGGGG 2092  
QY 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420

Db 2093 ACGGGAGGCGCTGACCTTGAACAGATGCTAAAGCAATTTTGAGTGTCAACACAATGATAAA 2152  
QY 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
Db 2153 ATTAGAGGATGGGTGGTTCTCTGTGAAGACTTCTCATCGTATAACTGCTGTGTGCAGAC 2212  
QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
Db 2213 ATTCTGCTCATGCTTCTAGATTTGAGCTTGGGACTGGAACCTTTTATGCAATGAAA 2272  
QY 461 TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe 480  
Db 2273 TATGGAGCATTTCTCTGTTCATGAGTAGGAGGACTCAGAGATACTGTGCAGCCCTTT 2332  
QY 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThr 500  
Db 2333 GATCCTTTTAAATGAGTCA-----GAGCTGGGTGGACCTTCAGTAGGGCTGAAGCT 2383  
QY 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520  
Db 2384 AGCCAGCTGATCCACGCATTTAGGAAATTTGCTTACTGAC--TTATCGTGAGTACAAAAAGAG 2442  
QY 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538  
Db 2443 TTGGGAGGGGATTCAGACACGTTGTATGACACAAGACTTAAGTTGGGATAATGC 2496  
RESULT 27  
US-10-044-543-25  
; Sequence 25, Application US/10044543  
; Publication No. US20030135883A1  
; GENERAL INFORMATION:  
; APPLICANT: Singletary, George  
; APPLICANT: Zhou, Lan  
; TITLE OF INVENTION: No. US20030135883A1el Starch Synthase Polynucleotides  
; TITLE OF INVENTION: and Their Use in the Production of New Starches  
; FILE REFERENCE: 1144D  
; CURRENT APPLICATION NUMBER: US/10/044,543  
; PRIOR FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: 09/388,743  
; PRIOR FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 2418  
; TYPE: DNA  
; ORGANISM: Typha latifolia  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2418)  
US-10-044-543-25  
Alignment Scores:  
Pred. No.: 2,65e-122 Length: 2418  
Score: 1103.00 Matches: 243  
Percent Similarity: 59.7% Conservative: 78  
Best Local Similarity: 45.2% Mismatches: 176  
Query Match: 38.1% Indels: 42  
DB: Gaps: 12  
US-10-628-525A-21 (1-539) x US-10-044-543-25 (1-2418)  
QY 15 GluGlyIleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSer 34  
Db 574 GAAGATCTTGTAGACGACAAATTTGATGTGTACATGTC-----AAAGAT 618  
QY 35 GluIleValValGlyLysGluGln-----AlaArgAlaLysValThr 48  
Db 619 GATTTGAATCTCTGGGGAAGAAATAGGTTCTCTTCTTTGCTGGGCAAAATGTC--- 675  
QY 49 GlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGly 69  
Db 676 ATGAACATCATAGTAGTTCTGTCAGAAATGTGCTCTTCTTGTGTCACAAACAGGTGGCTTGA 735

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QY 69 AspValCysGlySerLeuProValAlaLeuAlaAaArgGlyHisArgValMetValVal 88
DB 736 GAITGTCAGGAGCATGCGAAGGCTTTGGCCAGAGAGGACATAGGCTCATGGTTGG 795
QY 89 MetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGlu 108
DB 796 GCACCAAGGTATGGAACACTATGCTGAACCCCAAGATATAGGATCGCGAAATACACAG 855
QY 109 LysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyr 128
DB 856 GTTCAT-----GGCAGGATATGGAAGTAACTTATTATCCATGCTTAT 897
QY 129 ArgAspSerValAspTrpValPheValAspHisProSerTyr--HisArgProGlyAsn 147
DB 898 ATCGACGGTGTGAATTTGTTTATGATATGTCAGACTTCGTCACCGGGGGAATCGT 957
QY 148 LeuTyr--GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeu 166
DB 958 ATTTATGAGGGAACCGAGTG-----GATATCTTAAACGTATGATTGTTTC 1005
QY 167 CysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln 186
DB 1006 TGCAGGCGAGCTGTAGAGGTTCTTGSCATGTTCCATGTGTGGTCTTCTGTTATGAGAT 1065
QY 187 ---AsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAla 205
DB 1066 GGTAATTTGGCTTTCATCAGAAATGATGCGATCTCTCTGCTGTTTATCTGAAG 1125
QY 206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn 225
DB 1126 GCATATTATCGTGACAATGCTTGATGAATATGCTCGTCTGCTGTTCTGTTATACACAC 1185
QY 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGlu 245
DB 1186 ATAGCCACCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1245
QY 246 TrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLys 265
DB 1246 TACTTGGACCTTTTCAGTTGATGATGACCCCGTC-----GGA 1281
QY 266 GlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrVal 285
DB 1282 GGTGAACACCTCAATATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1341
QY 286 SerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeu 305
DB 1342 AGCCATGGTTATGCTAGGAGCTGAAACATCAGAAAGTGGTTGGGCGCTACATGAAAT 1401
QY 306 LeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrp 325
DB 1402 ATAAATGAAGTAACCTGGAAGTTTCAGGTATTTGAATGGCATGATGATCAAGAGTGG 1461
QY 326 AsnProAlaThrAspLysCysIlePro-----CysHisTyrSerValAspAsp 341
DB 1462 AGCCCGAATTTGATGTCACCTTAAATCCGATGGATACACAAATTTCTCTAGATCT 1521
QY 342 LeuSer--GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360
DB 1522 TTAGAGATGGTAAAGCCAGTATGTAAGGCTGCTTTGTCAGCGAGAGTCTGCTGCTGTT 1581
QY 361 ArgProAspValProLeuIleGlyPheIleGlyValGlyLeuAspTyrGlnLysGlyIleAsp 380
DB 1582 CGTGATATGTACCCATCATTCATTCATGAGGTGATGAGCTTACACACCAAGAGCGTCCAT 1641
QY 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400
DB 1642 CTCATTGCCAGGCCCATGCTGCTGATGATGTCAGTCATGATGTTCAAGTAGCTATGTTAGGC 1701
QY 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420
DB 1702 ACGGGGAGCAAGACCTTGAGAATTTACTGAGGAACCTTTGAGGGGTCAACACAGGGGCAAA 1761
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QY 421 PheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440
DB 1762 GTTAGAGCATGGTTGCATTTTCAGTAAGATGGCGCATAGAAATTACAGCAGGTGCCGAC 1821
QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460
DB 1822 ATCTCATGATGCTTCGAGGTTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGCAATGATG 1881
QY 461 TyrGlyThrValProValIleHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe 480
DB 1882 TATGAAACCATTTCCAGTCTGCTGTTGGGGCCCTTAGAGATACAGTACTCAATTT 1941
QY 481 AsnProPheGlyGluAsnGlyGlnGlyThrGlyTyrAlaPheAlaProLeuThrThr 500
DB 1942 GATCTTTTCAAGAGTCT-----GGTCTTGGTTGGACCTTCGACAGGCGAGGCA 1992
QY 501 GluAsnMetPheValAspIleAlaAsnGlyAlaAsnGlyHisValGlyProCys 538
DB 1993 GGAAGCTGATCCATGCTTGAATTAAGTCTT-GAATACATACTGGAATTACAAGGACAG 2051
QY 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCys 538
DB 2052 TTGGAAGGCTCTTCAACAAGAGGATGATGCAAGATCTTAGCTGGGATAATGC 2105

RESULT 28
US-10-336-753-50
; Sequence 50, Application US/10336753
; Publication No. US20030226176A1
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter L.
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; TITLE OF INVENTION: HOSTS
; FILE REFERENCE: 2461-52
; CURRENT APPLICATION NUMBER: US/10/336,753
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/09/402,254
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2010)
US-10-336-753-50

Alignment Scores:
Pred. No.: 1,87e-121 Length: 2010
Score: 1095.00 Matches: 245
Percent Similarity: 58.3% Conservative: 73
Best Local Similarity: 45.0% Mismatches: 166
Query Match: 37.8% Indels: 62
DB: 6 Gaps: 12

US-10-628-525A-21 (1-539) x US-10-336-753-50 (1-2010)
QY 10 LeuGlyLeuGluProGluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29
DB 460 GTTGTGCGCATGATGCTGGTTCTTTTGAACATTTATGGGACAAT-----504
QY 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49
DB 505 -----GATCTGGGCTTTGGCCGGGAGAAAT-----GTTATG 537
QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69
DB 505 -----GATCTGGGCTTTGGCCGGGAGAAAT-----GTTATG 537
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Db 538 AACGTGATCGTGGTGGCTGTAATGTTCTCCATGGTGCAGAAACAGGTGGTCTTGGAGAT 597  
 Qy 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMet 89  
 Db 598 GTTGTGGGAGCTTTTACCAAGCTTTAGCGAGAGAGGACATCTGTTATGTTGGTA 657  
 Qy 90 ProArgTyrLeuAenGlyThrSerAspLysAsnTyrAlaAenAlaPheTyrThrGluLys 109  
 Db 658 CCAAGGTAT-----GGGACTATGTGGAAGCGCTTTGTATATGGGAATC 699  
 Qy 110 HisIleArgIleProCysPheGlyGluHisGluValThrPhePheHisGluTyrArg 129  
 Db 700 CGGAATACTACAAGCTGCAGGACAGACTAGAGTGAATATTTCCATGCAATTTATT 759  
 Qy 130 AspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeu 148  
 Db 760 GATGGAGTCGACTTTGTGTTTCATTGATGCCCTCTTTTCCGGCACCGCTCAAGATGACATA 819  
 Qy 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168  
 Db 820 TATGGG-----GGAAGTAGCGAGCAATCATGAAGCGCATGATTTGTTTTCGAAG 870  
 Qy 169 AlaAlaCysGluAlaProLeuLeuGluLeuGlyGlyTyrIleTyrGlyGln---Asn 187  
 Db 871 GTTGTCTTGAGGTTCTTGGCAGCTTCATGCGGTGTGTGTGCTACGGAGATGGAAAT 930  
 Qy 188 CysMetPheValValAenAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLys 207  
 Db 931 TTGGTGTTCATTGCCAATGATTGGCACACTGCCTCGCTCTGCTCATACATACATCGCC 990  
 Qy 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAla 227  
 Db 991 TACAGAGACCATGGTAAATGCAATGACACTACACTCGCTCGCTCATACATACATCGCC 1050  
 Qy 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247  
 Db 1051 CACAGGGCGGTGGTCTCTAGATGAATTCCTGATGAGTTCCTGATGAGTTCCTGACACTT 1110  
 Qy 248 GlyAlaLeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGlyGlu 267  
 Db 1111 CAACATTTGAGCTGACGATCCGTC-----GGTGGCGAG 1146  
 Qy 268 AlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLys 287  
 Db 1147 CACGCCAACATCTTTGCGCGGTCTGAAGATGGCAGACCGGTGGTGTGACTGTGACGCGC 1206  
 Qy 288 GlyTyrSerTrpGluValThrAlaGluGlyGlnGlyLeuAenGluLeuLeuSer 307  
 Db 1207 GGTACTGTGGAGCTGAAGACAGTGAAGGCGGCTGGGGCTCCACGACATCATCCGT 1266  
 Qy 308 SerArgLysSerValLeuAenGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327  
 Db 1267 TCTAACGACTGGAAGATCAATGTCATCGTGAACGCGCATCGACCCAGGAGTGAACCCC 1326  
 Qy 328 AlaThrAspLysCysIlePro-----CysHisTyrSerValAspLeu--- 342  
 Db 1327 AAGGTGACGCTGCCTCGGTGCGACGGCTACACCAACTACTCTCCCTCGAGACACTCGAC 1386  
 Qy 343 SerGlyLysAlaLysCysLysGlyAlaLeuGlnGlyLeuGlyLeuProIleArgPro 362  
 Db 1387 GCTGGAAGCGGAGTGAAGCGGCGCTGACGGGAGCTGGGCTCTGGAAGTGGCGGAC 1446  
 Qy 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIle 382  
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 Qy 383 GlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402  
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 Qy 403 AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422  
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Qy 423 GlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442  
 Db 1627 GGGTGGGTGGGTCTCGGTGCTTATGCGCATCGCATCAGCGGGGCGCGCGTGTCTG 1686  
 Qy 443 LeuMetProSerArgPheGluProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGly 462  
 Db 1687 GTGATGCTTCCCGCTTCGAGCGCTCGGGCTGAACCAAGCTCTACGCGATGGCGTACGGC 1746  
 Qy 463 ThrValProValHisAlaThrGlyGlyLeuArgAspThrValGluAenPheAsnPro 482  
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 Qy 483 PheGlyGluAenGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAen 502  
 Db 1807 TTC-----GGCGAGCGCGGCTCGGTGGACTTTT----- 1836  
 Qy 503 MetPheValAspIleAlaAenCysAsnIleTyrIleGlnGlyThrGlnValLeu----- 520  
 Db 1837 -----GACCGCGCGGAGGCCAACAGCTGATCGA-GGCGCTCAGGCACCTGCCTCGA 1886  
 Qy 521 -----LeuGlyArgAlaAenGluAlaArgHisValLysArg 532  
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 Qy 533 LeuHisValGlyPro 537  
 Db 1947 CCTCAGCTGGGACCA 1961  
 RESULT 29  
 US-10-109-048-1143  
 ; Sequence 1143, Application US/10109048  
 ; Publication No. US20040107461A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COMMURI, PADMA  
 ; APPLICANT: KEELING, PETER L.  
 ; APPLICANT: RAMIREZ, NONA  
 ; APPLICANT: MCKEAN, ANGELA  
 ; APPLICANT: GAO, ZHONG  
 ; APPLICANT: GUAN, HANPING  
 ; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS  
 ; FILE REFERENCE: 2461-76  
 ; CURRENT APPLICATION NUMBER: US/10/109,048  
 ; CURRENT FILING DATE: 2003-03-04  
 ; PRIOR APPLICATION NUMBER: 60/279,720  
 ; PRIOR FILING DATE: 2001-03-30  
 ; NUMBER OF SEQ ID NOS: 1154  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 1143  
 ; LENGTH: 2865  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-10-109-048-1143  
 Alignment Scores:  
 Pred. No.: 3, 2e-121 Length: 2865  
 Score: 1095.00 Matches: 245  
 Percent Similarity: 58.3% Conservative: 73  
 Best Local Similarity: 45.0% Mismatches: 166  
 Query Match: 37.8% Indels: 62  
 DB: 7 Gaps: 12  
 US-10-628-525A-21 (1-539) x US-10-109-048-1143 (1-2865)  
 Qy 10 LeuGlyLeuGluProGluGlyIleAlaGlySerIleAspAsnThrValValAla 29  
 Db 1315 GTTGTGTCAGATGATGCTGCTTTTGAACATTATGGGGACAAT----- 1359  
 Qy 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49  
 Db 1360 -----GATTCGGGCTTTGGCCGGGAGAAT-----GTTATG 1392  
 Qy 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69



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Qy 45 AlalysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLysSer 64
Db 343 -----GTAATGAATATATCATATTGGTAGCTGCAGAAATGTGCACCATGGCTCAAAACA 393
Qy 65 GlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArg 84
Db 394 GGTGGGCTTGAGAGATGTTGGAGCTTACCTAAAGCATTTGGCCAAAGAGGACATCGT 453
Qy 85 ValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAla 104
Db 454 GTCATGTAGTGTCTCAAGATATGGAAACTATCTGAACCTTAAGGAATAGGGAATCTT 513
Qy 105 PheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhe 124
Db 514 -----AAAAGGTACAAGGTTGAT-----GGACAGGACATCGAGATTAAATATAC 555
Qy 125 PheHisGluTyrArgAspSerValAspTyrPheValPheValAspHisProSerTyrHisArg 144
Db 556 TATCATACTTACATCGAATTCGTGTGATTTTGTCTTCATCATAGTCTTATTTTCCGCCAT 615
Qy 145 ProGlyAsn---LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr 163
Db 616 ATTGGAATGATATATATGTT-----GGAAACCGAGTGGACATTTTGAAGAGATG 666
Qy 164 ThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyTyrIle 183
Db 667 GTATTGTTCTGCAAGCAGCAGTTGAGGTTCTTGGCATGTCCCATGTGGTGGATTCTGT 726
Qy 184 TyrGlyGln---AsnCysMetPheValValAsnAspTyrHisAlaSerLeuValProVal 202
Db 727 TATGGAGATGGGAATTTGGTTTTCATTGCCAACGATTTGGCATACCTCTTACTTCCAGTT 786
Qy 203 LeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuVal 222
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Db 847 ATTCAACAACATTGCACATCAGGGTCGTGGTCCGCTAGATGACTTCTCATATGTGGATTG 906
Qy 243 ProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgHisAla 262
Db 907 CCATGATCACATTGACTCGTTTAGA----- 933
Qy 263 LeuAspLys-----GlyGluAlaValAsnPheLeuLysGlyAlaValAlaThrAla 279
Db 934 CTGGATGATCCTGTTGGAGGTGAGCATTTTAAACATTTTGCAGCTGGTATAAGAGCTGCT 993
Qy 280 AspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGly 299
Db 994 GACCGTGTGGTTACAGTTAGCCATGGCTATGCTTGGAGTTAAACAACATCTGAAGGTGGT 1053
Qy 300 GlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGly 319
Db 1054 TGGGGATTGATGAGATTCATCAACAGTGCATTTGGAAATTCATGTTATTTGTAATGGA 1113
Qy 320 IleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerVal 339
Db 1114 ATCGATACCCATAGTTGGATCCAAAATTGAC-----GCTCACTTAAATTC 1161
Qy 340 AspAspLeuSer-----GlyLysAlaLysCysLysGly 350
Db 1162 GATGGTTTACCACTTCACTCCCTGGAACTCTTGAATGGAAAGGCCAGTGCAGAGCT 1221
Qy 351 AlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIle 370
Db 1222 GCTTTCACAGAGAGTTGGTCTGCTCTGTCGTGACGAGCTTCTTATTTCTTCCCTTCATT 1281
Qy 371 GlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMet 390
Db 1282 GGGAGATTAGACCATCAAAAAGGTATAGATCTCATAGCGGAGGCCATGCATGGCTCGTC 1341
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Qy 391 ArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMet 410
Db 1342 GGTCAAGATCTACAGATAATCATGCTGGGCACTGGGAGGCCAGACCTCGAGGATATGCTT 1401
Qy 411 ArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerValPro 430
Db 1402 CGAAGATTTCAGACGTGAGCATCGCGGTAAAGTTCAGGGGATGGGTGGGTTCTCAGTGA 1461
Qy 431 ValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluPro 450
Db 1462 ATGGCTCATCGGATCACAGCAGGTGCTGATGCCCTACTGATGCCCTCCAGGTTCCAACT 1521
Qy 451 CysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThr 470
Db 1522 TGTGGATTGAACCAACTTCACGCTATGATGTACGGAACAATTCCTGTTGTGATGCAGTA 1581
Qy 471 GlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGly 490
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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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37.0 2842 11 US-11-231-599-3 Sequence 3, Appl
35.9 2107 11 US-11-231-599-5 Sequence 5, Appl
28.4 2410 11 US-11-096-568A-18030 Sequence 18030, A
23.0 9024 11 US-11-231-599-37 Sequence 37, Appl
20.1 2886 8 US-10-504-599A-15 Sequence 15, Appl
16.1 3621 11 US-11-231-599-9 Sequence 9, Appl
15.7 5346 11 US-11-231-599-7 Sequence 7, Appl
12.2 11611 11 US-11-231-599-38 Sequence 38, Appl
6.8 1592 11 US-11-231-599-16 Sequence 16, Appl
5.3 1269 8 US-10-336-263A-11 Sequence 11, Appl
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; APPLICANT: MORELL, MATTHEW  
; APPLICANT: RAHMAN, SADOUR  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 054270/0126  
; CURRENT APPLICATION NUMBER: US/11/144,630  
; CURRENT FILING DATE: 2005-06-06  
; PRIOR APPLICATION NUMBER: US/09/508,377  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: AU PP 2509  
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; PRIOR APPLICATION NUMBER: PCT/AU98/00743  
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; PRIOR FILING DATE: 1997-09-12  
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442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461  
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462 GlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPheAsn 481  
Db GGTACAGTTCTCTGTAGTTTCATGGAAGTGGGGGCTCCGAGACACAGTCGAGACCTTTCAAC 1969

482 ProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGlu 501  
Db CTTTTTGTGCAAAAGAGGAGGAGGTACAGGTGGCGCTTCTCACCGCTAACCGTGGAC 2029  
502 AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeu 521  
Db AAGATGTT-GTGGCATTGCGAACCGCATGTCGACATTTCAGGAGCACACAGCGCTCTG 2088  
522 GlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
Db GGAGGGGCTCATGAAGCGAGGCATGACGAAGACCATACATACGTGGGACCATGCCG 2142  
RESULT 3  
US-11-144-630-13  
; Sequence 13, Application US/11144630  
; Publication No. US2006001051A1  
; GENERAL INFORMATION:  
; APPLICANT: KALEEN, ZHONGYILI  
; APPLICANT: MORELL, MATTHEW  
; APPLICANT: RAHMAN, SADEUR  
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS  
; FILE REFERENCE: 054270/0126  
; CURRENT APPLICATION NUMBER: US/11/144,630  
; CURRENT FILING DATE: 2005-06-06  
; PRIOR APPLICATION NUMBER: US/09/508,377  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: AU PP 2509  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: PCT/AU98/00743  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: AU PP 9108  
; PRIOR FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 10337  
; TYPE: DNA  
; ORGANISM: Triticum tauschii  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (10232)  
; OTHER INFORMATION: a, t, c, g, other or unknown  
US-11-144-630-13  
Alignment Scores:  
Pred. No.: 2,67e-127 Length: 10337  
Score: 1277.00 Matches: 345  
Percent Similarity: 23.2% Conservative: 19  
Best Local Similarity: 27.6% Mismatches: 21  
Query Match: 44.1% Indels: 865  
DB: 14 Gaps: 9  
US-10-628-525A-21 (1-539) x US-11-144-630-13 (1-10337)  
12 LeuGluProGluGlyIleAlaGluGlySerIleAspAsnThrValValValAlaSerGlu 31  
Db TTGCAACCA--GGATGCTGAGGATTCATCGACAGCATATCGTGCTGCAAGTAG 1519  
32 GlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIle 51  
Db CAGGATTCGAGATCATGCGAATGAGCAACCTCAAGCTAAAGTTACACGTAGCATC 1579  
52 ValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCys 71  
Db GTGTTTGTGACGTGGAAGCTCTCTTATGCAAAAGTCAGGGGGCTGGGAGATGTTGT 1639  
72 GlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValValMetProArg 91  
Db GGTTCGTACCAATGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1699  
92 TyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIle 111  
Db TACTTGAATGGGCTCTCTGATAAAACTATGCAAAAGGCATTATACACTCGAAGCACATT 1759

Qy	112	ArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSer	131
Db	1760	AGAGTCCATGCTTTGGGGGATCAGATGAATGACCTTTTTCATGAGTATAGACAAAC	1819
Qy	132	ValAspTtpVal-----	135
Db	1820	GTGCGATTGGT--GGGTACACAATCACCTTCTTATTCTCTGTTGAATTCTAGCAACTGTTT	1878
Qy	135	-----	135
Db	1879	ATCCTTGTTTACACTTCTTTTAGCCCTGCAAGACATATGTAATTCCATACTTTTGT	1938
Qy	135	-----	135
Db	1939	TATTTCCCTTGACTCTTGCTCATGAAGGTCAAATATCATATATCCATGGAAGTCATGC	1998
Qy	135	-----	135
Db	1999	ATGTCCTAGTATTTTTCGTGTCGGTGCTTTAACTTTCAGGGATTAACTAGCTGGATTT	2058
Qy	135	-----	135
Db	2059	GATAACTAAAGTTTATTTTATTGAAAAAAATTTAGTGTGGCTGAGCCACAGCCACGCA	2118
Qy	135	-----	135
Db	2119	GTGGCACCACCTGTTGCACATGATTTTTCGATTTCTGTTTGACCGAGCACTTCATGTAA	2178
Qy	135	-----	135
Db	2179	TAAAGTGTAATAATCATAAAGTACCAATTTTATTCTGCCAATTCACCTTAAGAGTATATAC	2238
Qy	135	-----	135
Db	2239	ATTTATCTTGGCCTCAATCATGGAGTACTGTGCATTGAGTGACCATCATTTGTTCTAAG	2298
Qy	135	-----	135
Db	2299	GAGAAATGTGGGTGCAAGGAAGACACTTTTGTCCCTTAATAAAGGAGGCACTCTGTT	2358
Qy	135	-----	135
Db	2359	GTCATATAGTAGAAGCAACAACTATTTCATAAGAGCTAACTATGGCAAAAGAACCAA	2418
Qy	135	-----	135
Db	2419	AAAAAGCATGCTAAGGCGGTGACACAAAGGTGAGGGGGCCCTTGAGCTGACAGCAACC	2478
Qy	135	-----	135
Db	2479	CCAAACTATTGCCATTGTTTTCATAATGAAGATCAATTTAGAAGCTCTCAGGAACCTCG	2538
Qy	135	-----	135
Db	2539	AAACAGTGGCTTCCGTCCACAGATCGTCTGTTAATAATTTTGTCCAGTGATACTTTT	2598
Qy	135	-----	135
Db	2599	TTGCTCTTACAAGAGTGCCTATGTTGCATATACATATTGTTAAGTTGTTTCATAGTTTAC	2658
Qy	135	-----	135
Db	2659	TTCTTATTCTAAACAGCAAGTGCCTAATGCTTGCATTTATTTTGGCTATTATTTTATTT	2718
Qy	136	-----PheValAspHisProSerTyrHisArgPro	145
Db	2719	CTCATTTCAATCAACACTTTTGTTCAGGTGTTTGTGATCATCCGTCATATCATAGACCA	2778
Qy	146	GlyAsnLeuTyrGlyAspLysPheGlyValaPheGlyAspAen-----	159
Db	2779	GGAAGTTTATATGGAGATAATTTTGGTCTTTTGGTGATTAATCAGGTACACTACACTATA	2838

QY	159		-----	-----	159
Db	2898	CTAAGCCTCTAGTTGACTAAAGTCGTAAAGTGTATACCTCTCGTGACGGCTGCTCATGT	2898		
QY	160	---GlnPheArgTyThrLeuLeuCysTYrAlaAlaCyseGlualProleuileuGI	178		
Db	2899	CGTGCAGTTCCAGATACACACTCTCTTGTCTATGCTGANGCGAGGCCCAATAATCTCTGA	2958		
QY	178	uLeuglyglyPyzileTyrgLynAnCysMetPheValValAsnAsptPhisAlase	198		
Db	2959	ATTGGAGGATATATTTATGGACAGAATTGCA TGTTTGTTGTAACGATTGGCATGCCAG	3018		
QY	198	rLeuValproval	202		
Db	3019	CCTTGTGCCAGT -GTACGTTGTTGTGGANCTGAAAAGTCCAATFCTTTATTTCATTCTCTG	3077		
QY	202	-----	-----	202	
Db	3078	CTTTGCAGTGTGCCCATGTCTACATTTCTTTTHATGCTTTTTTCATGCTGTCTTATATTT	3137		
QY	202	-----	-----	202	
Db	3138	GCAATATGCTTATGGAGTCTAAAAGTTACCGAGGGGAATAACTCTTAAGGATTTCTCTCA	3197		
QY	202	-----	-----	202	
Db	3198	ATCAAATTATCTTAGCTTTAGTTTAA CATTTA CTGTGCGAAACA TATGTGTTTGAGATT	3257		
QY	202	-----	-----	202	
Db	3258	TACAGTTTACAGANTTGC ACTTCACTAGTTTGTAGTAACTATCTGATGTTTTCCCAGAGAA	3317		
QY	202	-----	-----	202	
Db	3318	ATGCTAAAAGCTTTGTGCTCTTGATGCA TTGATAGAAAAAGAGTTTATGTACACTCCCCA	3377		
QY	202	-----	-----	202	
Db	3378	GAGGGGACC AAAAATTACAACCA CCCTTGAGAACTAGGGCTG CGGAAGAAGCGA	3437		
QY	202	-----	-----	202	
Db	3438	TGCAAGCCCACTGCCCCCTTGTAGTCAAAGCCGGCGT CAGCTTGATGTGTCAAGT	3497		
QY	202	-----	-----	202	
Db	3498	AAGTACAGTGTAGATTGGCGAAGTCCGTCGNAGATGACAGTTGTCGCTGCT	3557		
QY	202	-----	-----	202	
Db	3558	TCCAAATCCACAAACTATGAGCATGATCACTGGAGAGTACCTTTTCTCGCGGTGAGG	3617		
QY	202	-----	-----	202	
Db	3618	GGGTGACTGGTGTCTGCTGCCAGTTTTCAGATAATCTGAAAAATG CATGTTTTGA	3677		
QY	202	-----	-----	202	
Db	3678	TGATTTTAGTAICTTGGGACCTTGGGTACCACTTAAGCTTTCA CACAGTAATTTGCA GT	3737		
QY	202	-----	-----	202	
Db	3738	TACACCTATA AAAGTAA CGGTCA TGATATGC ATGTGTTTGGGTAGATCATGTGCTGTC	3797		
QY	202	-----	-----	202	
Db	3798	ATTTTAGGAATTAGGACATGCCAGAACCA CGTGAGGCTTATGGGCAATTCA TTGTTGCC	3857		
QY	202	-----	-----	202	
Db	3858	ATTATACGAGTCATGAATATGTTT CAGCAN GTTTG GACGCTACTGTTGTTGGGCAAT TTC	3917		
QY	202	-----	-----	202	

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Db 3918 AGATGCGTAATGCTAGCTGCTTGTGCTAGCTGGCTTATTTTGTGTACAGTATCGAT 3977
QY 202 ----- 202
Db 3978 GTTAGATGCATATTTCTTTTGTCTTGCTGTGCTGTTTGGCCATGTTGATTTCCCTTTTCTG 4037
QY 202 ----- 202
Db 4038 TCGCCAGTGTGCGATGTTAAATGGTTTCATTTACATATCAACTTTGTTGTGTCGACATCA 4097
QY 203 -----LeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSe 217
Db 4098 GTCATTTTATTTCAGGCTTTCTTGCTGCAAAATATACACCATACGGTGTGTTTACAGAGATTC 4157
QY 217 rArgSerIleLeuValIleHisAsnLeuAlaHisGln----- 229
Db 4158 CCGCAGCACCTTGTATTATACATAAATTTAGCACATCAGGTTTGGGTCTATCACCTTTCAAT 4217
QY 229 ----- 229
Db 4218 ATCCGTACATGGCTTTGTAACTGGTTTCACAGTATCGTCATCTATGTTATTTCAT 4277
QY 230 -----GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpT 247
Db 4278 GTCATTTAGGGTGTGGAGCTGCAAGTACATATCTCTGATCTGGGATTTGCCACCTGAATGCT 4337
QY 247 yrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyG 267
Db 4338 ATGGAGCTTTAGAAATGGGTATTTCCAGAAATGGCAAGGAGGATGCCCTTTTGAAGGGTG 4397
QY 267 luAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerL 287
Db 4398 AGGCAGTTAACTTTTGAAGGAGCAGTGTGACAGCAGATCGAATTTGACCGTCAGTC 4457
QY 287 yS----- 287
Db 4458 AGGTGAATACTCAATPACTTCTCTTTTCTTTTGGGGATGTTCTTCAGTTCAATTGCC 4517
QY 288 -----GlyTyrSerTrpGluV 293
Db 4518 TGTCTTTTCCCAATTAAGAAATGAATTAATCTTTTGTCTTCTAGGGGTATTTCATGGGAG 4577
QY 293 alThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValL 313
Db 4578 TCACAACTGCTGAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCCCCGAAAAGTGTAT 4637
QY 313 euAsn----- 314
Db 4638 TGAATGGTAATATATTTGAATCCACTTATCTTCTTCTGAAACATATTTACAGAAATAGA 4697
QY 315 -----GlyIleValAsnGly 319
Db 4698 TGGATGGGTGCAAGAATAAATTCAGTTTGTCTTTTCGGTATGAAGGAATTTGTAATGGA 4757
QY 320 IleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerVal 339
Db 4758 ATTGACATTAATGATTTGGAAACCCCAACACAGACAGTGTCTCCCTCATCTATTATTCTGTC 4817
QY 340 AspAspLeuSerGlyLys----- 345
Db 4818 GATGACCTCTCTGGAAGGTGTGTGGATAGTAGTACCCTATATATAATCATGTATCTGATC 4877
QY 345 ----- 345
Db 4878 TAGTACTTTCTTTTCTTTGCTAGTTTGTCTTCCCATGATGTTCTCACTAACTAACTCTAT 4937
QY 346 -----AlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeu 358
Db 4938 GTGGTTTGGCATACTTGTGAGGCCAAATGTAAGCTGAATTCAGAGAGGCTGGGTTTA 4997
QY 359 ProIleArgProAspValProLeu----- 366

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Db 4998 CCTGTAAGGGAGGATGTTCTCTCTGGTTAGATACAAACCCCTAAGATATATATTTTTTAAA 5057
QY 367 -----IleGlyPheIleGly 371
Db 5058 TCCCTAAAAAAACTTGGCGATCATCTCATTTAGCTTGTGATTCACAGATTGGCTTTATTGGA 5117
QY 372 ArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArg 391
Db 5118 AGACTGGATTACAGAAAGGCATTTGATCTCATTAATAATGGCCATTCAGAGCTCATGAGG 5177
QY 392 GluAspValGlnPheVal 397
Db 5178 GAGGACGTGCAGTTTGTA 5195
RESULT 4
US-11-231-599-1
; Sequence 1, Application US/11231599
; Publication NO. US20060035379A1
; GENERAL INFORMATION:
; APPLICANT: Morrell, Matthew
; APPLICANT: Li, Zhongyi
; APPLICANT: Rahman, Sadequr
; TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES
; FILE REFERENCE: 72715Supplemental
; CURRENT APPLICATION NUMBER: US/11/231,599
; CURRENT FILING DATE: 2005-09-21
; PRIOR APPLICATION NUMBER: US/10/018,418
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (176)..(2569)
; OTHER INFORMATION:
US-11-231-599-1
Alignment Scores:
Pred. No.: 2,75e-106 Length: 2939
Score: 1077.50 Matches: 234
Percent Similarity: 61.2% Conservative: 70
Best Local Similarity: 47.1% Mismatches: 166
Query Match: 37.2% Indels: 28
DB: 11 Gaps: 8
US-10-628-525A-21 (1-539) x US-11-231-599-1 (1-2939)
QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69
Db 1097 AACGTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1156
QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMet 89
Db 1157 GTTCCGGTGTCTTGTCCCAAGGCTTTGGCGAAGAGAGGACATCTGTTGTTGTTGGTGA 1216
QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109
Db 1217 CCAAGGTAT-----GGGACTATGAGGAAGCCTACCATGTCGAGTC 1258
QY 110 HisIleArgIleProCysPheGlyGluHisGluValThrPhePheHisGluTyrArg 129
Db 1259 CGAAAATACTACAGGCTGCTGCGACAGGATATGGAAGTGAATATTTCATGCTTATATC 1318
QY 130 AspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeu 148
Db 1319 GATGAGTTGATTTTGTGTTCATTGACGCTCTCTCTCCGACACCCGACGAGACAT 1378
QY 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168

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[illegible]

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Db      2417 CTGATCAGGGCGCTCGGGCACTGCTT--CCGACCTACCGGAGACTACAAAGAGAGCTGGAG 2417
Qy      523 ArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db      2476 GGGGCTCCAGGAGCGGGCATGTGCGAGGACTTCAGCTGGGAGCATGCCGC 2526

RESULT 5
US-11-231-599-3
; Sequence 3, Application US/11231599
; Publication No. US20060035379A1
; GENERAL INFORMATION:
; APPLICANT: Morrell, Matthew
; APPLICANT: Li, Zhongyi
; APPLICANT: Rahman, Sadequh
; APPLICANT: Appels, Rudolph
; TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 72715Supplemental
; CURRENT APPLICATION NUMBER: US/11/231,599
; CURRENT FILING DATE: 2005-09-21
; PRIOR APPLICATION NUMBER: US/10/018,418
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2842
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (89)..(2485)
; OTHER INFORMATION:
US-11-231-599-3

Alignment Scores:
Pred. No.: 1,52e-105 Length: 2842
Score: 1070.50 Matches: 246
Percent Similarity: 57.7% Conservative: 77
Best Local Similarity: 43.9% Mismatches: 189
Query Match: 37.0% Indels: 49
DB: 11 Gaps: 12

US-10-628-525A-21 (1-539) x US-11-231-599-3 (1-2842)
Qy      1 CysValAlaGluLeuSerArgGluAspLeuGlyLeuGluPro-----GluGly 16
Db      847 TGCAGCCCCCGTGTACAGAGACCTTTGGGACTTCAGAAATACATTCGGCTTCAGGA 906
Qy      17 IleAlaGluGly-SerIleAspAsnThrValValValAlaSerGlu----- 31
Db      907 ---GCCCGTGGAGGCCAAGATGCTGGCTGGGCTGTTGCAGATGATGCGGGCTCCTTTGA 963
Qy      32 -----GlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysVa 47
Db      964 ACATCACCAAGAACCATGATTCGGACCTTTGGCAGGGGAGAAC----- 1006
Qy      47 lThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLe 67
Db      1007 -GTCATGAACAGTGCTCGTGGCTGCTGAATGTTCTCCCTGGTGCANAACAGGTGGTCT 1065
Qy      67 uGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetVa 87
Db      1066 TGGAGATGTTGCGGTGCTTTGCCCAAGCTTTGGCGAGAGAGGACATCGTGTATGCT 1125
Qy      87 lValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrTh 107
Db      1126 TGTGTTACCAAGGTAT-----GGGACTATGAGGAAGCCTACCATGT 1167
Qy      107 rGluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGl 127
Db      1168 CGAGGTCCGAAATACCTACAAAGCTGCTCGACAGGATATGGAAGTGAATATTATTCATGC 1227
Qy      127 uTyrArgAspSerValAspTirValPheValAspHisProSerTyr---HisArgProGl 146

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Db 1228 TTATATCGATGAGATTGATTTGTTTCATTGACGCTCTCTCTCCGACCGCCGAGCA 1287  
 Qy 146 yAenLeuTyGlyAspLysPheGlyAlaPheGlyAspAenGlnPheArgTyThrLeuLeu 166  
 Db 1288 AGACATTTATGGG-----GGCAGCAGACAGAGAAATTTATGAAGCGCATGATTTTGT 1338  
 Qy 166 uCySvTyAlaAlaCysGluAlaProLeuLeuLeuGlyGlyGlyTyIleTyGlyGly 186  
 Db 1339 CTGCAAGCGCGTGTGAGGTTCCTTGGCAGCTTCATCGCGCGGTGCTTATGGGA 1398  
 Qy 186 n---AenCysMetPheValValAenAspTrpHisAlaSerLeuValProValLeuLeuAl 205  
 Db 1399 TGGAAATCTGGTGTATTATGCAATGATTGGCAGCAGCGCACTCTCGCTGTCTATCTGAA 1458  
 Qy 205 aAlaLysTyArgProTyGlyValTyLysAspSerArgSerIleLeuValIleHisAs 225  
 Db 1459 AGCATATTACAGGGACCATGGTTGTATGAGTACATCGCTCCATTATGTTGATACATA 1518  
 Qy 225 nLeuAlaHisGlnGlyValGluProAlaSerThrTyProAspLeuGlyLeuProProGl 245  
 Db 1519 CATCGGCACACAGCGCGTGGCCAGTAGATGAATTCCTCCGTTCCAGGATTGCCGTGACA 1578  
 Qy 245 uTrpTyGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLy 265  
 Db 1579 CTACCTG-----GAACACTTCAGACTGTACGACCCCGTGGG 1614  
 Qy 265 sGlyGluAlaValAenPheLeuLysGlyAlaValValThrAlaAspArgIleValThrVa 285  
 Db 1615 TGGTGAGCAGCGCACTACTTCGCGCGCGCTGAAGATGGCGGACAGGTGTGCTGTGT 1674  
 Qy 285 lSerLysGlyTySerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAenGluLe 305  
 Db 1675 GAGCCCGGTACTCTGTGGAGCTCAAGACGTGGAGGCGCGCTGGGGCTTCACGACAT 1734  
 Qy 305 uLeuSerSerArgLysSerValLeuAenGlyIleValAenGlyIleAspIleAenAspTr 325  
 Db 1735 CATACGGCAGAACGACTGGAAGACCGCGCGCATCGTCAACGCGCATCGACAACATGGAGTG 1794  
 Qy 325 pAenProAlaThrAspLysCysIlePro-----CysHisTySerValAspAs 341  
 Db 1795 GAACCCCGAGGTGGAGCTCCACTCAAGTCGACCGCTACACCACTTCTCCCTCGGGAC 1854  
 Qy 341 pLeu---SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProI 360  
 Db 1855 GTGGACTCCGCAAGCGCAGTGCAGAGAGCCCTGACGCGGAGCTGGGCTGCGAGT 1914  
 Qy 360 eArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyGlnLysGlyIleAs 380  
 Db 1915 CCGCGCGAGCTGCGCTGCTCGCTTCATCGCGCGCTGGACGGCAGAGGGCGTGGA 1974  
 Qy 380 pLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGl 400  
 Db 1975 GATCATCGGAGCGGACGATCGTCCCTGATCGTAGCAGGACGTGCGCTGCTATCTGGG 2034  
 Qy 400 ySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLy 420  
 Db 2035 CACCGCGCCACGACCTGGAGAGCATGCTGGGCATCTCGAGCGGGAGCACACAGCA 2094  
 Qy 420 sPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAs 440  
 Db 2095 GGTGCGCGGTGGTGGGTCTTCGCTGCGCTGGCGCAGCGGATCAGCGCGGCGCGCA 2154  
 Qy 440 pIleLeuLeuMetProSerArgPheGluProCysGlyLeuAenGlnLeuTyAlaMetGl 460  
 Db 2155 CGCGTCTCATGCGCTCCCGGTTCAGCGCGTGGCGGTGGAACCAAGCTTTACGCCATGGC 2214  
 Qy 460 nTyGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAenPh 480  
 Db 2215 CTACGGCACCGTCCCGCTGTGACCGCGTGGCGGGGTGAGGACACCGTCCCGCGT 2274  
 Qy 480 eAenProPheGlyGluAenGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrTh 500

Db 2275 CGACCCCTCAACCACTCC-----GGCCTCGGGTGGACGTTTCGACCGCGCGGAGGC 2325  
 Qy 500 rGluAenMetPheValAspIleAlaAenCysAenIleTyIleGlnGlyThrGlnValLe 520  
 Db 2326 GCACAAGCTGATGATGAGCGCTCGGCGCACTGCT-CCGCACTTACCGGGACTACAGGAGA 2384  
 Qy 520 uLeuGlyArgAlaAenGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
 Db 2385 GCTGGAGGGGCTCCAGGAGCGCGCATGTCCAGGACTTTCAGCTGGGAGCATGCCGC 2442

RESULT 6  
 US-11-231-599-5  
 ; Sequence 5, Application US/11231599  
 ; Publication No. US20060035379A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morrell, Matthew  
 ; APPLICANT: Li, Zhongyi  
 ; APPLICANT: Rahman, Sadequr  
 ; APPLICANT: Appels, Rudolph  
 ; TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES  
 ; TITLE OF INVENTION: THEREFOR  
 ; FILE REFERENCE: 72715Supplemental  
 ; CURRENT APPLICATION NUMBER: US/11/231,599  
 ; CURRENT FILING DATE: 2005-09-21  
 ; PRIOR APPLICATION NUMBER: US/10/018,418  
 ; PRIOR FILING DATE: 2002-05-09  
 ; NUMBER OF SEQ ID NOS: 59  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 5  
 ; LENGTH: 2107  
 ; TYPE: DNA  
 ; ORGANISM: Triticum aestivum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1791)  
 ; OTHER INFORMATION:  
 US-11-231-599-5

Alignment Scores:  
 Pred. No.: 3,15e-102 Length: 2107  
 Score: 1038.50 Matches: 229  
 Percent Similarity: 60.2% Conservative: 70  
 Best Local Similarity: 46.1% Mismatches: 171  
 Query Match: 35.9% Indels: 28  
 DB: 11 Gaps: 9

US-10-628-525A-21 (1-539) x US-11-231-599-5 (1-2107)

Qy 50 SerIleValPheValThrGlyGluAlaSerProTyAlaLysSerGlyGlyLeuGlyAsp 69  
 Db 319 AACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 378  
 Qy 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMet 89  
 Db 379 GTTGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 438  
 Qy 90 ProArgTyLeuAenGlyThrSerAspLysAsnTyAlaAenAlaPheTyThrGluLys 109  
 Db 439 CCAAGGTAT-----GGGACTATGAGAACCTACGAGATGTGGAGTCCGAGAA 486  
 Qy 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyArg 129  
 Db 487 TACTACAG-----GCTGCTGGACAGGATATGGAAGTGAATATTTCATGCTTATATC 540  
 Qy 130 AspSerValAspTrpValPheValAspHisProSerTyTyr---HisArgProGlyAenLeu 148  
 Db 541 GATGAGTGTGATTTGTGTTCATTCAGCTCTCTCTCTCCGACACCGAGAGGAGACATT 600  
 Qy 149 TyrGlyAspLysPheGlyAlaPheGlyAspAenGlnPheArgTyThrLeuLeuCysTy 168  
 Db 601 TATGGG-----GGCAGCAGACAGGAATATTGAAGCGCATGATTTGTTGTCAGAG 651  
 Qy 169 AlaAlaCysGluAlaProLeuIleLeuGluGlyTyIleTyIleGln---Aen 187

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Db 652 GCGCTGTTAGGTTCCATGGCAGCTTCCATGCGCGGTGTCCTTATGGGGATGGAAT 711
Qy 188 CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLys 207
Db 712 CTGGTGTATTGCAATGATTGGCACCGGCACTCTCTGCTGTCTATCTGAAGCATAT 771
Qy 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227
Db 772 TACAGGACCATGGTTTGTATGTCAGTACACTCGGTCCATTATGTTGATACATAACATCGCT 831
Qy 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247
Db 832 CACAGGCGCGTGGCCCTGTAGATGAATTCCTCGTTCCACGAGTTGCTGAGCACTACCTG 891
Qy 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspLysGlyGlu 267
Db 892 -----GNACACTTCAGACTGTACGACCCCGTGGGTGGTGA 927
Qy 268 AlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287
Db 928 CACGCCCACTACTTCGCGCGCGGCTGAAGATGCGGACGAGTTGTCGTGTGAGCCCC 987
Qy 288 GlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307
Db 988 GGGTACTGTGGAGCTGAAGAGCGGTGAGGGCGGCTTCCAGCATCATACG 1047
Qy 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327
Db 1048 CAGACGACTGGAAGACCCCGCGCATGTCACCGCATCGACATGAGTGGACCCC 1107
Qy 328 AlaThrAspLysCysIlePro-----CysHisTyrSerValAspAspLeu--- 342
Db 1108 GAGGTGAGCCCGCCACTCTAGTCCGAGCGGTACACCAACTTCTCCCTGAGGACGCTGGAC 1167
Qy 343 SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGlyLeuGlyLeuProIleArgPro 362
Db 1168 TCCGGCAGCGGAGTGCAGAGGCGCTCGACGGGAGCTGGGCGCTGCGAGTCCGCGCC 1227
Qy 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIle 382
Db 1228 GAGCTGCCGTCTCGCTTCATCGCGCGCTGACGGGCGAGGCGGTGGAGATCATC 1287
Qy 383 GlnLeuIlePheProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402
Db 1288 GCGGACGCCATGCGCTGGATCGTGAGCCAGGAGCTGCGATGATGCTGGGACCGGG 1347
Qy 403 AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422
Db 1348 CGCCAGCACTGGAGAGCATGCTGCAGCACTTCGAGCGGGAGCACCCAGACAGGTGGCGC 1407
Qy 423 GlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442
Db 1408 GGGTGGTGGGTCTCCGTGCGCTGGCGCCACCGATCACGGCGGGGCGGACGCGCTC 1467
Qy 443 LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGly 462
Db 1468 CTCATGCCCTCCGGTTCGTGGCGTGGCGCTGAACGAGCTCTACGCCATGGCCTACGGC 1527
Qy 463 ThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnPro 482
Db 1528 ACCGTCCCGTGTGACGCGCTGGCGGCGCTCAGGGACACCGTGGCGCGTTCGACCCC 1587
Qy 483 PheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsn 502
Db 1588 TTCACCACTCC-----GGGCTGGGTGGAGCTTCGACCGCGCCCGGCGGCAAG 1638
Qy 503 MetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGly 522
Db 1639 CTGATCGAGGCGCTGGGCACTGCCT-CCGCACTACCGAGACTTCAAGGAGAGCTGGAG 1697
Qy 523 ArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
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Db 1698 GGCCTCTCCAGGAGCGCGCATGTGCGAGGACTTTCAGCTGGGAGCACGCCGC 1748

## RESULT 7

US-11-096-568A-18030  
; Sequence 18030, Application US/11096568A  
; Publication No. US2006048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 18030  
; LENGTH: 2410  
; TYPE: DNA  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(2410)  
; OTHER INFORMATION: Ceres Seq. ID no. 12362462  
US-11-096-568A-18030

Alignment Scores:  
Pred. No.: 1,05e-78 Length: 2410  
Score: 823.00 Matches: 188  
Percent Similarity: 55.1% Conservative: 94  
Best Local Similarity: 36.7% Mismatches: 168  
Query Match: 28.4% Indels: 62  
DB: 11 Gaps: 13

US-10-628-525A-21 (1-539) x US-11-096-568A-18030 (1-2410)

Qy 34 SerGluIleValValGlyLysGluGlnAla-----43  
Db 407 AGTAAATACAGTGGCTAAAGAGAGCTACAGATAATGAATTCATCCAAAGACTACG 466  
Qy 44 -----ArgAlaLysValThr-----GlnSerIleValPheValThrGlyGlu 57  
Db 467 GGCATCGGGCACCTATTGTATGTTCTGCTGGATGACTATTGTATTTGTTGCACTGAA 526  
Qy 58 AlaSerProTyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProValAla 77  
Db 527 GTGCACCCATGGTGCAAAACTGGTGGCTCGGTGATGTTGTAGAGGAGTGTGCCCCAGCT 586  
Qy 78 LeuAlaAlaArgGlyHisArgValMetValMetProArgTyrIleuAsnGlyThrSer 97  
Db 587 TTGGCTGCTATGGGACACCGTGTCAATGACATAGCTCCTCGTTAT-----631  
Qy 98 AspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGly 117  
Db 632 ---GATCATATACAGATGTCATGGGATACAGTCTTGTGTGAGGTAATAATTGTTGAC 688  
Qy 118 GlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPheVal 137  
Db 689 ACGGTAGAAACTGTTGCTGCTCTTCCACTGCTACAAAGAGGAGTTGATCGTGTGTTTGT 748  
Qy 138 AspHisProSerTyr-----HisArgProGlyAsnLeuTyrGlyAsp 151  
Db 749 GATCATCTCTATGTTCTTGAAGAGTATGGGCAAGACTGGAGCAAAATTTGATGCTCT 808  
Qy 152 LysPheGlyAla---PheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAla 170  
Db 809 ACTACTGGAGACTGACTATCGAGTAAACAGTTGAGGTTCTGCGCTTGTGCTTGTGCT 868  
Qy 171 CysGluAlaProLeuIleLeuGluLeuGlyGly-----TyrIle-----TyrGly 185  
Db 869 TTGGAGGCTCCAAAGAGTTCTCAATTTCAACAATTTCTGAATATTTCTCTGGACCATATGG 928  
Qy 186 GlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAla 205  
Db 929 GAAGATGTTGCTCTGATGCAATGATTGGCACACTGTTATTTGCTATTTTGAAG 988

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QY 206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn 225
Db 989 AGCATGTATAGCCAAATGAAATTTATAAATGCTTAAGTTGCTTCTTCGCATACATAAT 1048
QY 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu 245
Db 1049 ATTGCCTATCAAGGTAGATTGTCGCCGAGCAGACTTCGATCTTCTTAATCTACTGACAGT 1108
QY 246 TrpTyrGlyAlaLeuGluTrpVal-----PheProGluTrpAlaArg 259
Db 1109 TTCTTGCCCATATTGATTTATTATGTAGTACATGTTTAAGCCTTTT----- 1153
QY 260 ArgHisAlaLeuAspLysGlyGluAlaValAlaAsnPheLeuLysGlyAlaValValThrAla 279
Db 1154 -----CTAGGGAGAAAGCTTAAGTATGATGACATGTTTAAGCCTTTT----- 1198
QY 280 AspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla----GluGly 298
Db 1199 GATCTGTTTCTTAACAGTCAGTCACATTTATGTCAGGAAGTCTCATCTCGGCCAGATAG 1258
QY 299 GlyGlnGlyLeuAsnGluLeuLeuSerArgLysSerValLeuAsnGlyIleValAla 318
Db 1259 GGTGTGTAGTTGGATGGTGTCTCTCGCACAA--AAGCCTCTAGAAATTGGAATCGTTAT 1315
QY 319 GlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSer 338
Db 1316 GGCATGGATGTTTGAATGGATCTCTCAACAGATAGTACATCAGCGTGAATATGAT 1375
QY 339 ValAspAspLeuSer---GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGly 357
Db 1376 GCAACAACGGTAATCAAGCAAGGGCTCTCAATAAAGAGAGTTTGCAGCAGAACTCGGA 1435
QY 358 LeuProIleArgProAspValProIleGlyPheIleGlyArgLeuAspTyrGlnLys 377
Db 1436 TTGCTGTGGACTCGAGCATCCCTGTATAGTTTTCGTGGCGCTCTCGAAGACAGAAA 1495
QY 378 GlyIleAspLeuIleGlnLeuIleProAspLeuMetArgLysValGlnPheVal 397
Db 1496 GGGTCGCACATACTCATTCAGCCATTCCAGAGTTCGTGGCGAAGATTCACAGATATC 1555
QY 398 MetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePhe 417
Db 1556 GTTCTTGGCAGCGGAAAGAAAGATGGAGGAGGAATAACGCAGCTGGAAGTGAATAT 1615
QY 418 LysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAla 437
Db 1616 CCMAACAACGGTAGAGGCATACGGAATTTCAATGTTCCATTGGCACACATGATGTTGCC 1675
QY 438 GlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyr 457
Db 1676 GGGGCTGACTTCATTATCGTCCACAGCAGGTTTGAGCCATGTTGTTCTATTTCAGCTGCA 1735
QY 458 AlaMetGlnTyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrVal 477
Db 1736 GGGATGAGATAGGATGATTCCTATCTGTTTCATCCACTGGAGGACTTGTGCACACGGTT 1795
QY 478 GluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaPro 497
Db 1796 GAG-----GAGGCGCTCACCGGATTCACATCATGGTTCT 1828
QY 498 LeuThrThrGluAsnMetPheValAspIleAlaAsn 509
Db 1829 TTCATGTGCGATGTGTAACCTGTAGACCCAGCCGAC 1864
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## RESULT 8

```
US-11-231-599-37
; Sequence 37, Application US/11231599
; Publication No. US20060035379A1
; GENERAL INFORMATION:
; APPLICANT: Morrell, Matthew
; APPLICANT: Li, Zhongyi
; APPLICANT: Rahman, Sadequr
```

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; APPLICANT: Appels, Rudolph
; TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES
; FILE REFERENCE: 72715Supplemental
```

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; CURRENT APPLICATION NUMBER: US/11/231,599
; CURRENT FILING DATE: 2005-09-21
; PRIOR APPLICATION NUMBER: US/10/018,418
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 37
; LENGTH: 9024
; TYPE: DNA
; ORGANISM: Triticum sp.
US-11-231-599-37
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## Alignment Scores:

Pred. No.:	6,75e-61	Length:	9024
Score:	666.00	Matches:	151
Percent Similarity:	59.6%	Conservative:	48
Best Local Similarity:	45.2%	Mismatches:	119
Query Match:	23.0%	Indels:	18
DB:	11	Gaps:	4

US-10-628-525A-21 (1-539) x US-11-231-599-37 (1-9024)

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QY 211 TyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGly 230
Db 7241 TATTCCTATCTTCGGTACTCCGTTGGGCTAATTTCTTCTTCATGTTGCATG-CAGGGC 7299
QY 231 ValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrGlyAlaLeu 250
Db 7300 CGTGCCCTGTAGATGAATTCCTGCTACCGAGTTGCTTGAGCCTACTCTG----- 7350
QY 251 GluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaValAla 270
Db 7351 -----GAACACTTCAGACTGACGACCCCGTGGTGGTGAACACGCCAAC 7395
QY 271 PheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSer 290
Db 7396 TACTTCGCGCGCGGCTGAAGATGCGGACACGAGTTGTGCTGAGGCCCGCGGTACCTG 7455
QY 291 TrpGluValThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLys 310
Db 7456 TGGGAGCTGAAGACGGTCGAGGGCGGCTGGGGCTTCACGACATCATACGGCAGAACGAC 7515
QY 311 SerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAsp 330
Db 7516 TGGAGACCCGCGGCATCGTCAACGGCATCGACAACTGAGTGGAAACCCCGAGGTGGAC 7575
QY 331 LysCysIlePro-----CysHisTyrSerValAspAspLeu---SerGlyLys 345
Db 7576 GCCCACCTCAAGTCGAGCGGCTACACCAACTTCTCCCTGAGGACCGCTGACCTCCGGCAG 7635
QY 346 AlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValPro 365
Db 7636 CGGCAGTCAGAGGAGCCCTCGACGCGGAGCTGGGCTCTGAGTCCGCGCCACGCTGCG 7695
QY 366 LeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIle 385
Db 7696 CTGCTCGGCTTCATCGCGCGCTGACGCGGAGAGGGCGGTGAGTGTGGCGCGCCGACGAC 7755
QY 386 IleProAspLeuMetArgLysValGlnPheValMetLeuGlySerGlyAspProGlu 405
Db 7756 ATGCCCTGGATCGTGAGCCAGACGTGACGTGGTGTGCTGGCGCGCCGCGCCACGAC 7815
QY 406 LeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpVal 425
Db 7816 CTGGAGACATGCTCGGCACTTCGAGCGGGAGCACACGACAGGTGCGGGTGGGTG 7875
QY 426 GlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetPro 445
Db 7876 GGGTTCTCCGTGCGCTGCGCACCGGATCACGGCGGGGGGAGCGCGCTCTCTCATGCC 7935
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QY 446 SerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValPro 465  
 Db 7936 TCCCGGTTCCAGCGGTGGGGCTGAACAGCTCTACGCCATGGCTACGGCACCGTCCCC 7995  
 QY 466 ValValHleAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGlu 485  
 Db 7996 GTCTGTACCGCGGTGGGGCTCAGGACACCGGTGGCGGCTTCGACCCCTTCAACCC 8055  
 QY 486 AsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheVal 505  
 Db 8056 TCC-----GGGCTCGGTGGAGCTTCGACCGCGCGGCGGCGCAAGCTGATCGAG 8106  
 QY 506 AspilealaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsn 525  
 Db 8107 GCGCTCGGCGACTGCTT-CCGCACTTACCGAGACTTCAAGGAGAGCTGGAGGGCCCTCCA 8165  
 QY 526 GluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
 Db 8166 GGAGCGCGCATGTCCGAGGACTTCAGCTGGAGGACGCCGC 8207

## RESULT 9

US-10-504-599A-15

; Sequence 15, Application US/10504599A

; Publication No. US20050272033A1

; GENERAL INFORMATION:

; APPLICANT: YAMAKAWA, HIROHITO

; APPLICANT: SUZUKI, ERIKO

; APPLICANT: MIYATAKE, KIYOKO

; APPLICANT: HAYAKAWA, KATSUYUKI

; TITLE OF INVENTION: WHEAT DETECTING METHOD

; FILE REFERENCE: 8036-1018

; CURRENT APPLICATION NUMBER: US/10/504,599A

; CURRENT FILING DATE: 2004-08-16

; PRIOR FILING DATE: PCT/JP02/09983

; PRIOR FILING DATE: 2002-09-26

; PRIOR FILING DATE: 2002-02-15

; PRIOR FILING DATE: 2002-03-29

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 15

; LENGTH: 2886

; TYPE: DNA

; ORGANISM: Triticum aestivum

; US-10-504-599A-15

## Alignment Scores:

Pred. No.: 2,81e-52 Length: 2886  
 Score: 581.00 Matches: 208  
 Percent Similarity: 36.2% Conservative: 103  
 Best Local Similarity: 24.2% Mismatches: 191  
 Query Match: 20.1% Indels: 362  
 DB: 8 Gaps: 21

US-10-628-525A-21 (1-539) x US-10-504-599A-15 (1-2886)

QY 11 GlyLeuGluProGluGlyIleAlaGlySerIleAspAsnThrValValAlaSer 30  
 Db 97 GCGTGAGGCCCGCGAGCCCGCGGATGGGCTCTCGGCATGAGGACCGCGGAGCTAGC 156  
 QY 31 -----GluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysVal 47  
 Db 157 GCGGCCCAACGCAAGCCGGAAGCGCACCGCGCGGCGGCTCTCCATGGTG 216  
 QY 48 ThrGln-----SerIleValPheValThrGlyGluAlaSerPro 60  
 Db 217 GTGCGGCCCAACCGCGAGCGCGCATGAACCTCGTGTCTCGCGCGCGAGATGGCGCC 276  
 QY 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAla--- 79  
 Db 277 TGGAGCAGACCGCGGCTCTCGCGAGCTCTCGGGGGGCTCTCCCGCCAGCCATGGCCGTA 336

QY 79 ----- 79  
 Db 337 AGCTAGACAGCACCACCTGTCTTCTCATATGTTTCATCTTCAGTTGCGAGCATCCCTGCC 396  
 QY 80 -----AlaArgGlyHisArgValMetValValMetPro 90  
 Db 397 GTTACACGGGTGGTGTGTCGTCAGGCCCAACGGCCACCGGGTCATGGTCATCTCCCG 456  
 QY 91 ArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHis 110  
 Db 457 CGCTAC-----GACCACTACAGGACCGCTGGGACACCAAG-CGTGCT 497  
 QY 111 IleArg----- 112  
 Db 498 CTCGAGGATCTTGAACCTTACCCGCAACTTTAAAGATCAAAATTCGCATGCTCTCTGCAC 557  
 QY 113 -----IleProCysPheGlyGly 118  
 Db 558 ATTTCTGAGGATCTTACTGACTGACTAACTGGATCTCGCAGATCAAGGTCGTTGACAAG 617  
 QY 119 GluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAsp 138  
 Db 618 TAGCAGAGGTGAGGTACTTCCACTGCTACAAGCGGGGTGGACCGGTGTTGCTGCAC 677  
 QY 139 HisProSerTyrHisArgProGlyAsn----- 147  
 Db 678 CACCCGTGCTTCT-GGAGNAGGTGACCGATCGTCTGCTGGACCGATCAAGCTAGCTCT 736  
 QY 147 ----- 147  
 Db 737 TCGTCTCTCAACCTTGTATAGCATGGTGTGATGATTTCAGTTGTTTCTGCTGCTGCAAT 796  
 QY 148 -----LeuTyrGlyAspLysPheGlyAla---Phe 156  
 Db 797 TTCCAGGTCCGGGCAAGACCAAGAGAGATCTACGGGCGCCGACGCCGCGACTAC 856  
 QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
 Db 857 GAGGACACCCAGCAGCGCTTCTGCGCAGCGCGGTGGNAGTGGCCGAGGATC 916  
 QY 177 LeuGluLeu-----GlyGlyTyr----- 182  
 Db 917 CTGAACCTCGACAAATAACCCCTACTTTTCTGGGCGCTACGGTAAGATCAAGATCAAGCAC 976  
 QY 182 ----- 182  
 Db 977 GCCTACTAGTCAAGCTAGAGTGTGTAACTCTGAACCTCTGAAGAACTTGATATTTCTT 1036  
 QY 182 ----- 182  
 Db 1037 GAGAGAGCTGGATGATCACCATTTTTTTTTGTATCTGGGTGCGGTGCTGCTCCCTGTTG 1096  
 QY 183 -----IleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal 200  
 Db 1097 CGCGCGCGCA-GGGGAGGACGTGGTGTGTCGTCGCAATGACTGGCACACGGGCTCTG 1155  
 QY 201 ProValLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 Db 1156 GCCTGCTACCTCAAGAGCAACTACCAAGTCCAATGGCATCTACAGGGCCGCAAGAGTTTG 1215  
 QY 220 ----- 220  
 Db 1216 CATCTTCTTCAAACTATATATCTCTCTGCAATTCATGATGATGATATCTTGCTCTTC 1275  
 QY 220 ----- 220  
 Db 1276 ATTTCTGAACAGGCATATCAATTTTGGGTTTCATCTTGGCTGAAATTTTACATTGCAACT 1335  
 QY 221 -----LeuValIleHisAsnLeuAlaHisGlnGlyValGluPro 233  
 Db 1336 TCATTTTCATGGCAGGTGGCATCTGTCATCTCAACATCTCTGTACAGGGCCGCTTCTCC 1395

QY 234 AlaSerThrTyrProAspLeuGlyLeuProGluTyrPheGlyAlaLeuGluTyrVal 253  
 DB 1396 TTCGACGACTTCGGCAGCTCAACCTGCCGACAGGTTCAAGTCGCTTGCATTCATC 1455  
 QY 254 PheProGluTyrAlaArgHisAlaLeuAspLys-----GlyGluAlaValAsn 270  
 DB 1456 -----GACGCTACGACAAAGCCGCTGAGGGCGCAAGATCAAC 1494  
 QY 271 PheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSer 290  
 DB 1495 TGGATGAAGCCGGAGTCTGACGCGCAGCAAGGTCTCAGCGTAGCCCTACTACGGC 1554  
 QY 291 TrpGluValThrThrAlaGluGly----GlyGlnGlyLeuAsnGluLeuSerSerArg 309  
 DB 1555 GAGGAGCTCATCTCTGGCAGCAGCCAGGGGCTCGAGCTCGACACATCATG-----CGC 1608  
 QY 310 LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThr 329  
 DB 1609 CTCACTGGGATCACCGGCATCGTCAACGCGATGATGTTAGCGAGTGGGACCCCAAG 1668  
 QY 330 AspLysCysIleProCysHisTyr----- 337  
 DB 1669 GACAAAGTTCCTCGCGCTCAACTACGACATCACACCGTGAGCAACACCAAGATTTCT 1728  
 QY 338 -----SerVal-As 340  
 DB 1729 TCCTCTTCTTCGGTGATCGCTGGTTCCTGGGTGGTTCACGACGAGGCAAGTGACA 1788  
 QY 340 pAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProI 360  
 DB 1789 GCGGTGGAGGAGGAGCGCTGACAAAGGAGCGCTGCAGCGCGAGGTGGGCTGCCGT 1848  
 QY 360 eArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAs 380  
 DB 1849 GGACCGAAGGTGCGCTGCGCTTCATCGCAGGCTGGAGGAGCAGACGAGGCGCCGA 1908  
 QY 380 pLeuIleGlnLeuIleProAspLeuMetArg---GluAspValGlnPheValMetLe 399  
 DB 1909 CGTGATGTCGCGGCATCCCGAGATCTGAGGAGGAGGAGCTCCAGATCGTTCCTCT 1968  
 QY 399 u----- 399  
 DB 1969 GGTACATCATCGAGCCCGCAACCCGACCCCATTTGCTGAAACTTCGATCAAGCAGACCTA 2028  
 QY 400 -----GlySerGlyAspProGluLeuGluAspTrpMetArgS 412  
 DB 2029 AGAATGATCGAATGATTCGAGGGGCGCCGGAAGAAGAGTTTCGAGCGGCTACTCAAGA 2088  
 QY 412 erThrGluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValS 432  
 DB 2089 GCATTGAGGAGAAATTCGCGAGCAGGTGAGGGCGGTGTCAGGTTCAACGCGCGCTGG 2148  
 QY 432 erHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysG 452  
 DB 2149 CTCACCATGATGTCGCGCGCGCGAGTCTCGCGCTCACACGCGCTTCGAGCGCTCGC 2208  
 QY 452 LysLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrVal----- 464  
 DB 2209 GCCTCATCGACTCCAGGGGATGCGCTACGGAACGGTAAACTTTTCTTTCGCAAGTC 2268  
 QY 465 -----P 465  
 DB 2269 CTTACTTCTGAGCAATCATGACCATGCGCCATGACCGAAGTTTCTCCAAATTTTCAGC 2328  
 QY 465 roValValHisAla---ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheG 484  
 DB 2329 CGTGGCGGTGCGCTCCACCGCGGCTGTGCGACACGATCGT----- 2372  
 QY 484 LysGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetP 504  
 DB 2373 -----GAGGCGAAGACCGGCTTCCACATGGCGCGCTCAGTGTGCGATGT-AAGT 2420  
 QY 504 heValAspIleAlaAsn----- 509

DB 2421 TCATCAATCTCTCTCAATAAATTTCTTCATCTTGTTCATCTCGGAGCTCAGGACATCATC 2480  
 QY 510 -----CysAsnIleTyrIleGlnGlyThrGlnV 519  
 DB 2481 AAACGGGTTTCCTTTTTCCTCTTGTGGCCAGTCGCAACGCTGGTGA-GCCGGCCGACGTG 2539  
 QY 519 aLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
 DB 2540 AAGAAGGTGGTGACCACTCGAAGCGCGCTCAAGGTCTGCGCACGCGCGC 2592  
 RESULT 10  
 US-11-231-599-9  
 ; Sequence 9, Application US/11231599  
 ; Publication No. US20060035379A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morrell, Matthew  
 ; APPLICANT: Li, Zhongyi  
 ; APPLICANT: Rahman, Sadequr  
 ; APPLICANT: Appels, Rudolph  
 ; TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES  
 ; FILE OF INVENTION: THEREFOR  
 ; FILE REFERENCE: 72715Supplemental  
 ; CURRENT APPLICATION NUMBER: US/11/231,599  
 ; PRIOR FILING DATE: 2005-09-21  
 ; PRIOR APPLICATION NUMBER: US/10/018,418  
 ; NUMBER OF SEQ ID NOS: 59  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 9  
 ; LENGTH: 3621  
 ; TYPE: DNA  
 ; ORGANISM: Triticum aestivum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(3177)  
 ; OTHER INFORMATION:  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1520)..(1520)  
 ; OTHER INFORMATION: n can be a or g or c or t, and the encoded amino acid  
 ; OTHER INFORMATION: cannot be a  
 ; OTHER INFORMATION: assigned with certainty.  
 US-11-231-599-9  
 Alignment Scores:  
 Pred. No.: 9,48e-40 Length: 3621  
 Score: 467.00 Matches: 154  
 Percent Similarity: 44.2% Conservative: 90  
 Best Local Similarity: 27.9% Mismatches: 183  
 Query Match: 16.1% Indels: 126  
 DB: 11 Gaps: 20  
 US-10-628-525A-21 (1-539) x US-11-231-599-9 (1-3621)  
 QY 42 GlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyr 61  
 DB 1811 CAATTGAAACAGAGAAATACATG-CGTATTATCCACATTGCCGTTGAGATGCCCGCGTT 1869  
 QY 62 AlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaArg 81  
 DB 1870 GCAAGGTTGGAGGCTTGGGGATGTTGTACAACTCTTTCACGTGCCATTCAAGATCTA 1929  
 QY 82 GlyHisArgValMetValValMetProArgTyr-----LeuAsnGlyThrSerAspLys 99  
 DB 1930 GGACATACATGTCGAGGTTATTCTCCGGAAGTACGACTGTTTGAACCAAGCAGTGTCAAG 1989  
 QY 100 Asn-----TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
 DB 1990 GATTACATTTATATCAAAAGTTTCTTGGGTGGTACGAAGTAAAGATATGGGTGGA 2049  
 QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136



Db 3725 GATTTACATTTATATCAAAAGTTTCTTGGGGTGTGTACAGAAATAAAAGTATGGTTGCA 3784  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136  
Db 3785 CGAGTCGAGAGACCTGACCGTTTACTTCTCCGGAACCTCAAAATGGGATGTTGGCGTT--- 3841  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 3842 -----GGATGTGTATATGGA----- 3856  
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 3857 AGCAATGATGACCGCAGATTTGGGTTCTTCTGTCTGTCTAGAGTTTATCTCCAG 3916  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196  
Db 3917 AATGAATTTTCTCCACATATAATA-----CATTCG-----CATGATTGGTCA 3958  
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 3959 AGTGCTCCGGTCGCGTGTATATAGGAACACTATCCCAATCCAGAATG---GCAAGC 4015  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 4016 ACTCGGGTTGTATTTACCATCCACATCTTGAA----- 4048  
Qy 237 TyrProAspLeuGlyLeuProGluTyrTrpTyrGlyAlaLeuGluTrpValPheProGlu 256  
Db 4049 -----TTTGGAGCA----- 4057  
Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
Db 4058 -----CATATATTGGTAAAGCAATG 4078  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
Db 4079 ACATACGTGTGATAAAGCCCAACTGTTCTCTACATATTCAAGGCGTG----- 4129  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 4130 ---GCAGGCCATGGC-----GCCATTGTCTCTCATCGTGAGAAATTTACGCGCAT 4177  
Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
Db 4178 CTCATATGGAATGTATCCAGATATCTGGGATCGGTACACTGACAAATTTATCCGGTCCCT 4237  
Qy 337 TyrSerValAspAsp---LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGlu 355  
Db 4238 TATACTTGTGAGAAATGTTGCGAAGCAAGAGAGCTGCAAAAAGGGCCCTTGCAGCAGAG 4297  
Qy 356 LeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyr 375  
Db 4298 TTTGGATTAACAG---CAAACTGATGTCTTATGTGCGGAATCATACCCGCTGTACAGCC 4354  
Qy 376 GlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGln 395  
Db 4355 CAGAGGGAATCCACTCATCAAGCAGCAATTCACCGAACTCTCGAAGCAACGGACAT 4414  
Qy 396 PheValMetLeuGlySerGly---AspProGluLeuGlu---AspTrpMetArgSerThr 413  
Db 4415 GTGGTTTGTCTGGTTTCAGTCCAGATCATCGAATACAAAGGCGATTTTTCAGATTGGCC 4474  
Qy 414 GluSer-----IlePheLysAspLysPheArgGlyTrpValGlyPheSerValPro 430  
Db 4475 GATGTCTTTCATGGTGTATACCATGGTAGGGTGAAGCTTGTCTCAACCTATGATGAGCCT 4534  
Qy 431 ValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluPro 450  
Db 4535 CTTTCTCACTGATATACGCTGGCTGGACTTCATTAATGTTCTTCAATCTCGAAGCC 4594  
Qy 451 CysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThr 470  
Db 4595 TGTGGCTTAACACAACCTTGTGCCATGCGTTATGATCGATCCCTATATAGTTTCGGAAGACT 4654

Qy 471 GlyGlyLeuArgAspThrValGluAsnPhe----- 480  
Db 4655 GGAGGACTTTCACGACACACAGCTTTCGACGCTAGACAATATAGAGACCGGCTCGGTCTCTT 4714  
Qy 481 -----AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
Db 4715 GGTCTTGAACCAATGGGTTTCAGTTTCGACGAGCGCAGCAATGGCGTGGATTATGCC 4774  
RESULT 12  
US-11-231-599-38  
; Sequence 38, Application US/11231599  
; Publication No. US20060035379A1  
; GENERAL INFORMATION:  
; APPLICANT: Morrell, Matthew  
; APPLICANT: Li, Zhongyi  
; APPLICANT: Rahman, Sadequr  
; APPLICANT: Appels, Rudolph  
; TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES  
; FILE REFERENCE: 72715Supplemental  
; CURRENT APPLICATION NUMBER: US/11/231,599  
; CURRENT FILING DATE: 2005-09-21  
; PRIOR APPLICATION NUMBER: US/10/018,418  
; PRIOR FILING DATE: 2002-05-09  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 11611  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
US-11-231-599-38  
Alignment Scores:  
Pred. No.: 3,02e-14 Length: 11611  
Score: 238.50 Matches: 108  
Percent Similarity: 36.4% Conservative: 56  
Best Local Similarity: 24.0% Mismatches: 131  
Query Match: 8.2% Indels: 156  
DB: 11 Gaps: 18  
US-10-628-525A-21 (1-539) x US-11-231-599-38 (1-11611)  
Qy 163 TyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyTyr 182  
Db 9024 TTTACTACTAGCTTATTTGGTGCATTTGGTGTTCCTTCTCTACTC-----TAC 9071  
Qy 183 IleTyrGlyGlnAsnCysMetPheValVal----- 192  
Db 9072 TATCTGAATGCTACTTGTGTTTTCGCAACAGTTGCTTTTATCCCTTCCATTTCTCAG 9131  
Qy 193 -----AsnAspTrpHis 196  
Db 9132 TTAATAAAACTTGCATCTGTATTTCACGTGACAGCATATAATACATTCGCATGTTGGTCA 9191  
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 9192 AGTGCTCCGGTCCGCTGGCTATATAGGNACACTATTCCAATCCAGAATG---GCAAGC 9248  
Qy 217 SerArgSerIleLeuValIleHisAsnLeu-----AlaHisGlnGlyValGluPro 233  
Db 9249 ACTCGGGTTGTATTATCCATCCACAATCTTGAATTTGGAGCACATTTAT---ATTGTAAA 9305  
Qy 234 AlaSerThrTyrProAspLeuGlyLeuProGluTyrTrpTyrGlyAlaLeuGluTrp--- 252  
Db 9306 GCAATGACATACTGTGATAAAGCCCAACTGT---GAGTGCCTTACTGTCTTGTAAATTTTA 9364  
Qy 253 ValPheProGluTrpAlaArgArg-----HisAlaLeuAspLysGlyGluAlaValAsn 270  
Db 9365 ATCTTCTGTTGGCGCACAGAAATCTTCCACATTTTACAGAAATCATCTTCTGTGTTT 9424  
Qy 271 PheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSer 290  
Db -----::: |||||

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Db 9425 TGTACGTATTCAACTATTTCACCC-----CAAACTTTTCAGGTTTCCTCCATACATATCA 9478
Qy 291 TrpGluValThrThrAlaGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 310
Db 9479 AGGACGCTG-----GCAGCCATGCT-----GCCATTGCTCCTCATCGT 9517
Qy 311 SerValLeuAenGlyIleValAenGlyIleAenGlyIleAenGlyIleAenGlyIleAenGlyIleA 330
Db 9518 GAGAAATCTACGGCATTTCTCAATGGAATTCATCCAGATATCTGGGATCCATACACTGAC 9577
Qy 331 LysCysIlePro-----CysHis----- 336
Db 9578 AATTATTATCCCGTACCAGATTTTTCACAGATGCAAGTAGATATATACCAAGCCACA 9637
Qy 337 -----Tyr-SerValAs 340
Db 9638 GATAGTTTATATGCTTAACATATGTTTTCATACTACTTCCAGGTCCCTTATACTTGTGAGAA 9697
Qy 340 pAspLeuSerGlyLysAlaLysCysLysGlyValAenGlyGlyGlyGlyGlyGlyGlyGlyGly 360
Db 9698 TGTGTCGAGGCAAGAGAGCTGCAGAAAGGCGCTTGCAGCAGAAAGTTTGGATTACAG-- 9755
Qy 360 eArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAs 380
Db 9756 -CAAACTGATCTCTTATGTCGAAATCATCCCGCTCTGACGCCCGCAAGGAATCCA 9814
Qy 380 pLeuIleGlnLeuIleLeProAspLeuMetArgGluAspValGln----- 395
Db 9815 CCTCATCAAGCAGCAATTCACCGAACCTCGAAAGCAACGACGAGGTTTCATCATCCCTT 9874
Qy 395 ----- 395
Db 9875 GTGAACGAATAACATCAACAGTTTGTGTTATAAAAGTTGCTTACTATTGTTTTGTT 9934
Qy 396 -----PheValMetLeuGlySe 401
Db 9935 TACTTCAAAACAAAGTCTGAAATGAAGTGTGTTGTTCTAGTGGTTTGTGTTGTTGTT 9994
Qy 401 rGly---AspProGluLeuGlu---AspTrpMetArgSerThrGluSer----- 416
Db 9995 AGCTCCAGATCATCGAATACAAAGCGATTTTTCAGATTTGCGCGATGCTCTTCACGGTGT 10054
Qy 416 ePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHis----- 433
Db 10055 TTACCACGGTAGGTGAAGCTGTCTTAACCTACGATGAGCCTCTTCTCACCTGGTGAG 10114
Qy 433 ----- 433
Db 10115 CTCCATATCTACACACCATCTAGCCAGCGCTTCATTATGGGAGCTGGAGACTACTTTTA 10174
Qy 434 -----ArgIleThrAlaGlyCysAspIleLeuLeuMe 444
Db 10175 TAATTTAGTTGATGATCATGCTGCTGAGATATACGCTGGCTCCGACTTCATTATTGT 10234
Qy 444 tProSerArgPheGluProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrVa 464
Db 10235 CCCTTCAATCTTGAAACCCCTGTCGCTTAACACAACTTGTGTCATGCGTTATGATCGAT 10294
Qy 464 lProValValHisAlaThrGlyGlyLeu 473
Db 10295 CCCTATAGTTCCGAAACCCGAGGTGTG 10322

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RESULT 13
US-11-231-599-16
; Sequence 16, Application US/11231599
; Publication No. US20060035379A1
; GENERAL INFORMATION:
; APPLICANT: Morrell, Matthew
; APPLICANT: Li, Zhongyi
; APPLICANT: Rahman, Sadequr
; APPLICANT: Appels, Rudolph
; TITLE OF INVENTION: GENES ENCODING WHEAT STARCH SYNTHASES AND USES
; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 72715Supplemental
; CURRENT APPLICATION NUMBER: US/11/231.599
; CURRENT FILING DATE: 2005-09-21
; PRIOR APPLICATION NUMBER: US/10/018.418
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 1592
; TYPE: DNA
; ORGANISM: Triticum sp.
US-11-231-599-16

Alignment Scores:
Pred. No.: 1.16e-10 Length: 1592
Score: 195.50 Matches: 56
Percent Similarity: 41.8% Conservative: 31
Best Local Similarity: 26.9% Mismatches: 44
Query Match: 6.8% Indels: 77
DB: Gaps: 6

US-10-628-525A-21 (1-539) x US-11-231-599-16 (1-1592)

Qy 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGlyLeuProIleArg 361
Db 495 GTCGAGGCAAGAGAGCTGCAGAAAGGCGCTTGCAGCAGAAAGTTTGGATTACAG---CAA 551
Qy 362 ProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381
Db 552 ACTGATGTCTCTTATGTCGGAATCATCCCGTCTGACGCCCGCAAGGAATCCACCTC 611
Qy 382 IleGlnLeuIleLeProAspLeuMetArgGluAspValGln----- 395
Db 612 ATCAAGCAGCAATTCACCGAACCTCGAAGCAACGAGGTTTCATCATCCCTTGTGA 671
Qy 395 ----- 395
Db 672 ACGAATAAACATCAACAGTTTGTGTTATAAAAGTTGCTTACTATTGTTGTTTACT 731
Qy 396 -----PheValMetLeuGlySerGly 402
Db 732 TCAAAACAAAGTCTGAAATGAAGTGTGTTGTTCTTAGTGGTTTGTCTTGGTTCACT 791
Qy 403 ---AspProGluLeuGlu---AspTrpMetArgSerThrGluSer-----IlePhe 417
Db 792 CCAGATCATCGAATACAAAGCGATTTTGCAGATTTGCGCGATGCTCTTCACGGTGTTC 851
Qy 418 LysAspLysPheArgGlyTrpValGlyPheSerValProValSerHis----- 433
Db 852 CACGTTAGGTGAAGCTTGTCTTAACCTACGATGAGCCTCTTCTCACCTGGTGAGCTCC 911
Qy 433 ----- 433
Db 912 AATATCTACACACCATCTAGCCAGCGCTTCATTATGGGAGCTGGAGACTACTTTATAAT 971
Qy 434 -----ArgIleThrAlaGlyCysAspIleLeuLeuMetPro 445
Db 972 TTAGTTGATGATCGATCATGCTGAGATATACGCTGGCTCCGACTTCATTATTGTCCT 1031
Qy 446 SerArgPheGluProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValPro 465
Db 1032 TCAATCTTGAACCCCTGTCGCTTAACACAACTTGTGTCATGCGTTATGATCGATCCCT 1091
Qy 466 ValValHisAlaThrGlyGlyLeu 473
Db 1092 ATAGTTCCGAAACCCGAGGTGTG 1115

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RESULT 14
US-10-336-263A-11
; Sequence 11, Application US/10336263A
; Publication No. US20050251882A1
; GENERAL INFORMATION:
; APPLICANT: D'Ordine, Robert L

```

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; APPLICANT: Dotson, Stanton B
; APPLICANT: Duff, Stephen M
; APPLICANT: Sisson, Pamela J
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTERIA
; TITLE OF INVENTION: US 10/336-263A
; FILE REFERENCE: 38-21 (52176) A
; CURRENT FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Nostoc punctiforme
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1269)
; OTHER INFORMATION:
US-10-336-263A-11

Alignment Scores:
Pred. No.: 4.13e-06 Length: 1269
Score: 152.50 Matches: 74
Percent Similarity: 39.0% Conservative: 49
Best Local Similarity: 23.5% Mismatches: 95
Query Match: 5.3% Indels: 97
DB: 8 Gaps: 14

US-10-628-525A-21 (1-539) x US-10-336-263A-11 (1-1269)
QY 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTrpGly 248
Db 388 CAAGGAGTAACAGGTTACACCTATCACTCATAGGAGCAGTCAA-----TACAAC 441
QY 249 AlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAla 268
Db 442 ACTATAGAAAATATTCCTCTGATGTCAGTGCAGGATTCGCGATGAA----- 489
QY 269 ValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGly 288
Db 490 -----AAACAGGTGTTAGAAACAGCAGCAGCAATTGTA----- 522
QY 289 TyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSer 308
Db 523 -----CGGACCACTCGCAAGACAGCAACATCGATCGCTAGTTCCACT 570
QY 309 ArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAla 328
Db 571 GAA-----GGCAATATCGATATT----- 588
QY 329 ThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCys 348
Db 589 -----ATCCCTGTGTGTACAGATATTTCAGCGTTTT----- 618
QY 349 LysGlyAlaLeuGlnLysGluLeuGly-----LeuProIleArgProAspValPro 365
Db 619 ---GGTTCATTGGCGGAGAGCAGCGGCTGAACTGGAATTCGCAAGATGCCAA 675
QY 366 LeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp---LeuIleGlnLeu 384
Db 676 GTTGATTATTATGTAGGGCGTTTGACCAACGCAAGGTATAGAAACCCCTAGTCGTGCA 735
QY 385 IleIleProAspLeuMetArgGlu-----AspValGlnPheValMetLeuLysGly 402
Db 736 GTCAACGAGTCTGAACATGACGACTCGAAGAAATCTCAAGCTAATTATTCGCGTGTAGT 795
QY 403 AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422
Db 796 ACTCCA-----GGTAACAGGACGCGCATAGAACGCGCATCGATTGAG 837
QY 423 GlyTrpValGly-----PheSerValProValSerHis 433
Db 838 CAAATCGTCCAGGAATTAGGAATCACTGACTTGACCATCTCTCTCTGCTGCTCAGTCAA 897

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QY 434 ArgIleThr-----AlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
Db 898 GATATTTTACCACATTATTCGCTGCGGATGCTGCGTTGTTCTTAGTCACTACGAA 957
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
Db 958 CCATTTGGACTGTTGCGATCGAAGCGATGGCAAGCGGTACGCGGTTGTGGCTAGTGAT 1017
QY 470 ThrGlyGlyLeuArgAspThrValGluAsn----- 479
Db 1018 GTCGGTGAGCTTCAATTTACTGTAGTTAATGAACAACTGGTTTATTAGCACCACCACA 1077
QY 480 -----PheAsnPro----- 482
Db 1078 GATGTAGTGTCTTTGCGTCTGCTATTGACCGAAATCTCTTTAATCCAGATGGCGAGAC 1137
QY 483 ---PheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAla 496
Db 1138 GAATTTGGTAAAGCTGGCAGAAAGCGTACTGAAAGCCAATTTAGT 1182

RESULT 15
US-11-082-389-41
; Sequence 41, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 41
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1270)
; OTHER INFORMATION: RXN02062
US-11-082-389-41

Alignment Scores:
Pred. No.: 5.43e-06 Length: 1293
Score: 151.50 Matches: 77
Percent Similarity: 36.3% Conservative: 42

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Best Local Similarity: 23.5% Mismatches: 100  
Query Match: 5.2% Indels: 109  
DB: 13 Gaps: 18

US-10-628-525A-21 (1-539) x US-11-082-389-41 (1-1293)

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QY 212 GlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyVal 231
DB 221 GGTGCACCTCGGATATGGAGGAGTTTCGTC-----CACGGCGTC 262
QY 232 GluProAla-----SerThrTyrPro----- 238
DB 263 GATCTGCTTGGAAAGCGGAACCTCGGATTAAGACACTGTCCACGGTTTACGCATG 322
QY 239 -----AspLeuGlyLeuProGluTyrTrpTyrGlyAlaLeuGlu 251
DB 323 GCAGAAGCTGCACAAACAGCTGGATGCTGCTCACTCACACACTTGGTATGCAGGTCCTTGGC 382
QY 252 -----TrpValPheProGluTyrPalaArgArgHisAlaLeuAsp 264
DB 383 GGCACCTTGCAGTCTCTCCAGCGCATTCCTCACGTGCTACCGCGCACTCTTTGGAG 442
QY 265 -----LysGlyGluAlaValAsn-----Phe 271
DB 443 CCAGATCGCCCATCGAAGCTGACACTTGGCGGTGGATACAGCGTGTCTCTGTGTCT 502
QY 272 LeuLysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrp 291
DB 503 GAAAAAATCCATGGAATACGCTGACGCGCTCATCTGTGTC----- 547
QY 292 GluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSer 311
DB 548 -----GCTCGCATGAAGATTCATCTCTCGTGTGCTACCTCCGTCGC 586
QY 312 Val-----LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327
DB 587 ATCAGCGCGACACGCGTGTGCTCTCACGGCATCACACTGATGTTGGCAGCCT 646
QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLys 347
DB 647 CGCCCG-----ACTTTCATGAC----- 664
QY 348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIle 367
DB 665 GCGAAGATTCCTACTCTCCCTCCCTAGGC-----GTTGACCCACAGCGGCCCATCGTC 718
QY 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp---LeuIleGlnLeuIleIle 386
DB 719 GCATTTTGGCGCGCATCACCCGCCAAAGGGGTGAGCACCTCATCAGGCGAGCGG 778
QY 387 ProAspLeuMetArgGluAspValGlnPheValMet---LeuGlySerGlyAsp---Pro 404
DB 779 -----CTTTTCAGCAGTCCGTGAGCTGTGCTCTGTGCGCGCGCCAGACACCC 832
QY 405 GluLeu-----GluAspTrpMetArgSerThrGluSerIle 416
DB 833 GAAATCGCAGCTCGCACCCACCGCTGGTGAAGAACTCCAGGCAAGCGCGAAGCAAT 892
QY 417 Phe-----LysAspLysPheArgGlyTrpValGlyPheSerVal 429
DB 893 TTCTGGGTTCCAGACATGCTGGCGACAGGACAAATCCAA----- 931
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
DB 932 -----GAGATTCTCACCGCTGCTGACACCTTCTGTGTGCGCCATTCATTACGAG 979
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
DB 980 CCACTGGGATCTGTGAACCTTGAAGCAATGGCTGCAACACCGCAGTGTGTGCGATCCGAC 1039
QY 470 ThrGlyGlyLeuArgAspThrVal 477
DB 1040 GTTGGAGGCATCCTCGAGGTGTT 1063
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## RESULT 16

US-11-082-389-43  
; Sequence 43, Application US/11082389  
; Publication No. US20050244935A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; FILE REFERENCE: BGI-131CPCN  
; CURRENT FILING DATE: 2005-03-16  
; PRIOR APPLICATION NUMBER: US/11/082,389  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930487.4  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446  
; SEQ ID NO 43  
; LENGTH: 1293  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1270)  
; OTHER INFORMATION: FRXA02062  
US-11-082-389-43

## Alignment Scores:

Pred. No.:	5,43e-06	Length:	1293
Score:	151.50	Matches:	77
Percent Similarity:	36.3%	Conservative:	42
Best Local Similarity:	23.5%	Mismatches:	100
Query Match:	5.2%	Indels:	109
DB:	13	Gaps:	18

US-10-628-525A-21 (1-539) x US-11-082-389-43 (1-1293)

```
QY 212 GlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyVal 231
DB 221 GGTGCACCTCGGATATGGAGGAGTTTCGTC-----CACGGCGTC 262
QY 232 GluProAla-----SerThrTyrPro----- 238
DB 263 GATCTGCTTGGAAAGCGGAACCTCGGATTAAGACACTGTCCACGGTTTACGCATG 322
QY 239 -----AspLeuGlyLeuProGluTyrTrpTyrGlyAlaLeuGlu 251
DB 323 GCAGAAGCTGCACAAACAGCTGGATGCTGCTCACTCACACACTTGGTATGCAGGTCCTTGGC 382
QY 252 -----TrpValPheProGluTyrPalaArgArgHisAlaLeuAsp 264
```

```
Db 383 GGCACCTTTCAGCTCGTCTCCACGGCAATTCCTCACGTGGCTACCGCGCACTCTTTGGAG 442
QY 265 -----LysGlyGluAlaValAsn-----Phe 271
Db 443 CCAGATCGCCCATGGAAGCGTGAGCAGCTTGGCGGTGGATACGACGTGCTCCTCGTCT 502
QY 272 LeuLysGlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrp 291
Db 503 GAAAAAATGCCAATGCAATACGCTGACGGGTATCGCTGTGTGCG-----547
QY 292 GluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSer 311
Db 548 -----GCTCGCATGAAAGATTCATCTCTCGTACCGCTCGC 586
QY 312 Val-----LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327
Db 587 ATCGAGCCGGCAACGCTGGTGTGCTCAACGGCATCGACACTGAGTTGGCGACCT 646
QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLys 347
Db 647 CGCCCG-----ACTTCGATGAC-----664
QY 348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIle 367
Db 665 GCGGAAGATTCGCTACTCGGCTCCCTAGGC-----GTTGACCCACAGCGGCCCATCGTC 718
QY 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp---LeuIleGlnLeuIleIle 386
Db 719 GCATTTGTGCGCGGCATCACCGCCCAAAAGGCGTCGACACCTCATCAAGGCGACGCG 778
QY 387 ProAspLeuMetArgGluAspValGlnPheValMet---LeuGlySerGlyAsp---Pro 404
Db 779 -----CTTTTCGACGAGTCCGCTGACGCTGTGCTGTGCGCGCGCACACCCCC 832
QY 405 GluLeu-----GluAspTrpMetArgSerThrGluSerIle 416
Db 833 GAAATCGCAGCTCGCACCCACCGCCCTGTTGGTGAAGAACTCCAGCAAGCGCGAAGGCATT 892
QY 417 Phe-----LysAspLysPheArgGlyTrpValGlyPheSerVal 429
Db 893 TTCTGGGTTTCAGACATGCTGGGCAAGCAATGGCTGCAACACCGCAGTTGTGCGCATCCGAC 1039
QY 470 ThrGlyGlyLeuArgAspThrVal 477
Db 1040 GTTGGAGGCATCCTGAGGTGTT 1063
```

```
RESULT 17
US-10-336-263A-1
; Sequence 1, Application US/10336263A
; Publication No. US20050251882A1
; GENERAL INFORMATION:
; APPLICANT: D'Ordine, Robert L
; APPLICANT: Dotson, Stanton B
; APPLICANT: Duff, Stephen M
; APPLICANT: Sisson, Pamela J
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTE
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 38-21 (52176) A
; CURRENT APPLICATION NUMBER: US/10/336,263A
; CURRENT FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1278
; TYPE: DNA
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; ORGANISM: Anabaena sp.
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1278)
; OTHER INFORMATION:
US-10-336-263A-1
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Alignment Scores:
Pred. No.: 7,8e-06 Length: 1278
Score: 150.00 Matches: 92
Percent Similarity: 38.8% Conservative: 63
Best Local Similarity: 23.1% Mismatches: 131
Query Match: 5.2% Indels: 114
DB: 8 Gaps: 21
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US-10-628-525A-21 (1-539) x US-10-336-263A-1 (1-1278)

```
QY 163 TyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle-LeuGluLeuGlyGlyT 182
Db 270 TTTACCGGAATTGT-----TGCCGAATTCACACGCTTCCAAAGCGCCCAAGGTTA 320
QY 182 rIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProVa 202
Db 321 TAACTATCAA-----CTCATTACACAAATTTACTGTTGTCATCTTGGTGGGAAT 371
QY 202 lLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuVa 222
Db 372 GCAACTG-----AAAAAGCAACAACCTTGTGTGT 401
QY 222 lIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLe 242
Db 402 GGTGCATACATACCACTCATTAGGACATCAATATCAACATCGATCGCAGATATA----- 456
QY 242 uProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAla---ArgArgHi 261
Db 457 -----CCCGCCATTCGCAATCAGCGATT 479
QY 261 sAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspAr 281
Db 480 AGCTATAGAA-----AAAGCTTGTTAGAGAGGTAGACAC 515
QY 281 gIleValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlnGl 301
Db 516 AGTAGTT-----GCCACCGCCCAAGACAGCAACA 548
QY 301 YLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAs 321
Db 549 TATGCGCGCCTGGTT---TCTAAGAAGGAGCGCATAGAGATGATTCTCTTGGCGGACTGA 605
QY 321 pIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAs 341
Db 606 CATTAAATACCTC-----618
QY 341 pLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleAr 361
Db 619 -----GGAACAATTGAA---AAGTCGCGCTCACGGGAAAAAATCGGGA-----ATTGA 662
QY 361 gProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp-- 380
Db 663 GCCTGATGCCAAGATGGTATTTTATAGTAGTCTTTGTATCCCGGTAAAGGATAGAAAC 722
QY 381 -LeuIleGlnLeuIleIleProAspLeuMetArg-----GluAspValGlnPheValMe 398
Db 723 CTTAGTCAGAGCGGTGTGCTCATCTAGTTGAGAGGTGAAGCAAACTCCAGTTAGTAAT 782
QY 398 tLeuGlySerGlyAspProGluLeuGluAspTrpMet-----ArgSerThrGluSe 415
Db 783 TGGTGTGTGATGCCGCTCCTGGTCAAAAGTGTAGGAGAGCGCGATCGCATTCGGAATAT 842
QY 415 rIlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIl 435
Db 843 TGTGGCTGAACTAGAAGTGAACGNTTGCACCCACCTTCGCTCGCTCGCTAGATCATGAAAT 902
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QY 435 eThr-----AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCys 451
Db 903 CCTCCCTTACTACTACGCTGGCTGATGTTGGCTGTTGCCAGTCACTACGAAACCTT 962
QY 451 sGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrG1 471
Db 963 TGGTTTGTATTGCTATTGAAGGATGGCTAGCMAAAGTCCCGTAATCCCGTAATGTAGG 1022
QY 471 YGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyTh 491
Db 1023 TGGATTGCAATTACAGTAGTT-----CCAGAAGTCAC 1055
QY 491 xGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPhe-----ValAsp----- 506
Db 1056 AGGT---TTACTTGCACCTCCACAGATGAGTCAGCTTTTGTCTACGCCATAGACCGCAT 1112
QY 507 -IleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnG1 526
Db 1113 ATTAGCCCAACC-AACTTG-----GCGAGATC 1138
QY 526 uAlaArgHisVallys-----ArgLeuHisValGlyProCys 538
Db 1139 AGCTAGGCACAGCGCGCCGCCAGCGAGTGGAAACCACTTTCAGCTGGCGCGGTGT 1193

RESULT 18
US-10-336-263A-9
; Sequence 9, Application US/10336263A
; Publication No. US20050251882A1
; GENERAL INFORMATION:
; APPLICANT: D'Ordine, Robert L
; APPLICANT: Dotson, Stanton B
; APPLICANT: Duff, Stephen M
; APPLICANT: Sisson, Pamela J
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTER
; FILE REFERENCE: 38-21 (52176) A
; CURRENT APPLICATION NUMBER: US/10/336, 263A
; CURRENT FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Nostoc punctiforme
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1272)
; OTHER INFORMATION:
US-10-336-263A-9

Alignment Scores:
Pred. No.: 2.39e-05 Length: 1272
Score: 145.50 Matches: 74
Percent Similarity: 40.2% Conservative: 53
Best Local Similarity: 23.4% Mismatches: 96
Query Match: 5.0% Indels: 93
DB: 8 Gaps: 15

US-10-628-525A-21 (1-539) x US-10-336-263A-9 (1-1272)

QY 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnMetTrpHisAlaSerLeuVal 200
Db 316 GGGTTTCTTACTTCC-----TTAATTTCATACCAACTACTGTTATCATCTTGGGTG 366
QY 201 ProValLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220
Db 367 GGTATGGAATG-----AAAAACAGCAATCCCTG 396
QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240
Db 397 ATTCAGGTACAT-----ACTTACCATTCTTTA 423
QY 241 GlyLeuProProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArg 260
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Db 424 GGAGCCGTTAAA-----TACAGAAGTATTGGTGATGTTCCCGTAATTGCAGCCCGCA 477
QY 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280
Db 478 TTAGCTGTAGAA-----AAAGCCCTGCTTGGAAACATATAGAC 513
QY 281 ArgIleValThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGln 300
Db 514 TGTGTAGTT-----GCAACAGTCCCAAGAACAAGAA 546
QY 301 GlyLeuAsnGlnLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320
Db 547 CACATCGGGTACTCGTTTCTAGCAAAAGGGAACATT----- 582
QY 321 AspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340
Db 583 -----GAAATGATTCCTGTGGCACTGACTGAC 612
QY 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360
Db 613 AAATTTGGGGGAATTCAGCGAAGT-----GCGGCGGAGAAAGTTGGCA-----ATT 660
QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp 380
Db 661 GCCCAGATGCCAAATAGTTCTATGTTGGTGGCTTTGACCGCGCAAGGAATTTGAA 720
QY 381 ---LeuIleGlnLeuIleIleProAspLeuMetArg-----GluAspValGlnPheVal 397
Db 721 ACCTTGGTAGAGCTGTTGCCAAGTCTAGTTTAAAGGGGTGAAGCTAACCTCCAGCTAGTA 780
QY 398 MetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePhe 417
Db 781 ATTGGCGGTGGTAGCGCTCCGCTCAGAGTGAT-----GCAATAGAA 822
QY 418 LysAspLys-----PheArg 422
Db 823 CCGCATCGCATTCGCTAGCATCGTGAAGTTCGGATTAGAAAATTTGTACACCTTTTGGC 882
QY 423 GlyTyrValGlyPheSerVal---ProValSerHisArgIleThrAlaGlyCysAspIle 441
Db 883 GGTCCGCTAGATGAATACTGTTCTCCCTCTCTACTAC-----GCCGCGCTGATGTC 933
QY 442 LeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461
Db 934 TCGTAGTCCCGCAGCCATTATGAACCTTTTGGTTAGTTGCTATTGAGGCAATGGCTAGT 993
QY 462 GlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrVal 477
Db 994 CAGACTCCAGCTGCTAGCTAGTAGTGATGTTGGTGGGTTCAGTTTACTGTT 1041

RESULT 19
US-10-336-263A-3
; Sequence 3, Application US/10336263A
; Publication No. US20050251882A1
; GENERAL INFORMATION:
; APPLICANT: D'Ordine, Robert L
; APPLICANT: Dotson, Stanton B
; APPLICANT: Duff, Stephen M
; APPLICANT: Sisson, Pamela J
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTER
; FILE REFERENCE: 38-21 (52176) A
; CURRENT APPLICATION NUMBER: US/10/336, 263A
; CURRENT FILING DATE: 2003-01-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Anabaena sp.
; FEATURE:
; NAME/KEY: gene
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/ LOCATION: (1)..(1269)  
/ OTHER INFORMATION:  
US-10-336-263A-3

Alignment Scores:  
Pred. No.: 0.000107 Length: 1269  
Score: 139.50 Matches: 74  
Percent Similarity: 40.7% Conservative: 48  
Best Local Similarity: 24.7% Mismatches: 107  
Query Match: 4.8% Indels: 71  
DB: 8 Gaps: 14

US-10-628-525A-21 (1-539) x US-10-336-263A-3 (1-1269)

```
QY 227 AlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrP 246
Db 382 GCATCCAGGAGCAACCAAGTTCACTTATCTTATAGGACGATCAAG----- 435
QY 247 TyrGlyAlaLeuGluTyrValPheProGluTyrPAlaArgHisAlaLeuAspLysGly 266
Db 436 TACAATCTATAGATACGATTCCTTTGGTTGCTACTAAAGCTTATCGGTAGAA----- 489
QY 267 GluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSer 286
Db 490 -----AAACAAGTATTAGAAACAGCAGCAAGAAATCGTT----- 522
QY 287 LysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeu 306
Db 523 -----GCTACCAGTCTCAAGAACAGCAACATATGCGTGTAGTT 564
QY 307 SerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsn 326
Db 565 TCTACTAAA-----GGTTACATTGATATC----- 588
QY 327 ProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAla 346
Db 589 -----GTTCTGCGGTACAGATATTACCGCTTTGGTTCAATTGCT 630
QY 347 LysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366
Db 631 -----AGCAAGCCGCAAGAGCAGAAATTAGGA-----ATTGATCAAGAACGAAAGTG 678
QY 367 IleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAsp---LeuIleGlnLeuIle 385
Db 679 GCTTGTATGATAGGAGCTTTGATCAACCTAAGGCATAGAACCTTAGTAGCGTCATG 738
QY 386 IleProAspLeuMetArgGlu-----AspValGlnPheValMetLeuGlySerGlyAsp 403
Db 739 AATGAGTCTCAATTGCGTGACAGCAATAAACTCAAACTAATTATTGCTGCTGTAGTACT 798
QY 404 ProGluLeuGluAspTrpMetArg-----SerThrGluSerIlePheLysAsp----- 419
Db 799 CTTGGTAATAGCGATGGCAGAGCGCGATCGCATTTGAGGCCATTGTGCAAGAAATGGCG 858
QY 420 -----LysPheArgGlyTrpValGlyPheSerValProValSerHisArg 434
Db 859 ATGACGGAATACATAGTTTCCAGGC-----CGCTCAGGCAAGATGCTCCTCGTCT 912
QY 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454
Db 913 TACTACGCTGCGGCTGATGTTTGGCGTTGTTCAGTCACATATGAACTTTTGGATTGGTG 972
QY 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474
Db 973 GCAATTTGAAGCAATGGCAAGTGGTACACCTGTAGTACCGAGCGATGTTGGTGGATCTCAA 1032
QY 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAla 494
Db 1033 TTTACGGTAGTTTCC-----GAGAAAACCGTTTATTG 1065
QY 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514
Db 1066 GTACCACCA-----AAAGATATTGCTGCGTTCAACATTGCAATT 1104
```

RESULT 20

US-11-098-686-9230  
/ Sequence 9230, Application US/11098686  
/ Publication No. US20060024696A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
/ TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
/ TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING  
/ FILE REFERENCE: 09531-128001  
/ CURRENT APPLICATION NUMBER: US/11/098,686  
/ PRIOR FILING DATE: 2005-04-04  
/ PRIOR APPLICATION NUMBER: PCT/US03/31318  
/ PRIOR FILING DATE: 2003-10-01  
/ PRIOR APPLICATION NUMBER: US 60/416,395  
/ PRIOR FILING DATE: 2002-10-04  
/ NUMBER OF SEQ ID NOS: 11433  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 9230  
/ LENGTH: 1341  
/ TYPE: DNA  
/ ORGANISM: Lawsonia intracellularis  
US-11-098-686-9230

Alignment Scores:  
Pred. No.: 0.000355 Length: 1341  
Score: 135.00 Matches: 95  
Percent Similarity: 33.9% Conservative: 68  
Best Local Similarity: 19.8% Mismatches: 156  
Query Match: 4.7% Indels: 162  
DB: 14 Gaps: 23

US-10-628-525A-21 (1-539) x US-11-098-686-9230 (1-1341)

```
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 25 GAATTTCTCCATAATTTA---AGTGGAGATTAGGAACAGCATGTTATGGAATGACTCAG 81
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValMetProArgTyrLeuAsnGlyThr 96
Db 82 GCTCTTATTCGATCAGGAGCCAAATTTGCTTTATTTCTTCCTCGA----- 126
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro----- 114
Db 127 -----TCAGAACACAGCTCAGCTATGTCGACAAATAAACATTTTCTTAAATA 177
QY 115 -----CysPheGlyGlyGluHisGluValThrPhePheHisGluTyr 128
Db 178 CGTTCTGCTGCTGATGTTTGTATTATACAAACATAAACAACTTGGTTACTTCACTCAACAA 237
QY 129 ArgAspSerValAspTrpVal-----PheValAspHisPro-----SerTyrHis 143
Db 238 TTTCAAGAAATC---TGAAGAAACAACTTTTCTATCCGTCCTCTATTAAAGCAACACTTCAT 294
QY 144 ArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr 163
Db 295 ---CCATATGTTCTCTAGTCAACACTTTCTGCTTATATTCTACTCAGAAATCATTTTA 351
QY 164 Thr-----LeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGlu 178
Db 352 ACTGAACACAAATGAATTTCTCTACAGTTAGTTTCAGCATGTGCTTTACCTCTTGT----- 405
QY 179 LeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSer 198
Db 406 TCTGTGTGA-----TATGGTCCACACTTAATGGAAGAAGTATTCGTTATAGCCAAGCT 459
QY 199 LeuValProValLeuAlaAlaLysTyr----- 208
Db 460 GCTGCACAAATAGCTATGAGAGAAATGATGATGTTATTCATGTCCTGATGATGACA 519
QY 209 ArgProTyrGlyValTyr-----LysAspSerArgSerIleLeuValIleHis----- 224
Db 520 TACCCCTGCTGGAATCATAGCTAAAAAAATAGTAATAAACCACTTATTATTGCCCATGTTCA 579
```

	QY	225	- - - - -	-----AsnLeuAlaHis	228
	Db	580	GCTACAGATTGGATCGATGTTGGTGA	CCTCACTAATCAGAATAATTCAAATATATAGA	AAG639
	QY	229	GlnGlyValGlUpProAlaS	SerThrTyP <sup>r</sup> roASPleuGlyLeuP <sup>r</sup> oCglUtpTyArgLy	248
	Db	640	GTTGGTCTTGAGCGGTGCTGATCATATATTGC	TCTCACG----	678
	QY	249	AlaLeuGluTrpValPheP <sup>r</sup> oCglUtpTrpAlalargH	isAlalaLeuApLys-	265
	Db	679	-----	---CACTACTCGTAATCTTATTATCAAAAAATATCATATT	717
	QY	266	--GlyGluAlavalAenPheLeuLysGlyAlavalThrala	aArgHisAlaLeuApLys-	284
	Db	718	CCAGAGAAAAMATTAGTTGTTTCATAATGCTGTACTTC	CAGCA----	762
	QY	285	ValSerLysGlyTyS <sup>r</sup> erTriPGlUvalThrThralagLu	GlyGlyGinGlyLeuaSnGlu	304
	Db	763	--TCTGGAAATTATACATGCCAG--	-----AAAAA	789
	QY	305	LeuLeuSerSerArgLysServallauSnGlyIlevalaEn	GlyIleaSpIleasn Asp	324
	Db	790	AGRAAATTCAAACA AAAAGTAGTACTC	-----	816
	QY	325	TrpAasnProAlathrAspLysCyelleP <sup>r</sup> ocysHistyr	ServValaspLeuSerGly	344
	Db	816	---	-----	816
	QY	345	LysAlaLysCylsygilyAlalaLeuGlnlysGluLeuGly	LeuProIIeaArgProaspVal	364
	Db	816	---	-----	816
	QY	365	ProlEutleglyPhelieglyArgLeuasPTyGrInLys	Gly-----Ilasap	380
	Db	817	-----TTCTTGGAAAGTAGTTACACATCAA AAAGCCCCTG	AAACACTTTTATAAAT	864
	QY	381	LeuileGlnLeullelleIP <sup>r</sup> oASpleuMetArgGluasp	ValGlnPheValMeLeugly	400
	Db	865	GCTGCATATCTGTITCCA AAAAMAATTA----	CAAAATGTATGTTTTATCATCGCTGGT	918
	QY	401	SerglyaspProGluLeuGluasPTripMetArgSerthr	GluseriillePheLyaSPlys	420
	Db	919	AGCGGGAT--ANGTTACCCTCAATGATCCGTAAAGT	AGTAGCTTCATTCGCCCTGGGAGT	975
	QY	421	PheaRglyTrpValGlyphe-----	ServalProValserHisarlgilletHraLaGly	438
	Db	976	CGTTTCCACTTTACTGGCTTTTACATAAACCAACAGT	GAACAT---ATATATTCTCTT	1032
	QY	439	CyeasptileLeuleuMetProSerArGPheGluP <sup>r</sup> oCys	GlyLeuaSnGlnLeutyAla	458
	Db	1033	AGCAATGTATGTATTAGCTTAGPATTTCTGAACCATTT	GGAATTACCACTTGAAGCT	1092
	QY	459	MetGlnTyrglyThrValProValHisAlathrglyLeu	AlagaSP <sup>r</sup> ThrValcLU	478
	Db	1093	ATAAGACATGGACACCTGTAA TTATATCAA AACAATCCG	GAGTAGTAGTAAAG	1152
	QY	479	Asn	479	
	Db	1153	AGT	1155	

**RESULT 21**

<hr/>	
US-11-098-686-8739	
; Sequence 8739, Application US/11098686	
; Publication No. US20060024696A1	
; GENERAL INFORMATION:	
; APPLICANT: Kipur, Vivek and Gebhart, Connie J.	
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES	
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING	
; FILE REFERENCE: 09531-128001	
; CURRENT APPLICATION NUMBER: US/11/098,686	
; CURRENT FILING DATE: 2005-04-04	
; PRIOR APPLICATION NUMBER: PCT/US03/31318	
<hr/>	
QY	225 -----AsnMetuAlaHis 228    :::    :::
Dbb	414064 GCTACAGAAATTTGATCGATGTGGTCACTCACCTAAATCAAGATAATTCTAAATATAGAAGA 414123    :::    :::
QY	229 GInglyValGluProAlaSerThrTyProAspLeuGlyLeuProGluTrpTyrgLy 248      ::       ::
Dbb	414124 GTTGSGTCTTGAGCGTCTGCATCATATTATTGCTGCAGC----- 414162    ::     ::
QY	249 AlaLeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAsplyg----- 265    ::     ::
Dbb	414163 -----CACTATACTCGTAATCTTTATTATGAAGAAAATATCATATT 414201    ::     ::

QY 266 ---GlyluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThr 284  
Db 414202 CCAGGAGAAAATAGTGTGTCATATGCTGACTTCCAGCA----- 414246  
QY 285 ValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlnGlyLeuAsnGlu 304  
Db 414247 ---TCTGGAATATATACATGGCAG-----AAAAAA 414273  
QY 305 LeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAsp 324  
Db 414274 AGAAATTCAAACAAAAGTATGACTTC----- 414300  
QY 325 TrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGly 344  
Db 414300 ----- 414300  
QY 345 LysAlaLysGlyGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspVal 364  
Db 414300 ----- 414300  
QY 365 ProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGly-----IleAsp 380  
Db 414301 -----TTCCTCGAAGAGTTACACATCAAAAAGCCCTGAACACTTTATAAAT 414348  
QY 381 LeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
Db 414349 GCTGCATATCTGTTTCAAAAATA-----CAAAATGATGTTTATCATGCTGCT 414402  
QY 401 SerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLys 420  
Db 414403 AGCGGGGAT---ATGTTACCTCAATGATCCGTAAAGTAGTTCATTACGCCCTTGGGAGT 414459  
QY 421 PheArgGlyTrpValGlyPhe-----SerValProValSerHisArgIleThrAlaGly 438  
Db 414460 CQTTTCCACTTACTGGCTTTTACATAACCAACAAAGTTGAACAT---ATATATTCTCTT 414516  
QY 439 CysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAla 458  
Db 414517 AGCAATGATATAGTTATGCTAGTATTTCTGAACCAATTTGGAATACACACTTGAAGCT 414576  
QY 459 MetGlnTyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGlu 478  
Db 414577 ATAAGACATGGAACACCTGTAATTATATCAAAACAATCCGGAGTTAGTGAAGTATTAAAG 414636  
QY 479 Asn 479  
Db 414637 AGT 414639

RESULT 22  
US-10-336-263A-7  
; Sequence 7, Application US/10336263A  
; Publication No. US20050251882A1  
; GENERAL INFORMATION:  
; APPLICANT: D'Ordine, Robert L  
; APPLICANT: Dotson, Stanton B  
; APPLICANT: Duff, Stephen M  
; APPLICANT: Sisson, Pamela J  
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE NUCLEIC ACID MOLECULES FROM CYANOBACTERIA  
; FILE REFERENCE: 38-21 (52176) A  
; CURRENT APPLICATION NUMBER: US/10/336,263A  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 1443  
; TYPE: DNA  
; ORGANISM: Nostoc punctiforme  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(1443)  
; OTHER INFORMATION:  
US-10-336-263A-7

Alignment Scores:  
Pred. No.: 0.00695 Length: 1443  
Score: 123.50 Matches: 73  
Percent Similarity: 39.1% Conservative: 97  
Best Local Similarity: 23.8% Mismatches: 93  
Query Match: 4.3% Indels: 95  
DB: 8 Gaps: 15  
US-10-628-525A-21 (1-539) x US-10-336-263A-7 (1-1443)  
QY 215 LysAspSerArgSerIleLeuValIleHisAsn-----LeuAlaHisGlnGly 230  
Db 364 CGAACAGGCGCGCTATACCTTGATTCACACTACTATTGGCTTCTGCTGGGTAGGA 423  
QY 231 ValGluProAlaSerThrTyrProAspLeuGlyLeuProPro-----GluTrp 246  
Db 424 TTAGAAGCTTAATCTCGA-----TTGGGACTACCCCAAGTTTCATACCTCATCTCT 474  
QY 247 TyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGly 266  
Db 475 ATAGGTGACAGTTAAATAC-----CGCAATATGGAAATATCCG 510  
QY 267 GluAlaValAsnPheLeuLysGlyAlaVal-----ValThrAlaAspArg 281  
Db 511 CGCAGATTTCTGCAATTCGTAATTTGTGGAGAGGGCAATTTTAGAACACAGCAGATTAT 570  
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlnGly 301  
Db 571 GTAATATCC-----ACTAGCCCTCAAGAAGCGGAAGAT 603  
QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321  
Db 604 TTACGTCAAGTTAAATTCGCAACATGCTGCTGATT----- 636  
QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341  
Db 637 -----AAAGCATTCCTCGGGATTAACTACTGAACAC 669  
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGly-----Leu 358  
Db 670 TTT-----GGTCTGTGCTAAGAAGTTGCTCGCCCAACAGATTG 708  
QY 359 ProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGly 378  
Db 709 GGGATTGCTTCAGATTCTCAGATAATCTTGTATGTAGGACGCTTTGACCCCGCAAGGA 768  
QY 379 IleAspLeuIle-----GlnLeuIleIlePro 387  
Db 769 GTTGAACCCCTGGTCAGAGCTTGGCCCAATTTGCTTCAGCATTTCACACTCTATCTAGTT 828  
QY 388 AspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGlu 407  
Db 829 GGTGGTTGCCGTGAAGAT-----GGAGCAGACTTCAAGAA----- 864  
QY 408 AspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly----- 423  
Db 865 -----CAACAGCGCATTTGAAGTTTGGTGAATGACTGGG-ATTGGAAGCGGTACAGT 917  
QY 424 -----TrpValGlyPheSerValProValSerHisArgIle-ThrAlaGlyCysAspIle 441  
Db 918 TTTCACTGGACGAATTTCTCAAGCACTGTTACTACTTACTTATCGCGCAGGG---GATAT 974  
QY 441 IleLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461  
Db 975 CTGCGTTGTACCGAGTTACTAGCCCTTTTGTAGTGGCGCATTTGAAGCAATGGCAGC 1034  
QY 461 rGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAs 481  
Db 1035 CAGAACACCCGTAATTTGCTAGTAATGTGGAGGATTTGCAGCATACGTTAGTGCAT----- 1089  
QY 481 nPropGlyGluAsnGly 487  
|||||



```
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThralaAspArg 281
Db 518 -----TTGCTAACATTACCTTGACCAACATAGATCGG 550
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrThralaGluGlyGlnGly 301
Db 551 GTTATATGTTCTTAAT-----ACATGCAAGAA----- 580
QY 302 LeuAsnGluLeuSerSerArgLysSer-----ValLeuAsnGlylleValAsnGly 319
Db 581 ----AATATGATTGTTAGACAGAAATTAAGTCTCGATATAATCTCAGTAATCCCAACGCA 637
QY 320 IleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerVal 339
Db 638 GTGGTCAGCGAAGATTTCACCAAGG----- 664
QY 340 AspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuPro 359
Db 665 --GATCCTACTGCTGGCCACCAAGAGAAACAAAGTAGGATAAG----- 706
QY 360 IleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlylle 379
Db 707 -----ATAGTGTCTGCGTGCATCGGAAGCTCTTTCCAAACAAAGGGTCC 751
QY 380 AspLeuIleGlnLeuIleProAspLeu-----MetArgGluAspValGlnPheVal 397
Db 752 GATTTACTTACTCGCATTAATTCGAAGTTTGTCTCATGAGATGTCGAATTATA 811
QY 398 MetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePhe 417
Db 812 GTAGCGGGCGATGGT---CCAAAGTTATAGATTTTCAACAAATGATTCAA----- 859
QY 418 LysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAla 437
Db 860 -----AGTCATAGACTACACAAAA 877
QY 438 GlyCysAspIleLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyr 457
Db 878 CGTGTGCAACTCTTA----- 892
QY 458 AlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrVal 477
Db 893 -----GGCTCTCTGCCA-----CATGAGAAA-----GTCAGGATGATTA 928
QY 478 GluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaPro 497
Db 929 -----TGTCAAGGTGACATATATTTACACGCTAGT 958
QY 498 LeuThrThrGlu-----AsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGln 515
Db 959 TTAACAGAGCATTGGTACATTTAGTTGAGCGGCATCTGTAAATTTGCTAATGTGA 1018
QY 516 GlyThrGlnVal 519
Db 1019 ACGACACAGATC 1030

RESULT 25
US-10-301-480-65765/c
; Sequence 65765, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65765
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-65765 (1-584)
Alignment Scores:
Pred. No.: 0.0393 Length: 584
Score: 112.00 Matches: 37
Percent Similarity: 44.3% Conservative: 25
Best Local Similarity: 26.4% Mismatches: 50
Query Match: 3.9% Indels: 28
Gaps: 7
```

```
US-10-628-525A-21 (1-539) x US-10-301-480-65765 (1-584)
QY 248 GlyAlaLeuGluTrpValPhe---ProGluTrpAla----- 258
Db 477 GGTTCCTTTTCTGGTCTCTTGTGCCAGCTCGAGTTTGGGGTCAGGAGAAAAGTCTTG 418
QY 259 -----ArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274
Db 417 GGCCTGCAGTTTACAAGACATTTCTAGACAGGCGAGCTTGTGTACCTGAGTC----- 364
QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294
Db 363 TCTCTTGGCAGCTTGGCCACCCTTCTCTGTATCTCTTGGTATATAAAATGGGAGTCTTCA 304
QY 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerArgLysSerValLeuAsn 314
Db 303 ACCAGTGAGGAGGAGAGACAGCTTCTTGTCTTGGCAGAGCTCTCAATCTATC----- 250
QY 315 GlylleValAsnGlylleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332
Db 249 TCACTTGCAGGTGGTATCAGGCTCACCTGATGG---TGTCAAGGAGACTTTTGTCCAATC 193
QY 333 -----IleProCysHisTyrSerValAspAspLeuSerGlyLysAla 346
Db 192 CACTGGGAAAAAGTGTCTGAGCTGTTCTTGTGTAGATCAGGTATCAGAAATGCC 133
QY 347 LysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366
Db 132 AGTTGTGTGCTGCTTCTCTG-----TTGGGTGAGGAGCTTCAAAACATTTCTGCCACTA 79

RESULT 26
US-10-301-480-679174/c
; Sequence 679174, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 679174
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-679174
Alignment Scores:
Pred. No.: 0.0393 Length: 584
Score: 112.00 Matches: 37
Percent Similarity: 44.3% Conservative: 25
Best Local Similarity: 26.4% Mismatches: 50
Query Match: 3.9% Indels: 28
Gaps: 7
```

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DB: 10 Gaps: 7
US-10-628-525A-21 (1-539) x US-10-301-480-679174 (1-584)
Qy 248 GlyAlaLeuGluTrpValPhe---ProGluTrpAla----- 258
Db 477 GGTTCCTTTTCTGGTCTTGTGCGCCAGCTTGTGGGTTCAGGAGAAAGTCTTG 418
Qy 259 -----ArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274
Db 417 GGCCTGCAGTTTACAAAGACATTTTCTAGACAGGCGAGCTTGTCTACCTGAGTC----- 364
Qy 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294
Db 363 TCTCTGCCAGCTGCCACCTTCTCTGTATCTCTGTATATAAAATGGAGTCTTCA 304
Qy 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsn 314
Db 303 ACCAGTGAGGAGGAGAGCAGCTTCTGTGTATCTCTGTATATAAAATGGAGTCTTCA 304
Qy 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsn 314
Db 303 ACCAGTGAGGAGGAGAGCAGCTTCTGTGTATCTCTGTATATAAAATGGAGTCTTCA 304
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys----- 332
Db 249 TCACCTGCAGGTGGTATCAGGCTCACCTGATGG---TGTACAGGAGGACTTTGTGCCAATC 193
Qy 333 -----IleProCysHisTyrSerValAspAspLeuSerGlyLysAla 346
Db 192 CACTGGGAAAAAGTGTCTCCTGAGCTGTTTCTGTGCTAGATCAGGTATCAGGAAATGCC 133
Qy 347 LysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366
Db 132 AGTTGTGATGGCTTCTCTCG-----TTGGGTGAGGAGCTTCAAAACATTTCTGCCACTA 79
RESULT 27
US-10-301-480-65766/c
; Sequence 65766, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US 10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65766
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-65766
Alignment Scores:
Pred. No.: 0.138 Length: 584
Score: 107.00 Matches: 36
Percent Similarity: 43.6% Conservative: 25
Best Local Similarity: 25.7% Mismatches: 51
Query Match: 3.7% Indels: 28
DB: 9 Gaps: 7
US-10-628-525A-21 (1-539) x US-10-301-480-65766 (1-584)
Qy 248 GlyAlaLeuGluTrpValPhe---ProGluTrpAla----- 258
Db 477 GGTTCCTTTTCTGGTCTTGTGCGCCAGCTTGTGGGTTCAGGAGAAAGTCTTG 418
Qy 259 -----ArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274
Db 417 GGCCTGCAGTTTACAAAGACATTTTCTAGACAGGCGAGCTTGTCTACCTGAGTC----- 364
Qy 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294
Db 363 TCTCTGCCAGCTGCCACCTTCTCTGTATCTCTGTATATAAAATGGAGTCTTCA 304
Qy 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsn 314
Db 303 ACCAGTGAGGAGGAGAGCAGCTTCTGTGTATCTCTGTATATAAAATGGAGTCTTCA 304
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys----- 332
Db 249 TCACCTGCAGGTGGTATCAGGCTCACCTGATGG---TGTACAGGAGGACTTTGTGCCAATC 193
Qy 333 -----IleProCysHisTyrSerValAspAspLeuSerGlyLysAla 346
Db 192 CACTGGGAAAAAGTGTCTCCTGAGCTGTTTCTGTGCTAGATCAGGTATCAGGAAATGCC 133
Qy 347 LysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366
Db 132 AGTTGTGATGGCTTCTCTCG-----TTGGGTGAGGAGCTTCAAAACATTTCTGCCACTA 79
RESULT 28
US-10-301-480-679175/c
; Sequence 679175, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US 10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 679175
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-679175
Alignment Scores:
Pred. No.: 0.138 Length: 584
Score: 107.00 Matches: 36
Percent Similarity: 43.6% Conservative: 25
Best Local Similarity: 25.7% Mismatches: 51
Query Match: 3.7% Indels: 28
DB: 10 Gaps: 7
US-10-628-525A-21 (1-539) x US-10-301-480-679175 (1-584)
Qy 248 GlyAlaLeuGluTrpValPhe---ProGluTrpAla----- 258
Db 477 GGTTCCTTTTCTGGTCTTGTGCGCCAGCTTGTGGGTTCAGGAGAAAGTCTTG 418
Qy 259 -----ArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274
Db 417 GGCCTGCAGTTTACAAAGACATTTTCTAGACAGGCGAGCTTGTCTACCTGAGTC----- 364
Qy 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294
Db 363 TCTCTGCCAGCTGCCACCTTCTCTGTATCTCTGTATATAAAATGGAGTCTTCA 304
Qy 295 ThrAlaGluGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsn 314
Db 303 ACCAGTGAGGAGGAGAGCAGCTTCTGTGTATCTCTGTATATAAAATGGAGTCTTCA 304
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys----- 332
Db 249 TCACCTGCAGGTGGTATCAGGCTCACCTGATGG---TGTACAGGAGGACTTTGTGCCAATC 193
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QY 333 -----IleProCysHisTyrSerValAspLeuSerGlyLysAla 346
Db 192 CACTGGAAAAAGTGTCTCTGAGCTGTTCTGCTAGATCAGGTATCAGGAATGCC 133
QY 347 LysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366
Db 132 AGTTGTGATGGCTTCTTCTG-----TTGGGTGAGGAGCTTCMAAACATCTCTGCCACTA 79

RESULT 29
US-10-932-182A-5377
; Sequence 5377, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5377
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-5377

Alignment Scores:
Pred. No.: 0.66 Length: 1353
Score: 105.00 Matches: 63
Percent Similarity: 36.3% Conservative: 40
Best Local Similarity: 22.2% Mismatches: 101
Query Match: 3.6% Indels: 80
DB: 9 Gaps: 12

US-10-628-525A-21 (1-539) x US-10-932-182A-5377 (1-1353)
QY 220 IleLeuValIleHisAsn-----LeuAlaHisGlnGlyValGluPro 233
Db 256 ATCCAGATGTTTCATCTCTCATGAGCTTCCACATTTGCCCATGAGGGGATCTGTCAT 315
QY 234 AlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTrpVal 253
Db 316 GCCAATACGATG-----GGATTAAGAAGACTGTC 342
QY 254 PheProGlu-----TrpAlaArgHis 261
Db 343 TTCACAGACCATTCATTTATGTTTCATATATCAATCTAATCTCGATTTGGGTGAACAG--- 399
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArg 281
Db 400 -----TTATTAACTTTTCTTGTGACAAATATAGTAGG 432
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGly 301
Db 433 GTTATCTGTGTTTCAAT-----ACATGCAAGAAATAATATGATTGTT 474
QY 302 LeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAsp 321
Db 475 AGAACAGAAATG-----AAACAGATATATTATTCGTTGATTCGGAACGACGATGGTC 525
QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341
Db 526 ACTGAAGATTTTAAGCCAGA-----GACCCTGATAAT 558
QY 342 LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArg 361
Db 559 AACACGAGAGAAAGACGGGTAAA----- 582
QY 362 ProAspValProIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 381
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Db 583 ---GATAAGATAGTATTGTTAGTATTGGAAGACTCTTTCCGAATAAAGGGTCTGATTG 639
QY 382 IleGlnLeuIleIleProAspLeu-----MetArgGluAspValGlnPheValMetLeu 399
Db 640 CTTACTCGTATCATTTCCAAAAGTTTGTCTCCACACATGAAGAAGTAGAATTTATAGTTGCT 699
QY 400 GlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAsp 419
Db 700 GGTGATGGT---CCCAAAATTCATTGATTTTCAACAAATGATTGAAACTTATAGACTGCAA 756
QY 420 LysPheArgGlyTrpValGlyPheSerValProValSerHisArg-----Ile 435
Db 757 AAACGTGTTCAACTTTTGGGA-----TCCGTTGCTCATGAAAAGGTAAGAGATGTT 807
QY 436 ThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGln 455
Db 808 TTGTGTCAGAGCGATATATATTGTCATGCTAGTTTGACAGAAGCATTTGGTACAATTCTA 867
QY 456 LeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAsp 475
Db 868 GTAGAGGCTGTCATCTCTGCAATTACTGATTGTTAACAACCCAGGTTGGGGGTATTCCAGAG 927
QY 476 ThrValGluAsn 479
Db 928 GTGCTACCCAAT 939

RESULT 30
US-10-932-182A-5377
; Sequence 5377, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5377
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-5377

Alignment Scores:
Pred. No.: 0.66 Length: 1353
Score: 105.00 Matches: 63
Percent Similarity: 36.3% Conservative: 40
Best Local Similarity: 22.2% Mismatches: 101
Query Match: 3.6% Indels: 80
DB: 9 Gaps: 12

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Db 316 GCCAATACGATG-----GGATTAAGAAGACTGTC 342
QY 254 PheProGlu-----TrpAlaArgHis 261
Db 343 TTCACAGACCATTCATTTATGTTTCATATATCAATCTAATCTCGATTTGGGTGAACAG--- 399
QY 262 AlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArg 281
Db 400 -----TTATTAACTTTTCTTGTGACAAATATAGTAGG 432
QY 282 IleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGly 301
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Db 475 AGAACAGAAATG-----AAACAGATATATTATTCGTTGATTCGGAACGACGATGGTC 525
QY 322 IleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp 341
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Post-processing: Minimum Match 0%

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# SUMMARIES

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5	2861	98.9	1749	49	US-10-336-753-52
6	2861	98.9	1752	28	US-09-625-406-12
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Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 52, Appl  
Sequence 52, Appl  
Sequence 12, Appl  
Sequence 12, Appl



## RESULT 1

US-09-625-406-20  
 ; Sequence 20, Application US/09625406  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keeling, Peter  
 ; APPLICANT: Guan, Hanning  
 ; TITLE OF INVENTION: Starch Encapsulation  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
 ; STREET: 5370 Manhattan Circle  
 ; CITY: Boulder  
 ; STATE: CO  
 ; COUNTRY: US  
 ; ZIP: 80303  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/625,406  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/941,445  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Winner, Ellen P  
 ; REGISTRATION NUMBER: 28,547  
 ; REFERENCE/DOCKET NUMBER: 89-97  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 499-8080  
 ; TELEFAX: (303) 499-8089  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1620 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: not relevant  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHEICAL: NO  
 ; FEATURES:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..1620  
 ; US-09-625-406-20

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## RESULT 2

US-10-628-525-20

; Sequence 20, Application US/10628525

; GENERAL INFORMATION:

; APPLICANT: Keeling, Peter

; Guan, Hanping

; TITLE OF INVENTION: Starch Encapsulation

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

; STREET: 5370 Manhattan Circle

; CITY: Boulder

; STATE: CO

; COUNTRY: US

; ZIP: 80303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/628,525

; FILING DATE: 28-Jul-2003

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/941,445

; FILING DATE: 30-SEP-1997

; APPLICATION NUMBER: US 60/026,855

; FILING DATE: 30-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Winner, Ellen P

; REGISTRATION NUMBER: 28,547

; REFERENCE/DOCKET NUMBER: 89-97

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 499-8080

; TELEFAX: (303) 499-8089

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1620 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: Not Relevant

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1620

; SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-10-628-525-20

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Pred. No.:

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Length:

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Query Match: 100.0%

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DB: 53

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QY 41 GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerPro 60

Db 121 GAGCAAGCTCGAGCTAAAGATAACACAAAGCAATGTCTTTGTAAACCGCGGAAGCTTCTCT 180

QY 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAla 80

Db 181 TATGCAAAAGTCTGGGGGCTTAGAGATGTTTGTGTTTCAATGCCAGTTGCTCTTGTCTCT 240

QY 81 ArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsn 100

Db 241 CGTGTCAACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACCTCCGATAAAGAT 300

QY 101 TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHis 120

Db 301 TATGCAAAATGCAATTTTACACAGAAAAACACATTCGATTCATGCTTTGGCGGTGAACAT 360

QY 121 GluValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisPro 140

Db 361 GAAGTTACCTTCTCCATGAGTATAGAGATTGAGTTGACTGGGTGTTTGTGTTGATCATCCC 420

QY 141 SerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGln 160

Db 421 TCATATACACAGACCTGGAAATTTATATGAGATAAGTTTGGTGTCTTTGGTGATAATCAG 480

QY 161 PheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGly 180

Db 481 TTCAGATACACACTCCTTTGCTATGTCATGTGAGGCTCCTTTGATCCTTGAATGGGA 540

QY 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuVal 200

Db 541 GGATATATTTATGGACAGATTGCATGTTGTTGTCATGATTGGCATGCCAGTCTAGTG 600

QY 201 ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220

Db 601 CCAGTCTCTTCTGCTGCAAAATATAGACCATATGTTGTTTATAAAGACTCCCGCAGCAT 660

QY 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240

Db 661 CTTGTAATACATAATTTTAGCACAATCAGGGTGTAGAGCTGCAAGCACATATCTGACCTT 720

QY 241 GlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260

Db 721 GGGTTGCCACTGAATGTTATGGAGCTCTGGAGTGGGTATTTCCCTGAATGGCGGAGG 780

QY 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280

Db 781 CATGCCCTTGACAGGGTGAGGAGTAAATTTTTTGAAGGGTGCAAGTTGTGACAGCAGAT 840

QY 281 ArgIleValThrValSerLysGlyTyrSerTyrGluValThrThrAlaGluGlyGln 300

Db 841 CGAATCGTACTGTTCAGTAAGGGTTATTTCTGGGGAGGTGACAACTGCTGAAGGTGACAG 900

QY 301 GlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320

Db 901 GGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAAATTTGAATGGAAT 960

QY 321 AspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340

Db 961 GACATTAATGATTGGAACCTGCCACAGCAAAATGATATCCCTGTCATTAATTCGTGTTGAT 1020  
 Qy 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIle 360  
 Db 1021 GACCTCTCTGGAAAGGCCAAATGTAAGGTGCATTGCGAAGGAGCTGGGTTTACCTATA 1080  
 Qy 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyLysAsp 380  
 Db 1081 AGGCTGATGTTCTCTGATTGGCTTTATTTGGAAGGTGGATTATTCAGAAAGGCATTGAT 1140  
 Qy 381 LeuIleGlnLeuIleLeuProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 Db 1141 CTCAATCAACTTATCATCAGATCTCATCGGGAAGATGTTCAATTTGTCATGCTTGA 1200  
 Qy 401 SerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLys 420  
 Db 1201 TCTGSGTGAACCCAGAGCTTGAAGATTGGATGAGATCTACAGATCGATCTTCAAGGATAA 1260  
 Qy 421 PheArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
 Db 1261 TTTCTGTTGATGGGTGGATTAGTGTTCAGATTTCACCGAATAACTGCGCGCTCGAT 1320  
 Qy 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
 Db 1321 ATATTGTTAATGCAATCCAGATTGCAACCTTGTTGGTCTCAATCAGCTATATGCTATGCG 1380  
 Qy 461 TyrGlyThrValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPhe 480  
 Db 1381 TATGGCAGAGTCTCTGTTGTCATGCACTGGGGGCTTAGAGATACCGTGGAGAACTTC 1440  
 Qy 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThr 500  
 Db 1441 AACCCCTTTGGTGGAAATGAGAGCAGGGTACAGGGTGGGCATTTCGCACCCCTTAACCA 1500  
 Qy 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520  
 Db 1501 GAACAATGTTTGTGACATTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1560  
 Qy 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
 Db 1561 CTGGGAAGGGCTAATGAAGCGAGGCATGTCAAAAGACTTCACGTGGGACCATGCCGC 1617

RESULT 3

US-10-628-525A-20  
 ; Sequence 20, Application US/10628525A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KEELING, PETER  
 ; APPLICANT: GAUN, HANPLING  
 ; TITLE OF INVENTION: STARCH ENCAPSULATION  
 ; FILE REFERENCE: 15056-04  
 ; CURRENT APPLICATION NUMBER: US/10/628, 525A  
 ; PRIOR FILING DATE: 2003-07-28  
 ; PRIOR APPLICATION NUMBER: 09/625,406  
 ; PRIOR FILING DATE: 2000-07-25  
 ; PRIOR APPLICATION NUMBER: 08/941,445  
 ; PRIOR FILING DATE: 1997-09-30  
 ; PRIOR APPLICATION NUMBER: 60/026,855  
 ; PRIOR FILING DATE: 1996-09-30  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: PatentIn Ver. 3.3  
 ; SEQ ID NO 20

LENGTH: 1620  
 TYPE: DNA  
 ORGANISM: Zea mays  
 FEATURES:  
 NAME/KEY: CDS  
 LOCATION: (1)..(1617)  
 US-10-628-525A-20

Alignment Scores:  
 Pred. No.: 0 Length: 1620  
 Score: 2893.00 Matches: 539  
 Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 53 Gaps: 0  
 US-10-628-525A-21 (1-539) x US-10-628-525A-20 (1-1620)  
 Qy 1 CyValAlaGluLeuSerArgGluAspLeuGlyLeuGluProGluGlyIleAlaGluGly 20  
 Db 1 TGGCTCGCGAGCTGAGCAGGAGGACCTCGGCTCGAACCCTGAAGGGATTGCTGAAGGT 60  
 Qy 21 SerIleAspAsnThrValValAlaSerGluGlnAspSerGluIleValValGlyLys 40  
 Db 61 TCCATCGATAACACAGTAGTGTGGCAAGTAGACCAAGATTCTGAGATTGTGGTGGAAAG 120  
 Qy 41 GluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerPro 60  
 Db 121 GAGCAGCTCGAGCTAAGTAAACAAAGCATTGCTTTGTAAACCGCGGAGGCTTCCTCT 180  
 Qy 61 TyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAla 80  
 Db 181 TATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTTGCTTGTGCT 240  
 Qy 81 ArgGlyHisArgValMetValMetProArgTyrLeuAsnGlyThrSerAspLysAsn 100  
 Db 241 CGTGGTCAACCGTGTGATGGTGTGTAATGCCCAGATATTTAAATGCTACCTCCGATAAG 300  
 Qy 101 TyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHis 120  
 Db 301 TATGCAAAATGCAATTTTACACAGAAAACACATTCGGATTCATGCTTTGGCGGTGAAC 360  
 Qy 121 GluValThrPhePheHisGluTyrArgAspSerValAspTyrValPheValAspHisPro 140  
 Db 361 GAAGTTACCTTCTTCCATGATATAGATTCAGTTGACTGGGTGTTTGTGTGATCATCCC 420  
 Qy 141 SerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGln 160  
 Db 421 TCATATACACAGACCTCGAATTTATATGGAGATAAGTTTGGTGGCTTTTGGTGTATAATC 480  
 Qy 161 PheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGly 180  
 Db 481 TTCAGATACACACTCCTTTGCTATGCTGATGAGGCTCCTTTTGAATTCCTTTGAATTTGG 540  
 Qy 181 GlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrPheHisAlaSerLeuVal 200  
 Db 541 CGATATATTTATGGACAGAAATTCATGTTTGTCAATGATTTGGCATGCCAGTCTAGTG 600  
 Qy 201 ProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle 220  
 Db 601 CCAGTCTCTTCTGCTGCAAAATATAGACCATATGTTGTTTATAAAGACTCCCGCAGCAT 660  
 Qy 221 LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu 240  
 Db 661 CTGTATATACATATTTAGCACATCAGGGGTGTAGAGCCTGCAAGCACATATCTCTGACCT 720  
 Qy 241 GlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArg 260  
 Db 721 CGGTTGCCACCTGAATGGTATGAGCTCTGGAGTGGGTATTCCTCAATGGCGGAGGAGG 780  
 Qy 261 HisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValValThrAlaAsp 280  
 Db 781 CATGCCCTTGCACAGGGGTGAGCAGTTAAATTTTTGAAAGGTGCAGCTTTGTGACAGCAT 840  
 Qy 281 ArgIleValThrValSerLysGlyTyrSerTyrGluValThrAlaGluGlyGlyGln 300  
 Db 841 CGAATCGTGACTGTCAAGTAAAGGGTTATTCGTGGAGGTCACAACTGCTGNAGGTGACAG 900  
 Qy 301 GlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIle 320  
 Db 901 GGCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTATTATAAAGCGAATTTGTAATGCAATT 960  
 Qy 321 AspIleAsnAspTyrAsnProAlaThrAspLysCysIleProCysHisTyrSerValAsp 340  
 Db 961 GACATTAATGATTGGAAACCTCCACAGACAAATGATGATCCCTGTCATTTCTGTTGAT 1020

QY 341 AspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProfil 360  
 DB 1021 GACCTCTCTGGAAAGGCCAATGTAAGGTGCAATGTCAGAAAGAGCTGGGTACTATA 1080  
 QY 361 ArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyLeuAsp 380  
 DB 1081 AGGCTGTGATGTTCTCTGATTGGCTTTATTGGAAGGTGGATTATCAGAAAGCATTTGAT 1140  
 QY 381 LeuIleGlnLeuIlePheProAspLeuMetArgGluAspValGlnPheValMetLeuGly 400  
 DB 1141 CTCATTTCAACTTATCATACAGATCTCATGCGGGAAGATGTTCAATTTGTCTATGCTTGA 1200  
 QY 401 SerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLys 420  
 DB 1201 TCTGTGTACCCAGAGCTTGAAGATTGGATGAGATCTACAGATCGATCTTCAAGATATA 1260  
 QY 421 PheArgGlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAsp 440  
 DB 1261 TTTCTGTGGATGGTTGGATTAGTTGTTCCAGTTTCCACCGAATAACTGCGCGCTGCCAT 1320  
 QY 441 IleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGln 460  
 DB 1321 ATATTGTTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTATATGCTATGCAG 1380  
 QY 461 TyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPhe 480  
 DB 1381 TATGSCACAGTTCCTGTGTGTCATGCACTGGGGGCTTAGAGATACCGTGAGAACTTC 1440  
 QY 481 AsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThr 500  
 DB 1441 AACCCCTTTCGGTGAGAAATGAGAGCAGGGGTACAGGGTGGGCATTGCAACCCCTAACCCACA 1500  
 QY 501 GluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeu 520  
 DB 1501 GAANACATGTTTGTGGACATTCGAACTCGAATATCTACATACAGGGAACACAAAGTCTCTC 1560  
 QY 521 LeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539  
 DB 1561 CTGGGAAGGGCTAATGAAGCAGGCAATGTCAANAGACTTCACGTGGACCATGCCGC 1617

RESULT 4

US-09-402-254-52  
 ; Sequence 52, Application US/09402254  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Guan, Hanning  
 ; APPLICANT: Keeling, Peter L.  
 ; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN  
 ; TITLE OF INVENTION: HOSTS  
 ; FILE REFERENCE: 2461-52  
 ; CURRENT APPLICATION NUMBER: US/09/402,254  
 ; CURRENT FILING DATE: 1999-10-01  
 ; EARLIER APPLICATION NUMBER: PCT/US98/06660  
 ; EARLIER FILING DATE: 1998-04-03  
 ; EARLIER APPLICATION NUMBER: 60/042,939  
 ; EARLIER FILING DATE: 1997-04-04  
 ; NUMBER OF SEQ ID NOS: 77  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 52  
 ; LENGTH: 1749  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1749)  
 US-09-402-254-52  
 Alignment Scores:  
 Pred. No.: 0 Length: 1749  
 Score: 2861.00 Matches: 539  
 Percent Similarity: 92.5% Conservative: 0  
 Best Local Similarity: 92.5% Mismatches: 0  
 Query Match: 98.9% Indels: 44

DB: 24 Gaps: 1  
 US-10-628-525a-21 (1-539) x US-09-402-254-52 (1-1749)  
 QY 1 CysValAlaGluLeuSerArgGlu-----8  
 DB 1 TGCCTCGCGGAGCTGAGCAGGGAGGGCGCGCGCGCGCGCTGCCACCCCGCTGCTG 60  
 QY 8 -----8  
 DB 61 GCGCCCCCGCTCGTCCCGGCTTCTCTCGCGCGCGCGCGCGAGCCCGCGGTGAGCGCGCA 120  
 QY 9 -----AspLeuGlyLeuGluProGluGly 16  
 DB 121 TCGACGCGCGCGCGCTGCCCGACCGCGCGCTCGGGGACCTCGGTCTCGAACTGNAGGG 180  
 QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaLaserGluGlnAspSerGluIle 36  
 DB 181 ATTGCTGAAGGTTCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 240  
 QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
 DB 241 GTGGTTGGAAGGAGCAAGCTCGAGCTAAAGTAAACAAAGCATTTGCTTTGTAACCGGC 300  
 QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
 DB 301 GAAGCTTCTCTTATGCAAGCTCTGGGGGTCTAGGAGATGTTTGTGGTTCATTTGCCAGTT 360  
 QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
 DB 361 GCTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
 DB 421 TCCGATAAGAAATATGCAAAATGCAATTTTACACAGAAATAACACATTCGGATTCCATGCTTT 480  
 QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
 DB 481 GCGGTGAACTGAAGTTACCTTCTTCCATGAGTATAGAGATTTCAGTTGACCTGGGTGTTT 540  
 QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
 DB 541 GTTGATCATCCTCATATCACAGACTCGAAATTTATATGAGATAAAGTTTGGTGTCTTT 600  
 QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
 DB 601 GGTGATAATCATGTCAGTACAGATACACACTCTCTTGTCTATGCTGCAATGAGGCTCCTTTGATC 660  
 QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
 DB 661 CTGTGAATTTGGAGGATATATTTATGACAGAAATTCATGTTGTTGTCATGATTGGCAT 720  
 QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
 DB 721 GCCAGTCTAGTCCAGTCTCTTCTGCTGCAAAATATAGACCATATGTTGTTTATAAAGAC 780  
 QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
 DB 781 TCCCGCAGCATTTCTGTATATACATAATTTAGCACATCAGGGGTGAGAGCTCGAACGACA 840  
 QY 237 TyrProAspLeuGlyLeuProGluTyrPyrGlyAlaLeuGluTyrPyrValPheProGlu 256  
 DB 841 TATCTGACCTTGGGTTCGCACCTGATGATGAGCTCTCGAGTGGGTATTTCCCTGAA 900  
 QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
 DB 901 TGGGCGAGGAGCATGCCCTTGACAAAGGTGAGGAGTTAATTTTGAAGGTGCGAGTT 960  
 QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrPyrGluValThrAla 296  
 DB 961 GTGACAGAGATCGAATCGTGTCTGAGTAGGGTTATTCGTGGAGGTGCAACTGCT 1020  
 QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316



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Db 1021 GAAGTGGACAGGCCCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGGAATT 1080
Qy 317 ValaenGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 1081 GTRAAATGGAATTGACATTAATGATTGGAACCTGCCACAGCAAAATGTATCCCTGTGCAT 1140
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 1141 TATTCTGTTGATGACCTCTCTGGAAGGCCAAATGTAAAGGTGCTATTCAGAAAGAGCTG 1200
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1201 GGTTCACCTAATAGGCTGATGTCCTCTGATTGGCTTTATTGGAAGTTGGATTATCAG 1260
Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1261 AAAGGCATTGATCTCATCACTCAATCAATCAGATCTCATCGGAGAGATGTTCAATTT 1320
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
Db 1321 GTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTCGATC 1380
Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436
Db 1381 TTCAGGATAAATTTTCGTGATGGGTGGATTAGTGTCCAGTTTCCCAACCGAATAACT 1440
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1441 GCCGGCTCGGATATATTGTAATGCCATCCAGATTGCACTTGTGGTCTCAATCAGCTA 1500
Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1501 TATGCTATGCAATGATGCGACAGTTCCTGTTGTCATGCAACTGGGGGCTTAGAGATACC 1560
Qy 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496
Db 1561 GTGGAGAACTTCAACCTTTTCGTGGTGAAGTGGAGAGAGGGTACAGGGTGGGCAATTCGCA 1620
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
Db 1621 CCCCTAACACACAGAAACATGTTTGGACATTCGCACTGCAATATCTACATACAGGA 1680
Qy 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 1681 ACACAGTCTCTCTGGGAAGGGCTAATGAAGCGAGGCATGTCAAAAGACTTCACGTGGCA 1740
Qy 537 ProCysArg 539
Db 1741 CCATGCCGC 1749
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## RESULT 5

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US-10-336-753-52
; Sequence 52, Application US/10336753
; GENERAL INFORMATION:
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; TITLE OF INVENTION: HOSTS
; FILE REFERENCE: 2461-52
; CURRENT APPLICATION NUMBER: US/10/336,753
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/09/402,254
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 1749
; TYPE: DNA
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; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1749)
US-10-336-753-52
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## Alignment Scores:

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Pred. No.: 0 Length: 1749
Score: 2861.00 Matches: 539
Percent Similarity: 92.5% Conservatives: 0
Best Local Similarity: 92.5% Mismatches: 0
Query Match: 98.9% Indels: 44
DB: 49 Gaps: 1
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US-10-628-525A-21 (1-539) x US-10-336-753-52 (1-1749)

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Qy 1 CysValAlaGluLeuSerArgGlu-----8
Db 1 TGCCTCGCGAGCTGAGCAGAGGGGGCCGCCGCCGCGCTGCCACCCTGGCTGCTG 60
Qy 8 -----8
Db 61 GCGCCCCCGCTCGTGCCTCGCTCTCTCGCGCCGCCGCCGCGCGAGCCCGGCA 120
Qy 9 -----AspLeuGlyLeuGluProGluGly 16
Db 121 TCGACGCCGCCGCCCTGCGCGAGCGCGCTGGGGGACCTCGGTCTCGAACCTGAAGG 180
Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36
Db 181 ATTGCTGAAGGTTCATCGATAACACAGTAGTTGTGGCAAGTCAGCAAGATTCTGAGATT 240
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 241 GTGGTTGGAAAGAGAGCAGCTCGAGCTAAAGTAAACAAGCAAGCATTTGTTGAACGGC 300
Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 301 GAAGCTTCTCTTATGCAAAAGTCTGGGGGTCTAGGAGATGTTTGTGTTTCATTGCCAGTT 360
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrIleuAsnGlyThr 96
Db 361 GCTCTTGTGCTCGTGGTCACTCGGTGATGGTGTGTAATCCAGATATTTAAATGGTACC 420
Qy 97 SerAspLysAsnTyrAlaAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
Db 421 TCCGATAGAAATATGCAAAATGCAATTTTACACAGAAAACACATTCGGATTCCATGCTTT 480
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136
Db 481 GCGCGTGAACATGAAGTTACCTTCTTCCATGATATAGAGATTTCAGTTGAGTGGTGT 540
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156
Db 541 GTTGATCATCTCCCTCATATCACAGACTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT 600
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 601 GGTGATATTCAGTTCAGATACACACTCTCTTCTGCTATGCTGTCATGTGAGGCTCTCTTTGATC 660
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196
Db 661 CTTGAATTGGGAGGATATATTTATGGACAGAAATTCATGTTGTTGTTGTCATGATTCGCAT 720
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 721 GCCAGTCTAGTGCCAGTCTCTTCTGCTGCAAAATATAGACCATATGCTGTTTATAAAGAC 780
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 781 TCCCCGAGCATTTCTTGTATATCATTAATTTAGCACATCAGGGGTGAGAGCTTCGACAGCA 840
Qy 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256
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; PRIOR APPLICATION NUMBER:	60/026,855				
; PRIOR FILING DATE:	1996-09-30				
; NUMBER OF SEQ ID NOS:	40				
; SOFTWARE:	PatentIn Ver. 3.3				
; SEQ ID NO 12					
; LENGTH:	1752				
; TYPE:	DNA				
; ORGANISM:	Zea mays				
; FEATURE:					
; NAME/KEY:	CDS				
; LOCATION:	(1)..(1749)				
US-10-628-525A-12					
<hr/>					
Alignment Scores:					
Pred. No.:	0	Length:	1752		
Score:	2861.00	Matches:	539		
Percent Similarity:	92.5%	Conservative:	0		
Best Local Similarity:	92.5%	Mismatches:	0		
Query Match:	98.9%	Indels:	44		
DB:	53	Gaps:	1		
<hr/>					
US-10-628-525A-21 (1-539) x US-10-628-525A-12 (1-1752)					
Qy	1 CysValAlaGluLeuSerArgGlu-----	8			
Db	1 TGCCTCGCGAGACTGAGCAGGGAGGCCGCGCCGCGCTCGATCGCACCCCGCTGCTG	60			
Qy	8 -----	8			
Db	61 GCGCCCCGCTGTGTCCCGGCTTCCTCGCGCCGCGCGACGACCCACGGTGAGCGCGCA	120			
Qy	9 -----	16			
Db	121 TCGACGCGCGCCCGTGCACGCGCGCTGGGGGACCTCGGTCTCGAACTGAGGG	180			
Qy	17 IleAlaGluGlySerIleAspAsnThrValValAlaLasSerGluGlnAspSerGluIle	36			
Db	181 ATTGCTGAAGTTCCATCGATAACAACAGTAGTTGTGGCAAAGTGGCAAGATTCTGAGATT	240			
Qy	37 ValValGlyLyseGluGlnAlaArgAlayValThrGlnSerIleValPheValThrGly	56			
Db	241 GTGGTTGGAAGGAGCAGCTCGAGCTTAAGTAAACAAAAGCATTTGTCTTTGTAAACCGCG	300			
Qy	57 GluAlaSerProTyrrAlaLyseSerGlyGlyLeuGlyAspValCysGlySerLeuProVal	76			
Db	301 GAAGCTTCTCTTATGCAAGTCTGGGGGTCTAGAGAGATGTTTGTGTTTCATTGCCAGTT	360			
Qy	77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrrIleuAsnGlyThr	96			
Db	361 GCTCTTGCTGCTGTGTGTGCACGCTGTGATGGTTGTAATGCCCAGATATTTAAATGGTACC	420			
Qy	97 SerAspLyseAsnTyrrAlaAsnAlaPheTyrrThrGluLyseHisIleArgIleProCysPhe	116			
Db	421 TCCGATTAAGAATTAATGCAAAATGCAATTTACACAGAAAAACACATTCGGATTCCATGCTTT	480			
Qy	117 GlyGlyGluHisGluValThrPhePheHisGluTyrrArgAspSerValAspTrpValPhe	136			
Db	481 GGCGGTGAACATGAAGTTACCTTCTTCCATGAGTATAGAGATTCAAGTTGACCTGGGTGTTT	540			
Qy	137 ValAspHisProSerTyrrHisArgProGlyAsnLeutyrrGlyAspLysePheGlyAlaPhe	156			
Db	541 GTTGATCATCCCTCATATCACAGACCTGGAAATTTATATGGAGATAAGTTTTGTGCTGCTTT	600			
Qy	157 GlyAspAsnGlnPheArgTyrrThrLeuLeuCysTyrrAlaAlaCysGluAlaProIleulle	176			
Db	601 GGTGATTAATCAAGTTACAGATACACACTCCCTTTGCTATGCTGCATGTGAGGCTCCTTTGATC	660			
Qy	177 LeuGluLeuGlyGlyTyrrIleTyrrGlyGlnAsnCysMetPheValValAsnAspTrpHis	196			
Db	561 CTGGATTGGAGGAGATATTTATGGACAGAAATTCGCAATGTTTGTGTCATGATTGGCAT	720			
Qy	197 AlsSerLeuValProValLeuLeuAlaAlalystyrrArgProTyrrGlyValtyrLyseasp	216			

RESULT 9  
US-11-096-568A-26590  
; Sequence 26590, Application US/11096568A

US-11-096-568A-26590  
; Sequence 26590, Application US/11096568A

GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therapy  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 26590  
; LENGTH: 2970  
; TYPE: DNA  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc. feature  
; LOCATION: (1) - (2970)  
; OTHER INFORMATION: Ceres Seq. ID no. 13579604  
US-11-096-568A-26590

Alignment Scores:  
Pred. No.: 0 Length: 2970  
Score: 2861.00 Matches: 539  
Percent Similarity: 92.5% Conservative: 0  
Best Local Similarity: 92.5% Mismatches: 0  
Query Match: 98.9% Indels: 44  
DB: 69 Gaps: 1

US-10-628-525A-21 (1-539) x US-11-096-568A-26590 (1-2970)

QY	1	CysValAlaGluLeuSerArglu	-----8
DB	719	TGCGTGGCGAGCTGAGCAGGAGGGCCGCGCGCGCGCGCTGCCACCCCGCTGCTG 778	
QY	8	-----8	
DB	779	GGCGCCCGCTCGTGCCTGGCTTCTCGCGCGCGCGCGCGAGCCACCGGGTGAGCGCGCA 838	
QY	9	-----AspLeuGlyLeuGluProGluGly 16	
DB	839	TCGACGCGCCCGCTGCCGACGCGCGCTGGGGGACCTCGGTCTCGAACCTCGAAGGG 898	
QY	17	IleAlaGluGlySerIleAspAsnThrValValAlaIleSerGluGlnAspSerGluIle 36	
DB	899	ATTGCTGAAGGTTCCATCGATAACACAGTAGTGTGGCAAGTGAGCAAGATTCTGAGATT 958	
QY	37	ValValGlyGlyGluAlaArgAlaValThrGlnSerIleValPheValThrGly 56	
DB	959	GTGGTTGGAAGGAGCAGCTCGAGCTAAGTAACACAAAGCATTTGTCTTTGTAACCGGC 1018	
QY	57	GluAlaSerProTyrAlaIleSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76	
DB	1019	GAAGCTTCTCTTATGCAAGTCTGGGGTCTAGGAGATGTTTGTGTTTCATTGCCAGTT 1078	
QY	77	AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96	
DB	1079	GCTCTTGCTGCTCGTGGTCCCGTGTGATGGTTGTAATGCCAGATATTTAAATGGTACC 1138	
QY	97	SerAspIleAsnTyrAlaAsnAlaPheTyrThrGluIleHisIleArgIleProCysPhe 116	
DB	1139	TCCGATAAGAATTATGCAAAATGCAATTTTACACAGAAACACATTCGGATTCCATGCTTT 1198	
QY	117	GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136	
DB	1199	GGCGGTGACATGAAGTTACCTTCTTCATGATATAGAGATTTCAGTTGACTGGGTGTTT 1258	
QY	137	ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspIlePheGlyAlaPhe 156	
DB	1259	GTTGATCATCCCTCATATCAGACCTGGAAATTTATATGAGATAAGTTTGGTGGCTTTT 1318	
QY	157	GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176	
DB	1319	GGTGATAATCAGTTCCAGATACACATCTCTTTGCTATGCTGATGTGAGGCTCCCTTTGATC 1378	
QY	177	LeuGluLeuGlyGlyIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196	

DB	1379	CTTGAAATTTGGGAGGATATATTTATGACAGAAATTCAGATGTTTGTGTCATGATTGGCAT 1438	
QY	197	AlaSerLeuValProValLeuLeuAlaIalatyfyrArgProTyrGlyValTyrIysAsp 216	
DB	1439	GCCAGTCTAGTGCCAGTCCCTTCTTCTGCTCAAAATATAGACCATATGGTGTATTAAGAC 1498	
QY	217	SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProIleAspThr 236	
DB	1499	TCCCGCAGCATTCTTTGTAATACATAATTTAGCACATCAGGGGTAGAGCCTCAAGCACCA 1558	
QY	237	TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256	
DB	1559	TATCTGTACCTTGGGTGGCCACCTGAATGGTATGAGCTCTGGAGTGGGTATTCCTCTGAA 1618	
QY	257	TrpAlaArgArgHisAlaLeuAspIysGlyGluAlaValAsnPheLeuIysGlyAlaVal 276	
DB	1619	TGGCGCAGGAGCATGCCCTTGACAAAGGTGAGGCAGTTAATTTTGAAGGTGCAGTT 1678	
QY	277	ValThrAlaAspArgIleValThrValSerIysGlyTyrSerTyrGluValThrAla 296	
DB	1679	GTGACAGCAGATCGAATCGTGAATGAGGTATTCGTGGAGGTCACAACTGCT 1738	
QY	297	GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgIysSerValLeuAsnGlyIle 316	
DB	1739	GAAGGTGACAGGCGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTATTTAAACCGAATT 1798	
QY	317	ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspIysCysIleProCysHis 336	
DB	1799	GTAAATGGAATTGACATTAATGATTTGGAACCTGTCACAGACAAATGTATCCCTGTCTAT 1858	
QY	337	TyrSerValAspAspLeuSerGlyIysAlaIysCysIysGlyAlaLeuGlnIysGluLeu 356	
DB	1859	TATCTGTGTGATGACCTCTCTGGAAAGGCCAAATGTAAGGTGCATTCGAGAGGAGCTG 1918	
QY	357	GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376	
DB	1919	GGTTTACCTATAGGCTGATGTTCTCTGATGGCTTTATGGAGGTGGATATATCAG 1978	
QY	377	IysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396	
DB	1979	AAAGGCATTGATCTCATTTCAACTTATCATACAGATCTCATCGGGGAAGATGTTCAATTT 2038	
QY	397	ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416	
DB	2039	GTCATGCTTGGATCTGGTGACCCAGAGCTTGAAGATTGGATGAGATCTACAGAGTGCATC 2098	
QY	417	PheIysAspIysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436	
DB	2099	TTCAAGGATTAATTTCTGGATGGGTGGATTTAGTGTTCAGTTTCCACCGAATAACT 2158	
QY	437	AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456	
DB	2159	GCCGCTCGCATATATTTGTAATGCCATCCAGATTCGAACCTTTGTGGTCTCAATCAGCTA 2218	
QY	457	TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476	
DB	2219	TATGCTATGCAATGAGTGGCACAGTTCCTGTTGTCATGCAACTGGGGGCTTAGAGATACC 2278	
QY	477	ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496	
DB	2279	GTGGAGAACTTCAACCTTTTCGGTGAGATGGAGAGCAGGGTACAGGGTGGGCACTTCGA 2338	
QY	497	ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516	
DB	2339	CCCCTAACCAACAGAAAACATGTTTGTGACATTCGAACTGCAATATCTACATACAGGA 2398	
QY	517	ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValIysArgLeuHisValGly 536	
DB	2399	ACAAAGTCTCTCTGGGAAGGGCTAATGAGCGAGGCATGTCAAAAGACTTCCACGTGGGA 2458	
QY	537	ProCysArg 539	









437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
438 GCGGCGCGGATATATTTAAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 774  
439 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
440 TATGCTATGCGATGATGCGACAGTTCCTTGTGTCATGCACTGGGGCCCTTAGAGATACC 714  
441 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAla 496  
442 GTGAGAGAACTTCAACCCCTTTCGGTGAGATGGAGAGCAGGATACAGGGTGGCATTCGCA 654  
443 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
444 CCCCTAACCCAGAAAACATGTTTGTGGACATTCGGAATTCGAATATCTACATACAGGA 594  
445 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValIysArgLeuHisValGly 536  
446 ACACAGTCTCTCTGGAGAGGCTTATGAAGCGGAGGATGTCAAAAGACTTTCAGTGGGA 534  
447 ProCysArg 539  
448 CCATGCCGC 525

RESULT 12  
US-60-094-436-12  
; Sequence 12, Application US/60094436  
; GENERAL INFORMATION:  
; APPLICANT: Lightner, Jonathan E.  
; APPLICANT: Broglie, Karen E.  
; APPLICANT: E. I. du Pont de Nemours and Company  
; TITLE OF INVENTION: Modification of Starch Biosynthetic Enzyme Gene  
; TITLE OF INVENTION: Expression to Produce Starches in Grain Crops  
; FILE REFERENCE: BB-1147-P1  
; CURRENT APPLICATION NUMBER: US/60/094,436  
; CURRENT FILING DATE: 1998-07-28  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Microsoft Word Version 7.0A  
; SEQ ID NO 12  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-60-094-436-12

Alignment Scores:  
Pred. No.: 0 Length: 2008  
Score: 2832.00 Matches: 538  
Percent Similarity: 92.3% Conservatives: 0  
Best Local Similarity: 92.3% Mismatches: 1  
Query Match: 97.9% Indels: 45  
DB: 74 Gaps: 1

US-10-628-525A-21 (1-539) x US-60-094-436-12 (1-2008)

Qy 1 CysValAlaGlnLeuSerArgGlu----- 8  
Db 119 TGGTTCGCGAGCTGAGCAGGAGGGGCGCGCGCGCGCTGCCACCGCGCTGCTG 178  
Qy 8 ----- 8  
Db 179 GCGCCCGCGCTGTCGCGCGCTTCTCGCGCGCGCGCGCGCGCGCGCGCGCA 238  
Qy 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 239 TCGACGCCCGCGCGCTGCGCGCGCGCGCGCGCTCGGTCTCGNACCTGAGGG 298  
Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 299 ATTGCTGAAGGTTCCATCGATAACACAGTAGTGTGCGCAAGTTCGAGATT 358  
Qy 37 ValValGlyGlyGlnAlaArgAlaIysValThrGlnSerIleValPheValThrGly 56  
Db 359 GTGGTTGGAAAGAGCAGCTCGAGCTAAAGTAACACAAAGCATTTGTCTTTGAACCGGC 418

Qy 57 GluAlaSerProTyrAlaIysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 419 GAAGCTTCTCTTATGCAAAAGTCTGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT 478  
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
Db 479 GCTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538  
Qy 97 SerAspIysAsnTyrAlaAlaAlaPheTyrThrGluIysHisIleArgIleProCysPhe 116  
Db 539 TCCGATGAAGATTTATGCAATGATTTTACAGAAAACACATTCGGATTCGATGCTTT 598  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPhe 136  
Db 599 GCGCGTGAAACATGAAGTTACCTTCTTCCATGAGTATAGAGATTCAGTTGCTGGTCTTT 658  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspIysPheGlyAlaPhe 156  
Db 659 GTTGTATCTCCTCATATCATCAGACCTGGAAATTTATATGAGATAAGTTTGGTCTTTT 718  
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 719 GGTGATATTCAGTTCAGATACACACTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 778  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
Db 779 CTTGAATTTGGAGGATATATTTATGACAGAAATTCGATGTTTGTTCATGATGGCAT 838  
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 839 GCCAGTCTAGTGCAGTCTCTTGTCTGCAAAATATAGACCATATGCTGTTTATAAAGAC 898  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 899 TCCCGCAGCATTCCTGTATACATAATTTAGCACATCAGGGGTAGAGCTTCGAGGACCA 958  
Qy 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 959 TATCTCTGACCTTGGGTTGCCCTGAATGGTATGGAGCTCTGGAGTGGGTATTTCCCTGAA 1018  
Qy 257 TrpAlaArgHisAlaLeuAspIysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
Db 1019 TGGCGGAGGAGGATGCCCTTGCAAGGGGTAGGCGAGTTAAATTTTGAAGAGGTGCGAGTT 1078  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
Db 1079 GTGACAGCAGATCGAATCTGACTGTCTGAGTAAAGGGTATTTCTGGGAGGTCACAACTGCT 1138  
Qy 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316  
Db 1139 GAAGGTGGACAGGCGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAACGGAAAT 1198  
Qy 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1199 GTAAATGGAATTCACATTAATGATTCGAAACCTCTGCCACAGACAAATGATATCCCTGCTCAT 1258  
Qy 337 TyrSerValAspAspLeuSerGlyIysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
Db 1259 TATCTGTTGATGACCTCTCTGGAAGGGCAATGTAAGGGTGCATTTGCAGAGAGGAGCTG 1318  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1319 GGTTTACCTATTAAGGCTGATTTCTCTGATTTGGCTTTATTTGGAAGGTGGATTTATCAG 1378  
Qy 377 LysGlyIleAspLeuGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396  
Db 1379 AAAGGCATTCGATCTCAATCACTTATCATACAGATCTCATCGGGAAGATGTTCAATTT 1438  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416  
Db 1439 GTCATGCTTGGATCTGGTACCAGAGCTTGAAGATTTGATGATGATCTTACAGAGTCGATC 1498

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QY 417 PheLysAspLysPheArgGlyTTPValGlyPheSerValProValSerHisArgIleThr 436
Db 1499 TTCAAGGATAAAATTTCTGGATGGGTGGATTTAGTGTTCAGTTTCCACCGAATAACT 1558
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1559 GCGGGCTGGCATATATTTGTAATGCCATCCAGATTCGAACCTTGTGGTCTCAATCAGCTA 1618
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1619 TATGCTATGAGTATGCGACAGTTCTGTTCATGCAACTGGGGGCTTAGAGATACC 1678
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTTPAlaPheAla 496
Db 1679 GTGGAGAACTTCAACCCCTTTGCGTGAGATGAGAGACAGGGTACAGGGTGGGCAATTCGCA 1738
QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
Db 1739 CCCCTAACCCACAGAAAACATGTTT-GTGGACATTTGCCAACTGCCAAATATCTACATACAGGGA 1797
QY 517 ThrGlnValLeuLeuGlyValArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 1798 ACACAACTCTCTCGGAAGGGCTAATGAAGCGAGGCATGTCAAAGACTTCACGCGGGA 1857
QY 537 ProCysArg 539
Db 1858 CCATGCCGC 1866

RESULT 13
US-60-094-436-9
; Sequence 9, Application US/60094436
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Broglie, Karen E.
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Modification of Starch Biosynthetic Enzyme Gene
; FILE REFERENCE: BB-1147-P1
; CURRENT APPLICATION NUMBER: US/60/094,436
; CURRENT FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 9
; LENGTH: 2491
; TYPE: DNA
; ORGANISM: Zea mays
US-60-094-436-9

Alignment Scores:
Pred. No.: 0 Length: 2491
Score: 2832.00 Matches: 538
Percent Similarity: 92.3% Conservative: 0
Best Local Similarity: 92.3% Mismatches: 1
Query Match: 97.9% Indels: 45
DB: 74 Gaps: 1

US-10-628-525A-21 (1-539) x US-60-094-436-9 (1-2491)
QY 1 CysValAlaGluLeuSerArgGlu----- 8
Db 262 TCGTCGCGGAGCTGACGAGGGAGGGCCCGCGCGCGCGCTGCGTCCGCCCGCTGCTG 321
QY 8 ----- 8
Db 322 GCGCCCCGCTCGTCCCGCTTCCTCTGCGCGCGCGCGCGCGAGCCCGGGTGAGCGCGCA 381
QY 9 -----AspLeuGlyLeuGluProGluGly 16
Db 382 TCGACGCGCGCCCGTGTGCCGACGCGCGCCCTGGGGGACCTCGGTCTCGAACCTGAAGG 441
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36
Db 442 ATTGTGAAGGTTCCATCGATAACACAGTAGTTGTGGCAAGTGAGCAAGATTCTGAGATT 501
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QY 37 ValValGlyGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 502 GTGGTTGGAAAGAGAGAGCTGAGCTAAAGTAACACAAAGCATTTGCTTTGTAAACCGGC 561
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 562 GAAGCTTCTCCTTATGCAAAAGTCTGGGGCTCTAGGAGATGTTGTGGTTCATTCGCCAGTT 621
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrIleuAsnGlyThr 96
Db 622 GCTCTTGCTGCTCGTGGTCACCGTGTGATGGTGTAAATGCCAGATTTTAAATGGTACC 681
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
Db 682 TCCGATAGAAATATGCAANTGCAATTTTACACAGAAAACACATTCGGATTCCTGCTTT 741
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTTPValPhe 136
Db 742 GCGGTGAAACATGAAGTTACCTTCTCCATGAGTATAGAGATTCAGTTGACCTGGGTGTT 801
QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156
Db 802 GTTGATCATCCCTCATATCACAGACCTCGAAATTTATATGAGATAAGTTTGGTGTCTTT 861
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 862 GGTGATAATCAGTTCAGATACACACTCTCTTCTGTCATGTCATGTGAGGCTCTCTTGATC 921
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTTPHis 196
Db 922 CTTGAATTTGGGAGGATATATTTATGACAGAAATTCATGTTGTTGTCATGATGGCAT 981
QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 982 GCCAGTCTAGTCCAGTCTCTTCTGTCGCAAAATATAGACCATATGCTGTTTATAAAGAC 1041
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 1042 TCCCGCAGCAATCTTGTAAATACATAATTTAGCACATCAGGGGTGAGAGCTCGAAGCA 1101
QY 237 TyrProAspLeuGlyLeuProGluTTPTyrGlyAlaLeuGluTTPValPheProGlu 256
Db 1102 TATCTGACCTTGGGTTCGCACCTGATGGTATGAGGCTCTGAGTGGGTATTCCTCGAA 1161
QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
Db 1162 TGGGCGAGGAGCATGCCCTTGACAAGGTGAGGCGAGTTAATTTTGAAGGTGCAGTT 1221
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
Db 1222 GTGACAGCAGATCGAATCTGTCTGTAGTAAAGGTTATTCGTGGAGGTGCACACTGCT 1281
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316
Db 1282 GAAAGTGGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTAAACGGAAT 1341
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 1342 GTAAATGGAATTTGACATTAATGATTGGAACCTCGCCACAGACAAAATGTATCCCTGTCTCAT 1401
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysValLysGlyValLeuGlnLysGluLeu 356
Db 1402 TATCTGTGTGATGACCTCTCTGGAAGGCCAANTGTAAAGGTGCATTCGCAAGGAGCTG 1461
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1462 GGTTTTACCTATAAGSCCTGATGTTCTCTCTGATTGGCTTTTATTGGAAGGTGATGATTATCAG 1521
QY 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1522 AAAGGCATTTGATCTCATTTCAACTTATCATACAGATCTCATCGGGAAGATGTTCAATTT 1581
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397 ValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGluSerIle 416  
1582 GTATGCTGGATCTGGTGAAGCTTGAAGATTGGATGATCTACAGATCGATC 1641  
417 PhelysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
1642 TTCAGGATAAATTCGTGGATGGTTGGATTAGTGTTCAGTTTCCACCGAATAACT 1701  
437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456  
1702 GCGGCTGCGCATATATGTTAAATGCCATCCAGATTCGAACCTTGTGTCTCAATCAGCTA 1761  
457 TyrAlaMetGlnTyrGlyThrValProValHisAlaThrGlyGlyLeuArgAspThr 476  
1762 TATGCTATGACATGATGACAGATTCCTGTTGTCATGCAACTGGGGGCTTAGAGATACC 1821  
477 ValGluAsnPheAsnProPheGlyGluAsnGlyGlnGlyThrGlyTyrAlaPheAla 496  
1822 GTGGAGAACTTCAACCTTTCGGTGAGATGGAGAGAGAGGATACAGGGTGGCATTCGCA 1881  
497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516  
1882 CCCTAACCAACAGAAACATGTT- GTGGACATTGGCAACTGCAATATCTACATACAGGA 1940  
517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536  
1941 ACACAGTCTCTCTGGGAGGGCTAATGAAGCGAGGATGTCAAAGACTTCAAGTGGGA 2000  
537 ProCysArg 539  
2001 CCATGCGC 2009

## RESULT 14

US-09-077-564-1  
Sequence 1, Application US/09077564  
GENERAL INFORMATION:  
APPLICANT: Knight, Mary E.  
APPLICANT: Keeling, Peter L.  
TITLE OF INVENTION: Modification of Starch Synthesis in  
TITLE OF INVENTION: Plants  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZENECA Ag Products  
STREET: 1800 Concord Pike  
CITY: Wilmington  
STATE: DE  
COUNTRY: USA  
ZIP: 19850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/077,564  
FILING DATE: 14-DEC-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB96/02990  
FILING DATE: 04-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9524938.9  
FILING DATE: 06-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hohenschutz, Liza D.  
REGISTRATION NUMBER: 33,712  
REFERENCE/DOCKET NUMBER: SEE 45052/UST  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 886-1699  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2992 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: NUMBER 1  
US-09-077-564-1

## Alignment Scores:

Pred. No.: 0 Length: 2992  
Score: 2757.00 Matches: 523  
Percent Similarity: 90.9% Conservative: 8  
Best Local Similarity: 89.6% Mismatches: 8  
Query Match: 95.3% Indels: 45  
DB: 20 Gaps: 1

US-10-628-525A-21 (1-539) x US-09-077-564-1 (1-2992)

QY 1 CysValAlaGluLeuSerArgGlu-----8  
Db 719 TGGTTCGCGAGCTGAGCAGGAGGGCGCGCGCGCTGCCACCGCGCTGCTG 778  
QY 8 -----8  
Db 779 GCGCGCGCGCTGCTGCGCGCGCTTCTCGCGCGCGCGCGCGCGCGCGCA 838  
QY 9 -----AspLeuGlyLeuGluProGluGly 16  
Db 839 TCGACGCCGCGCGCGCTGCGCGCGCGCGCGCGCGCTCGTCTCGAACCTGAAGGG 898  
QY 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36  
Db 899 ATTGCTGAAGGTTCCATTCGATTAACACAGTAGTTGTGCAAGTTCAGAGATT 958  
QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 959 GTGGTTGGAAGAGCAGCTCGAGCTAAAGTAACCAAGCAATTGTCTTTGTAACCGGC 1018  
QY 57 GluAlaSerPro-TyrAlaLysSerGlyLeuGlyAspValCysGlySerLeuProVa 76  
Db 1019 GAAGCTTCTCTTAATCGAAAGTCTCGGGGTCTAGGAGATGTTGTGTTTCATTCGCAGT 1078  
QY 76 lAlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyTh 96  
Db 1079 TGCTCTTGCTCGCGGTACCGGTGTATGTTGTAATGCCAGACATTTAAATGTGATC 1138  
QY 96 rSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPh 116  
Db 1139 CTCGGATAAGAATTATGCAAAATGCAATTTTACTCAGAAAACACATTCGGGATTCATTCTT 1198  
QY 116 eGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTyrValPh 136  
Db 1199 TGGCGGTGAACATGAAGTTACCTTCTCCATGAGTATAGAGATTTCAGTTGACGTGGGT 1358  
QY 136 eValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPh 156  
Db 1259 TGTGATCATCCCTCATATACAGACCTGGAATTTATATAGGAGATAAGTTTGGTCTTT 1318  
QY 156 eGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuI 176  
Db 1319 TGTGATAATCAGTTCCAGATACACACTCTTCTGATGCTGCGATGAGGCTCCTTTGGT 1378  
QY 176 eLeuGluLeuGlyGlyTyrIleTyrGlnAsnCysMetPheValValAsnAspTyrPh 196  
Db 1379 CCTTGAATGGGAGGATATATTATTCGACAGAAATTCATGTTGGTTGTCATGATTGGCA 1438  
QY 196 sAlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAs 216  
Db 1439 TGCAGTCTAGAGCCAGTCTCTTCTGCTGCAAAATATAGACCATATGTTGTTTATATAAGA 1498  
QY 216 pSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerTh 236  
Db 1499 CTCCCGCAGCATTCCTTGTAAATACATAAATTTAGCACATCAGGGGTAGAGCCTCAAGCAC 1558

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QY 236 rTyrProAspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProG1 256
Db 1559 ATATCTCGACCTTGGGTGGCCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTCCTGA 1618
QY 256 uTrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVa 276
Db 1619 ATGGCGAGGAGCATGCCCTTGACAAAGGTGAGGCAGTAAATTTTGAAGGTGCACT 1678
QY 276 lValThrAlaAspArgLleValThrValSerLysGlyTyrSerTrpGluValThrAl 296
Db 1679 TGTGACAGCATCGAATCGTCACTCTCAGTAAAGGTATATTCATGGAGGTCAACAATGC 1738
QY 296 aGluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyI1 316
Db 1739 TGAAGGTGACAGGCGCTCAATGAGCTCTTAAGCTCCAGAAAGATGATTAACCGAAT 1798
QY 316 eValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHi 336
Db 1799 TGTAAATGGAATGACATTAATGATTTGGAACCTGCGCACAGCAAAATGATGCCCTGTCA 1858
QY 336 sTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLe 356
Db 1859 TTATTCGTGTGATGACCTCTCTGAAAGGCTAAATGTAAAGGTGCATTCGAAAGGAGCT 1918
QY 356 uGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyValArgLeuAspTyrG1 376
Db 1919 GGGTTTACCTATAAGCCCTGATGTTCTCTGATTTGGCTTTATTTGGNAGATTGGATTATCA 1978
QY 376 nLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPh 396
Db 1979 GAAAGCATATGATCTCATTAATATCATACAGATCTCATGCGGAAGATGTTCAAT 2038
QY 396 eValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerI1 416
Db 2039 TGTCAATGCTTGGATCTGGTGACCCAGACTTGAAGATTGGATGAGATCTACAGAGTCGAT 2098
QY 416 ePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleTh 436
Db 2099 CTTCAAGGATAAATTTCTGGTGGATGGGTGGATTAGTTTCCAGTTTCCACCGAATAAC 2158
QY 436 rAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLe 456
Db 2159 TGGCGGTGGCATATATTTGTAATGCCATCCAGATTCGAACTTGGTCTCAATCAGCT 2218
QY 456 uTyrAlaMetGlnTyrGlyThrValProValHisAlaThrGlyGlyLeuArgAspTh 476
Db 2219 ATATGCTATGCAATATGGCACAGTTCTCTTGTCCATGCACTGGGGGCTTAGAGATAC 2278
QY 476 rValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAl 496
Db 2279 CGTGGAACACTTCAACCTTTCTGGTGAGAAATGGAGAGCAGGTACAGGTGGGCATTCCG 2338
QY 496 aProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnG1 516
Db 2339 ACCCTTAACACAGAAACATGTTTGTGGACATTTGCAACTGCAATATCTACATACAGGG 2398
QY 516 yThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValG1 536
Db 2399 AACACAAGTAATAATGGGAAGGCTTAATGAAGCCAGGCATGTCAAAAGAGATTCCAGTGGG 2458
QY 536 yProCysArg 539
Db 2459 ACCATGCCGC 2468
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## RESULT 15

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US-10-767-701-13043
; Sequence 13043, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
```

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; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 13043
; LENGTH: 2670
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS52_1
US-10-767-701-13043
```

```
Alignment Scores:
Pred. No.: 0 Length: 2670
Score: 2753.00 Matches: 522
Percent Similarity: 90.3% Conservative: 6
Best Local Similarity: 89.2% Mismatches: 11
Query Match: 95.2% Indels: 47
DB: 61 Gaps: 1

US-10-628-525A-21 (1-539) x US-10-767-701-13043 (1-2670)
QY 1 CysValAlaGluLeuSerArgGlu----- 8
Db 270 TCGTTCGCGAGCTGAGCAGGAGGCTCCGCGCGAGCGCGCGCGCTGCCACCCGCG 329
QY 8 ----- 8
Db 330 CTGCTGGCGCCCCGCTCGTGCCTTCCTCGCGCGCGCTCCGAGCCCCGAGGGGTGAG 389
QY 9 -----AspLeuGlyLeuGluPro 14
Db 390 CCGGCGTCGACACCCCGCCCGCTGCGCGCGCGCTCTCGGCGACCTCGGTCTCCAACT 449
QY 15 GluGlyIleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSer 34
Db 450 GAAGGATTTGCTGAGGGTTCCATCGATGAGACAGTAGTTGTGGCAAGTCAGCAAGATTCT 509
QY 35 GluIleValValGlyGluGlnAlaArgAlaLysValThrGlnSerIleValPheVal 54
Db 510 GAGATCGTGTGGAAAGGAGCAAGCTCGAGTAAAGTAACACAAGACATTGCTTTGTA 569
QY 55 ThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeu 74
Db 570 ACTGGCGAAGCTTCTCTTATGCAAGCTCGGGGTCTAGGAGATGTTTGTGTTCAATG 629
QY 75 ProValAlaLeuAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsn 94
Db 630 CCAGTTGCTCTTGTCTGCTCGTGCCTGATGTTGTAATGCCAGATATTTAAAT 689
QY 95 GlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIlePro 114
Db 690 GGTACTCTGTAAAGATTTACGCAATGCAATTTTACACAGAAAGCACATTCCGATTCCA 749
QY 115 CysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrp 134
Db 750 TGTCTTGGCGGTGAACATGAGTTACCTTTTCCATGAGTACAGAGATTCACTGACTGG 809
QY 135 ValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGly 154
Db 810 GTGTTTGTGATCATCCCTCATATCACAGACCTGGAATTTTATATGAGAGATAAGTTTGT 869
QY 155 AlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaPro 174
Db 870 GCTTTTGTGTAATCAGTTTCAGATACAGCTCCCTTGTCTATGCTGATGAGGCTCTCT 929
QY 175 LeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAsp 194
Db 930 TTGGTCTCTGAATTCGGAGGATATATTATGACAGAAATTCATGTTGTTGTTGTAATGAT 989
QY 195 TrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyr 214
Db 990 TGGCATGCCAGTCTAGTGCAGTCTCTTCTGTCGCAAAATATAGACCATATGTTGTTTAT 1049
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Qy 215 LysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAla 234  
Db 1050 AAAGACTCCGCGCAGCATCTCTGTAAATACATAATTTAGCACATCAGGCGTAGAGCCGTGCA 1109  
Qy 235 SerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPhe 254  
Db 1110 AGCACAATCTCGACCTGGGTGGCCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTC 1169  
Qy 255 ProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
Db 1170 CCTGAATGGCGCAGGAGCATGCCCTTGACAGGGGTGAGCGAGTAAATTTTGAAGGT 1229  
Qy 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTyrGluValThr 294  
Db 1230 GCAGTTGTGACAGCAGATCGAATTTGTGACTGTCTAGTAAGGTTATTTCATGGAGGTCA 1289  
Qy 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsn 314  
Db 1290 ACTGCTGAAGGTGACAGGGGTCTCAATGAGCTCTTAAGCTCCCGAAGAGGTGATTAAAC 1349  
Qy 315 GlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThrAspLysCysIlePro 334  
Db 1350 GGAATTTGAATGGAATTTGACATTAATGATTTGACCTCGACGCGACAAATGATTCCT 1409  
Qy 335 CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354  
Db 1410 TGTCAATATTCTGTGATGACCTCTCTGGAAAGCCAAATGTAAGTGCATTCGAGAAG 1469  
Qy 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374  
Db 1470 GAGCTGGGTTTACCTATAAGCCCTGAAGTTCTCTGATGGTTTTATTGGAAGATTGGAT 1529  
Qy 375 TyrGlnLysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspVal 394  
Db 1530 TATCAGAAAGGCATTGATCTCATCTCACTTATCATACCACATCTCATCGCGGACGAGCT 1589  
Qy 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyrMetArgSerThrGlu 414  
Db 1590 CAATTTGTCTGCTGCTGATGCTGAGCCAGCTCGAAGACTGGATGAGATCTACAGAG 1649  
Qy 415 SerIlePheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArg 434  
Db 1650 TCGGACTTCAAGGATAAATTTCTGGATGGGTGGATTTTATGTTTCCAGTTTCCACCGA 1709  
Qy 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454  
Db 1710 ATAACTGCCGCTCGGATATTTGTTAATGCCATCCAGATTCGACCTTGTGTCTCAAT 1769  
Qy 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474  
Db 1770 CAGCTATATGCTATGAGTATGACACAGTTCTGTGTTGCTCCACTGGGCGCTTAGA 1829  
Qy 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTyrAla 494  
Db 1830 GATACTGTGGAGAACTTCAACCTTTCTGGTGGAGATGGAGACAGGGGTACAGGGTGGCA 1889  
Qy 495 PheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIle 514  
Db 1890 TTGCGACCCCTAACCGGAAACATGTTTGTGGTGGAGATGGAGACAGGGGTACAGGGTGGCA 1948  
Qy 515 GlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHis 534  
Db 1949 CAAGGAGCACAAATCTCTCTGGGAGGGCTCATGAAGGGGCTATGTAAGAGACTTCAC 2008  
Qy 535 ValGlyProCysArg 539  
Db 2009 GTGGGACCATGCGCGC 2023

## RESULT 16

US-09-654-617-451753

; Sequence 451753, Application US/09654617

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong Annotated Plant Genes  
; FILE OF INVENTION: 38-21(15097)D  
; CURRENT REFERENCE: US/09/654,617  
; CURRENT APPLICATION NUMBER: 2000-09-05  
; CURRENT FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 451753  
; LENGTH: 2216  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
US-09-654-617-451753

Alignment Scores: Pred. No.: 0 Length: 2216  
Score: 2735.00 Matches: 508  
Percent Similarity: 98.1% Conservative: 5  
Best Local Similarity: 97.1% Mismatches: 10  
Query Match: 94.5% Indels: 0  
DB: 29 Gaps: 0

US-10-628-525A-21 (1-539) x US-09-654-617-451753 (1-2216)

Qy 17 IleAlaGluGlySerIleAspAenThrValValAlaSerGluGlnAspSerGluIle 36  
Db 1 ATTGCTGAAGGTTCCATCGATGAGACAGTAGTTGTGCAAGTGAGCAAGATTCTGAGATC 60  
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56  
Db 61 GTGGTTGGAAAGGAGCAGCTCGAGCTAAAGTAACCAAGCATTGCTTTGTAACGGC 120  
Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76  
Db 121 GAAGCTTCTCTTATGCAAGTCTGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT 180  
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96  
Db 181 GCTCTTGTGCTCGTGGTCACCGTGTGATGTTGTAATGCCAGATATTTAAATGGTACC 240  
Qy 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116  
Db 241 TCTGATAAGAAATTTACCGAAATGCAATTTTACAGAAAGACACATTCGATTCATGCTTT 300  
Qy 117 GlyGlyGluHisGluValThrPhePheHisGlyTyrArgAspSerValAspTyrValPhe 136  
Db 301 GCGGTTGAACATGAGTTACCTTTTCCATGACTACAGAGATTTCAGTTGACTGGGTGTT 360  
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156  
Db 361 GTTGATCATCCCTCATATCACAGACCTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT 420  
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
Db 421 GGTGATAATCAGTTTACAGTACAGCTCTCTTGTGCTGCTGATGAGGCTCTCTTTGGTC 480  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTyrHis 196  
Db 481 CTGTAATTTGGAGGATATATTTATGACAGAAATTTGCAATGTTTGTGTAATGATTGGCAT 540  
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 541 GCCAGTCTAGTGCAGCTCTCTTCTGCTGCAAAATATAGACCATATGTTGTTTATAAGAC 600  
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 601 TCCCGCAGCATTTCTGTAATACATAATTTAGCACATCAGGGGTGAGCCCTGCAAGCACA 660  
Qy 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 661 TATCTCTGACCTTGGGTTGCCACTGTAATGGTATGGAGCTCTGGAGTGGGTATTTCCCTGAA 720  
Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276

```
Db 721 TGGGCAAGGAGGCATGCCCTTGACAGGGTGAGGCAGTTAAATTTTGAAGGTGCAGTT 780
Qy 277 ValThrAlaAspArgIleValThrValSerIleGlyTyrSerTrpGluValThrAla 296
Db 781 GTGACAGCAGATCGAATGTGACTGTGCAGTAAGGGTTATTTCATGGGAGGTCAACTGCT 840
Qy 297 GluGlyGlyGlnGlyLeuAenGluLeuSerArgLysSerValLeuAenGlyIle 316
Db 841 GAAGGTGGACAGGTCTCAATGAGCTCTTAAGTCCCGAAGAGTGTATTAAACGAATT 900
Qy 317 ValAenGlyIleAspIleAenAspTrpAenProAlaThrAspLysCysIleProCysHis 336
Db 901 GTAAATGGAAATTGACATTAAATGTAATGGAACCTCGCAGCGACAAATGTATCCCTGTGCAT 960
Qy 337 TyrSerValAspAspLeuSerGlyIleAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 961 TATTCCTGTGATGACCTCTCTGGAAGGCCAAATGTAAAGTGCAATTGCGAAGGAGCTG 1020
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1021 GGTTTACCTATAAGGCTGAGTCTCTGATTTGTTTATTGGAAGATTGGATTATCAG 1080
Qy 377 LysGlyIleAspLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1081 AAAGGCATTGATCTCATTTCACTTATCATACACATCTCATCGGAGCGACGTTCAATTT 1140
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
Db 1141 GTCATGCTTGGATCTGGTGACCCAGAGCTCGAAGACTGGATGAGATCTTACAGAGTCGGAC 1200
Qy 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
Db 1201 TTCAGGATATAATTTCTGTGATGGGTGGATTAGTTAGTTGTTCCAGTTTCCACCGAATACT 1260
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAenGlnLeu 456
Db 1261 GCGGGTGGCATATATTGTAAATGCCATCCAGATTCCAACTTGTGGTCTCAATCAGCTA 1320
Qy 457 TyrAlaMetGlyTyrGlyThrValProValValHisAlaThrGlyClyLeuArgAspThr 476
Db 1321 TATGCTATCGAGTATGGCAGTTCCTGTGTGCCATGCAACTGGGGGCTTATAGAGATCT 1380
Qy 477 ValGluAsnPheAsnProPheGlyGluAenGlyGluGlnGlyThrGlyTrpAlaPheAla 496
Db 1381 GTGGAGAACTTCAACCTTTTCGGTGAGATGGAGAACAGGTACAGGTGGGCTTCGCA 1440
Qy 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAenCysAenIleTyrIleGlnGly 516
Db 1441 CCCCTAACCCAGGAAACATGTTGTGGACATTTGCCAATTCGCAATTCGACATACAAGCA 1500
Qy 517 ThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHisValIleArgLeuHisValGly 536
Db 1501 GCACAATCTTCTGGGAAGGGCTCATGAAGGGGGCATGTCAAAAGACTTCACGTGGGA 1560
Qy 537 ProCysArg 539
Db 1561 CCATGCCGC 1569
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## RESULT 17

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US-09-684-016-451753
; Sequence 451753, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 451753
; LENGTH: 2216
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; TYPE: DNA
; ORGANISM: Sorghum bicolor
US-09-684-016-451753
Alignment Scores: 0 Length: 2216
Pred. No.: 2735.00 Matches: 508
Score: 98.1% Conserv: 5
Percent Similarity: 97.1% Mismatches: 10
Best Local Similarity: 94.5% Indels: 0
Query Match: 29 Gaps: 0
DB:
US-10-628-525A-21 (1-539) x US-09-684-016-451753 (1-2216)
Qy 17 IleAlaGluGlySerIleAspAsnThrValValAlaSerGluGlnAspSerGluIle 36
Db 1 ATTGCTGAAGGTTCCATCGATCAGACAGTAGTGTGGCAAGTGAGCAAGATTCTTGAGATC 60
Qy 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 61 GTGGTTGGAAAGGAGCAGAGCTCGAGCTAAAGTAAACAAAGCATGTCTTTGTAAGTGGC 120
Qy 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 121 GAAGCTTCTCCTTATGCAAGTCTGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT 180
Qy 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrIleuAenGlyThr 96
Db 181 GCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Qy 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
Db 241 TCTGATAGAATTAAGCAATGCAATTTTACACAGAAAGCACATTCGGATTCATGCTTT 300
Qy 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136
Db 301 GCGGTGAAACATGAAGTTACCTTTTCCATGAGTACAGAGATTTCAGTTCAGTGGGTGTT 360
Qy 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156
Db 361 GTTGATCATCCTCATATACAGACCTGGAAATTTATATGGAGATAAGTTTGGTGTCTTT 420
Qy 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 421 GGTGATATCAGTTCAGATACAGCTCTCTTCTGCTATGCTGATGTGAGGCTCTCTTGGTC 480
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAenCysMetPheValValAenAspTrpHis 196
Db 481 CTTGAATTGGGAGGATATATTTATGACACAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 541 GCGAGTCTAGTGGGCTGCTCTTCTGCTGCAAAATATAGACCATATGCTGCTGCTGCTGCTGCT 600
Qy 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 601 TCCCGCAGCATTTCTGTAATACATAATTTAGCACATCAGGGTGTAGAGGCTCGAAGCACA 660
Qy 237 TyrProAspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGlu 256
Db 661 TATCCTGACCTTGGGTTGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAenPheLeuLysGlyAlaVal 276
Db 721 TGGGAAGGAGGATGCCCTTGACAGGGGTAGGAGGATTAATTTTGAAGGTTGAGTT 780
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
Db 781 GTGACAGCAGATCGAATTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Qy 297 GluGlyGlyGlnGlyLeuAenGluLeuSerSerArgLysSerValLeuAenGlyIle 316
Db 841 GAAGGTGGACAGGCTCTCAATGAGCTCTTAAGCTCCCGAAGAGTGTATTAAACCGAATT 900
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QY 317 ValLenglylleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 901 GTAATGGAATGATTAATGATGGAACCTCGACGCAAAATGATCCCTTGTCAT 960
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 961 TATTCGTGTGATGACCTCTCGGAAGCCAAATGTAAAGTGCATTCGCAAGAGAGCTG 1020
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
Db 1021 GGTTTACCTAAGGCCCTCAAGATTCCTCTGATTTGTTTATTTGGAAGATTGGATTATCAG 1080
QY 377 LysGlyIleAspIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396
Db 1081 AAGGCGATTGATCTCAATTCATCAATTCATCAATTCATCAATTCATCAATTCATCAATTT 1140
QY 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416
Db 1141 GTCATGCTTGATCTGATGACCCAGAGCTCGAGACTGGATGAGATCTACAGAGTCGGAC 1200
QY 417 PheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThr 436
Db 1201 TTCAAGGATAAATTTGCTGATGCTGATTTGATTTAGTTTCCAGTTTCCACCGGATTAAT 1260
QY 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeu 456
Db 1261 GCCGGCTCGCATATATTTAAATGCCATCCAGATTCGAACCTTGCTGCTCAATCAGCTA 1320
QY 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476
Db 1321 TATGCTATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 477 ValGluAsnPheAsnProPheGlyGluAsnGlyGlnGlnGlyThrGlyTyrPalaPheAla 496
Db 1381 GTGAGAACTTCAACCTTTTCGGTGAGATGGAGAACAGGGTACAGGGTGGGCTTCGCA 1440
QY 497 ProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGly 516
Db 1441 CCCCTAACCCAGGAAACATGTTTGTGGACATTCGGAACCTGCAATTCGACATACAGGA 1500
QY 517 ThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHisValLysArgLeuHisValGly 536
Db 1501 GCACAAATCTTCTGGGAAGGGCTCATGAAAGAGGGGATGTCAAAAGACTTCAAGTGGGA 1560
QY 537 ProCysArg 539
Db 1561 CCATGCGC 1569
```

## RESULT 18

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US-10-425-115-184334
; Sequence 184334, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 184334
; LENGTH: 1988
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_996C.1
; US-10-425-115-184334
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Alignment Scores:

Pred. No.: 0 Length: 1988

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Score: 2681.00 Matches: 499
Percent Similarity: 99.8% Conservativity: 3
Best Local Similarity: 99.2% Mismatches: 1
Query Match: 92.7% Indels: 1
DB: 51 Gaps: 0
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US-10-628-525A-21 (1-539) x US-10-425-115-184334 (1-1988)

```
QY 37 ValValGlyLysGluGlnAlaArgAlaLysValThrGlnSerIleValPheValThrGly 56
Db 2 ATGGTGGAAAGGAGCAGCTCGAGCTAAAGTAACACAAACATGCTCTTTGTAACTGGC 61
QY 57 GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal 76
Db 62 GAAGCTTCTCTTATGCAAAAGTCTGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT 121
QY 77 AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr 96
Db 122 GCTCTTGCTGCTCGTGGTCACTCGCTGATGTTGTAATGCCAGATATTTAAATGGTACC 181
QY 97 SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe 116
Db 182 TCCGATTAAGATTTATGCAATGATTTTACACAGAAACACATTCGATTCGATGCTTT 241
QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe 136
Db 242 GCGGCTGAACATCAAGTTACCTTCTTCCATGAGTATAGAGATTCAGTTGACTGGTGT 301
QY 137 ValAspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPhe 156
Db 302 GTTGATCATCCCTCATATCATCACAGCTCGAAATTTATATGAGATTAAGTTGGTGTCT 361
QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176
Db 362 GGTGATTAATCAGTTTCAGATACACACTCTTTGTCTATGCTGATGAGGCTCTTTGGTC 421
QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196
Db 422 CTGAAATGGGAGGATATATTTATGGACAGAAATTCATGTTGTTGTTGTTGTTGTTGTT 481
QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 482 GCAGTCTATGTCAGCTCTCTTCTGTCAGAAATATAGACCATATGTTGTTGTTGTTGTT 541
QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 542 TCCCGCAGCATCTCTTGTAAATACATAATTTAGCACATCAGGGTGTAGAGCTCGAAGCA 601
QY 237 TyrProAspLeuGlyLeuProProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256
Db 602 TATCCTGACCTTGGGTTGCCACCTGAATGGTATGGAGCTCTGGAGTGGGTATTCCTGAA 661
QY 257 TrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276
Db 662 TGGCGAGGAGGAGCATCCCTTGAAGGGGTAGGCGAGTTAAATTTTGAAGGTGTCAGTT 721
QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296
Db 722 GTGACAGCAGATCAATCGTACTGTCTAGTAAAGGTTATTCATGGGAGGTACACACTGCT 781
QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIle 316
Db 782 GAAGGTGGACAGGGCTCAATGAGCTCTTAAGCTCCAGAAAGAGTGTATTTAAACGGAA 841
QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336
Db 842 GTAAATGGAAATTCATTAATGATGGAACCTCGCCACACAGCAAAATGTATCCCTGTG 901
QY 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356
Db 902 TATTCGTGTGATGACCTCTCTGGAAAGGCCAAATGTAAAGGTGCATTCGAAAGAGGCTG 961
QY 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376
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Db 387 TGGTTGGATTAGTTCAGTTTCCACCGAATAAATGCGCGCTCGATATATTGTTA 328
Qy 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463
Db 327 ATGCCATCCAGATTGGAACCTTGGTGTCTCAATCAGCTATATGCTATGCGAGTATGGCACA 268
Qy 464 ValProValValHisAlaThrGlyLeuArgAspThrValGluAsnPheAsnProPhe 483
Db 267 GTTCTCTGTGTCATGCAACTGGGGGCTTAGAGATACCGTGGAGAACTTCAACCCCTTC 208
Qy 484 GlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503
Db 207 GGTGAGAAATGGAGCAGGCTACAGGTGGGCTTCAGCCCTTAACACAGAAACATG 148
Qy 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523
Db 147 TT-GTGACATTGCGAACTGCAATATCTACATACAGGAGACACAAAGTCTCTCTGGGAGG 89
Qy 524 AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
Db 88 GCTAATGAACGAGGCATGTCAAAAGACTTTCAGTGGGACCATGCCGC 41

RESULT 20
US-10-219-999-13937
; Sequence 13937, Application US/10219999
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)C
; CURRENT APPLICATION NUMBER: US/10/219,999
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/324,109
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 13937
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1308)
; OTHER INFORMATION:
US-10-219-999-13937

Alignment Scores:
Pred. No.: 0 Length: 1855
Score: 2538.00 Matches: 471
Percent Similarity: 99.8% Conservative: 0
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 87.7% Indels: 1
DB: 43 Gaps: 0

US-10-628-525a-21 (1-539) x US-10-219-999-13937 (1-1855)

Qy 68 GlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetVal 87
Db 1 GGAGATGTTTGTGTTTCATTCGCCAGTTGCTTGTGCTCGTGTGCTCGTGTGCTGTTG 60
Qy 88 ValMetProArgTyrLeuAsnGlyThrSerAspLeuAsnTyrAlaAsnAlaPheTyrThr 107
Db 61 GTAATGCCAGATATTTAAATGTTAGTCTCCGATAGAAATTTATGCAATATGCAATTTTACACA 120
Qy 108 GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPheHisGlu 127
Db 121 GAAAAACACATTCGGATTTCATCTTGGCGGTGAACATGAAGTTACCTTCTTCCATGAG 180
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Qy 128 TyrArgAspSerValAspTyrValPheValAspHisProSerTyrHisArgProGlyAsn 147
Db 181 TATAGAGATTTCAGTTGACTGGGTGTTTGTGATCATCCCTCATATCACAGACCTTGGAAAT 240
Qy 148 LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys 167
Db 241 TTATATGGAGATAAGTTTGGTGTCTTTTGGTATAAATCAGTTTCAGATACACACTCTCTTGC 300
Qy 168 TyrAlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn 187
Db 301 TATGCTGCAATGAGGCTCTTTGATCTTGAATTTGGAGGATATATTTATGGACAGAT 360
Qy 188 CysMetPheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAlaAlaLys 207
Db 361 TGCATGTTTGTGTCATGATGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG 420
Qy 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227
Db 421 TATAGACCATATGTTGTTTATAAGACTCCCGCAGCATTTCTGTATAATACATAATTTAGCA 480
Qy 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247
Db 481 CATCAGGTGTAGAGCTGCAACACATATCTCTGAGCTTGGGTGCGACCTGAATGTAT 540
Qy 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGlu 267
Db 541 GGAGCTCTGGAGTGGGTATTTCCCTGAATGGCGAGGAGCATGCTCTTGACAGGGTGAG 600
Qy 268 AlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287
Db 601 GCAGTTAAATTTTGAAGGTGCACTGTGACAGCAGATCGAATCGTACTGTCTGAGTAAG 660
Qy 288 GlyTyrSerTyrGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307
Db 661 GGTATTCTGTGGAGGTCAACTGCTGAAGGTGGACAGGCTCTCAATGAGCTCTTAAGC 720
Qy 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnPro 327
Db 721 TCCAGAAAGAGTGTATTAACCGAATGTTAAATGGATTTGACATTAATGATGGACCT 780
Qy 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLys 347
Db 781 GCCACAGACAAATGTATCCCTGTCTATTTCTGTTGATGACCTCTCTGGAAGGCGCAA 840
Qy 348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuLe 367
Db 841 TGTAAAGGTGCAATGCGAAGGAGCTGGGTGTACCTATAGGCTGTGATGTTCTCTGATT 900
Qy 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIlePro 387
Db 901 GGCTTTATTTGGAAGGTGCGATTATCAGAAAGGCAATGATCTCATTTCACTTATCATACCA 960
Qy 388 AspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGlu 407
Db 961 GATCTCATCGGGAAGATGTTCAATTTGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Qy 408 AspTyrMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPhe 427
Db 1021 GATTGATGAGATCTACAGAGTCGATCTTCAAGGATAAATTTCTGTTGATGGGTGATTT 1080
Qy 428 SerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArg 447
Db 1081 AGTGTTCAGTTTCCACCGAATTAATCGCGCTGGATATATTTGTTAATGCCATCCAGA 1140
Qy 448 PheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValVal 467
Db 1141 TTGCAACCTTGTGCTCTCAATCAGCTATATGCTATGCTATGCTATGCTATGCTATGCTAT 1200
Qy 468 HisAlaThrGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGly 487
Db 1201 CATGCAACTGGGGGCTTACAGATACCGTGGAGAACTTCAACCCCTTTCGTGAGATGGA 1260
```



APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E.  
APPLICANT: Tabaska, Jack E.  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(5313)B  
CURRENT APPLICATION NUMBER: US/10/425,114A  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 19497  
LENGTH: 1855  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3150-035-F10\_F11  
US-10-425-114A-19497

Alignment Scores:  
Pred. No.: 0 Length: 1855  
Score: 2538.00 Matches: 471  
Percent Similarity: 99.8% Conservative: 0  
Best Local Similarity: 99.8% Mismatches: 1  
Query Match: 87.7% Indels: 1  
DB: 51 Gaps: 0

US-10-628-525A-21 (1-539) x US-10-425-114A-19497 (1-1855)

QY 68 GlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetVal 87  
DB 1 GGAGATGTTTGGTGGTTCATTGGCCAGTGGCTCTTGGCTGGTGGTCCCGTGGTGGT 60

QY 88 ValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThr 107  
DB 61 GTAATGCCAGATATTAAATGATGTAATGATGTAATGATGTAATGATGTAATGATGTA 120

QY 108 GluLysHisIleArgLeuProCysPheGlyGluHisGluValThrPhePheHisGlu 127  
DB 121 GAAAAACACATTCGGATTCATGCTTTGGCGGTGAACATGAACTTACCTTCTTCATGAG 180

QY 128 TyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsn 147  
DB 181 TATAGAGATTCAGTTGACCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 240

QY 148 LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys 167  
DB 241 TTATATGGAGATTAAGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300

QY 168 TyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn 187  
DB 301 TATGCTGTCATGAGGCTCTTTGATCTTGAATGGAGGATATATTTATGGACAGAT 360

QY 188 CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLys 207  
DB 361 TGCATGTTTGTTCATGATGGCATGGCATGGCATGGCATGGCATGGCATGGCATGGCAT 420

QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227  
DB 421 TATAGACCATATGTTGTTTATAAAGACTCCCGGAGCATCTTGTATATACATATTTAGCA 480

QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247  
DB 481 CATCAGGTGTAGAGCTGCAAGCACATATCTGACCTTGGTGGTGGTGGTGGTGGTGGT 540

QY 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspLysGlyGlu 267  
DB 541 GGAGCTCTGGAGTGGGTATTTCCCTGAATGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 600

QY 268 AlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys 287  
DB 601 GCAGTTAAATTTTGAAGGTGCAATGTTGTGACAGCAGATCGAATCGTACTGTGAGTAA 660

QY 288 GlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307  
DB 661 GGTATTTCGTGGGAGGTCAACCTGCTGAAGGTGGACAGGCTCAATGAGCTCTTAAGC 720

QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327  
DB 721 TCCAGAAAGAGTGTATTAAACGGAATTTGAAATGGAATTCACATTTATGATTTGAACCT 780

QY 328 AlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLys 347  
DB 781 GCCACAGACAAATGATCCCTGTCTATTCTGTTGATGACCTCTCTGAAAGGCCCAA 840

QY 348 CysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIle 367  
DB 841 TGTAAAGGTGCAATTGCAGAGGAGCTGGGTTTACCTATATAGGCTGATGTTCTCTGATT 900

QY 368 GlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIlePro 387  
DB 901 GGCTTTATTGGAAAGGTGGATTTATCAGAAAGGATTCATCTCACTTATCATACCA 960

QY 388 AspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGlu 407  
DB 961 GATCTCATGCGGGAAGATGTTCAATTTGTCATGCTTGGATCTGCTGACCCAGAGCTTGA 1020

QY 408 AspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyThrValGlyPhe 427  
DB 1021 GATTGATGAGATCTACAGATCGATCTTCAAGGATAAATTTCTGATGGTGGATT 1080

QY 428 SerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArg 447  
DB 1081 AGTGTTCAGTTTCCACCGAATAACTGCCGGCTGGCATATATTGTAATGCCATCCAGA 1140

QY 448 PheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValVal 467  
DB 1141 TTCGAACCTTGGTCTCAATCAGCTATATGCTATGCTATGCTATGCTATGCTATGCT 1200

QY 468 HisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGly 487  
DB 1201 CATGCAACTGGGGCTTACAGATACCGTGGAGAACTTCAACCTTTCTGCTGAGATGGA 1260

QY 488 GluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIle 507  
DB 1261 GAGCAGGTATACAGGTGGGCTTCCACCCCTTAACCCACAGAAACATGTTTGTGGACATT 1319

QY 508 AlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAla 527  
DB 1320 GGAATCTCAATATCTACATACAGGGAACACAGTCTCTCTGGAAAGGGCTAATGAGCG 1379

QY 528 ArgHisValLysArgLeuHisValGlyProCysArg 539  
DB 1380 AGGCATGTCAAAAGACTTCCAGCTGGGACCATGCCGC 1415

RESULT 23  
US-60-312-544-3744  
Sequence 3744, Application US/60312544  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Edgerton, Michael D  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Liu, Jingdong  
APPLICANT: Stein, Joshua  
TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT  
FILE REFERENCE: 38-10(52726)A  
CURRENT APPLICATION NUMBER: US/60/312,544  
CURRENT FILING DATE: 2001-08-15  
NUMBER OF SEQ ID NOS: 10730  
SEQ ID NO 3744  
LENGTH: 1854  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:

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; NAME/KEY: CDS
; LOCATION: (3)...(1307)
; OTHER INFORMATION: Clone ID: LIB3150-035-F10_FLI
US-60-312-544-3744

Alignment Scores:
Pred. No.: 0 Length: 1854
Score: 2532.00 Matches: 470
Percent Similarity: 99.8% Conservative: 0
Best Local Similarity: 99.8% Mismatches: 1
Query Match: 87.5% Indels: 1
DB: 78 Gaps: 0

US-10-628-525A-21 (1-539) x US-60-312-544-3744 (1-1854)

QY 69 AspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValVal 88
DB 3 GATGTTGGTTCATTTGCGAGTTGCTCTTGCTGCTCGTGGTCAACCGTGTGATGGTTGTA 62
QY 89 MetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGlu 108
DB 63 ATGCCAGATATTTAAATGGTACCTCCGATAGAATTATGCAATGCAATTTACAGAA 122
QY 109 LysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyr 128
DB 123 AAACACATTCGGATTCATGCTTGGCGGTGAACATGAAGTTTACCTTCTTCATGAGTAT 182
QY 129 ArgAspSerValAspTyrValPheValAspHisProSerTyrHisArgProGlyAsnLeu 148
DB 183 AGAGATTCAATGACTGGGTGTTGTTGATCATCCCTCATATACAGACCTCGAAATTTTA 242
QY 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168
DB 243 TATGAGATAAGTTTGGTCTTTGGTGATATTCAGTTCAGATACACATCTCTTTGCTAT 302
QY 169 AlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCys 188
DB 303 GCTGCATGTGAGGCTCTTTGATCTTGAATGGGAGGATATATTATGGACAGAAATTCG 362
QY 189 MetPheValValAsnAspTyrHisIleSerLeuValProValLeuLeuAlaIalysTyr 208
DB 363 ATGTTTGTGTCAATGATGGATCCAGTCTAGTGCACATCTCTTCTGTCGCAAAATAT 422
QY 209 ArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHis 228
DB 423 AGACCATATGTTGTTTAAAGACTCCCGACATCTCTGTATATCATATTTAGACAT 482
QY 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGluTyrTyrGly 248
DB 483 CAGGGGTAGAGCCTGCAAGCACATATCTGACCTTGGGTGGCCACCTGAATGGTATGGA 542
QY 249 AlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAla 268
DB 543 GCTCTGGAGTGGGTATTCCTGAATGGGCGAGGAGGCGATGCCCTTGACAAAGGTCAGGCA 602
QY 269 ValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGly 288
DB 603 GTTAAATTTTGAAGGTGCAGTTGTGACAGCAGATCGATCTGACTGTCAGTAAAGGT 662
QY 289 TyrSerTyrGluValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSer 308
DB 663 TATTCGTGGAGGTCAACAATCTGCTGAAGGTGACAGGGGCTCAATGAGCTCTTAAGCTCC 722
QY 309 ArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAla 328
DB 723 AGAAAGAGTGTATTAACCGAAATTTGAATGAATTTGACATTAATGATTTGGAAACCTGCC 782
QY 329 ThrAspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCys 348
DB 783 ACAGACAAATGTATCCCTGTCTATTCTGTGTGATGACCTCTCTGGAAGGCCAAATGT 842
QY 349 LysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGly 368
```

```
DB 843 AAAGGTGCATTGCAGAAAGGAGCTGGGTTTACCTATATAAGGCTGATGTTCTCTGATTGGC 902
QY 369 PheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIlelleProAsp 388
DB 903 TTTTATTGGAAGGTTGATTTATCAGAAAGCAATGATCTCATTTCACTTATCATACCAGAT 962
QY 389 LeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAsp 408
DB 963 CTCATGCGGGAAGATGTTCAATTTGTCATGCTTGGATCTGGTGACCCAGAGCTTTGAAGAT 1022
QY 409 TrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSer 428
DB 1023 TGGATGAGATCTACAGAGTCGATCTTCAAGGATAAATTTCTGTTGGATGGGTTGGATTTAGT 1082
QY 429 ValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPhe 448
DB 1083 GTTCCAGTTTCCACCGCAATAACTGCGGCTCGCATATATTGTTAATGCCATCCAGATTTC 1142
QY 449 GluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHis 468
DB 1143 GAACTTGTGGTCTCAATCAGCTATATGCTATGCAAGTATGGCACAGTTCTCTGTTGCCAT 1202
QY 469 AlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGlu 488
DB 1203 GCAACTGGGGGCTTAGAGATACCGTGGAGAACTTCAACCTTTCGGTGAGAAATGGAGAG 1262
QY 489 GlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAla 508
DB 1263 CAGGTTACAGGTTGGGCTTTCACCCCTTAACACAGAAACATGTT-GTGGACATTGGC 1321
QY 509 AsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArg 528
DB 1322 AACTGCATATCTCATACAGGAAACACAGTCTCTCTGGGAAGGCTTAATGAGCGAGG 1381
QY 529 HisValLysArgLeuHisValGlyProCysArg 539
DB 1382 CATGTCAAAGACTTTCAGTGGGACCATGCCGC 1414

RESULT 24
PCT-US03-41098-141
; Sequence 141, Application PC/TUS0341098
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations, AG
; TITLE OF INVENTION: STRESS-RELATED POLYPEPTIDES AND USES THEREFOR
; FILE REFERENCE: 1392-10-20 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/41098
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/436,564
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patencin version 3.2
; SEQ ID NO 141
; LENGTH: 1881
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1881)
PCT-US03-41098-141

Alignment Scores:
Pred. No.: 0 Length: 1881
Score: 2525.50 Matches: 475
Percent Similarity: 95.8% Conservative: 31
Best Local Similarity: 80.5% Mismatches: 33
Query Match: 87.3% Indels: 51
DB: 2 Gaps: 3

US-10-628-525A-21 (1-539) x PCT-US03-41098-141 (1-1881)

QY 1 CysValAlaGluLeuSerArgGlu-----:::
|||||
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DB: 2 Gaps: 3
US-10-628-525A-21 (1-539) x PCT-US03-41200-307 (1-1881)
QY 1 CysValAlaGluLeuSerArgGlu-----8
DB 100 TCGGTGGCGAGCTGAGCAGGACGCTGGGTGGGTGGCGCAGCGCGCGCTGGCCACCGCGCGCG 159
QY 8 -----8
DB 160 CTGGTGAGCAGCCGGTCTCGCGACCTTCCTCGTGGCCGACGCTGACGCGCACCCGCGGCC 219
QY 9 -----AspLeuGly-----11
DB 220 ACGCAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGTTCGCGGACTCCGCGCGTGGGGGAG 279
QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValValAla 29
DB 280 ATCGAGCCCGATCTAGAAGGTCTACAGAAGATTCCATCGACAAACAATTTTGTGGCT 339
QY 30 SerGluGlnAspSerGluIleValValGlyIleGluGlnAlaArgAlaIleValThrGln 49
DB 340 AGTGAGCAGGAGCTGAGATCATGATGATGAAGGAGCAAGCTCAAGCTAAAGTAACACGC 399
QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaIleAspSerGlyGlyLeuGlyAsp 69
DB 400 ACGGTGTCTTGTAAACCGGTGAAGCTTCTCTTATGCAAGCTCAGGTGGACTAGAGAT 459
QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMet 89
DB 460 GTTGTGGTTCATCGCAATGCTCTGTCTCTCTGTGGTGTGATGATGATGATGATGATG 519
QY 90 ProArgTyrLeuAsnGlyThrSerAspIleValAlaAsnAlaPheTyrThrGluIle 109
DB 520 CCGAGATACGAACGGCGCTTGAACAAAAATTTGCAACGCAATTTTACACTGAGAG 579
QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
DB 580 CACATTAAAGATTCCATGCTTTCGCGGAGAACATGAATTTACTTTTTCACGAGTATAGG 639
QY 130 AspSerValAspTyrValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149
DB 640 GATTCGTGTGATGGGTGTGTGTGATCATCCTCATATAGAGTCTGCAAAATTTGTAT 699
QY 150 GlyAspIlePheGlyValPheGlyValPheGlyValPheGlyValPheGlyValPheGly 169
DB 700 GGAGATAATTTTGGTGTCTTGGCGATATATAGTTTTCAGATACACACTCTGTGTATGCG 759
QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyIleTyrIleTyrGlyIleAsnCysMet 189
DB 760 GGTGTGAAGCCCATTAATTTCTGACTGGGAGATATATCTATGGACAGAAATGCATG 819
QY 190 PheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAlaIleValTyrArg 209
DB 820 TTTGTGTGAATGATGTGGCATGCCAGTCTGTGGCAGTCTTCTGTGTCGCAAAATATAGA 879
QY 210 ProTyrGlyValTyrIleAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229
DB 880 CCATATGGTGTTCAGGAGTCCCGAGTGTCTGTGATACATAAATCTAGCATATAG 939
QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAla 249
DB 940 GGTGTGGAGCTCCGAGTACATATCTGACCTGGGATTTGCCACCTGAATGGTATGAGCA 999
QY 250 LeuGluTyrValPheProGluTyrAlaArgHisAlaLeuAspIleGlyGluAlaVal 269
DB 1000 TTAGAATGGTGTTCAGAGTGGGCAAGCGCGCATGCCCTTGCAAGGGTGGAGCATC 1059
QY 270 AsnPheLeuIleGlyValAlaValThrAlaAspArgIleValThrValSerIleGlyTyr 289
DB 1060 AATTTTTTAAAGGCGAGTGTGACAGCAGATCGAATGTGACTGTGACCGCGGGTAT 1119
QY 290 SerTyrGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArg 309
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## RESULT 26

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US-10-533-176-141
; Sequence 141, Application US/10533176
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations, AG
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: STRESS-RELATED POLYPEPTIDES AND USES THEREFOR
; FILE REFERENCE: 1392-10-20 PCT
; CURRENT APPLICATION NUMBER: US/10/533,176
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/436,564
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 141
; LENGTH: 1881
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1881)
US-10-533-176-141
```

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DB 1120 TCATGGAGGTCCACAACCTGCTGAAGGTGGCGAAGCCCTCAATGAGCTCTTAAGCTCCCG 1179
QY 310 IysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThr 329
DB 1180 AAGAGTGTATTGAATGGAATGTAATGAATGCAATTAATGAATGGAACCCATCCACA 1239
QY 330 AspIysCysIleProCysHisTyrSerValAspAspLeuSerGlyIleAlaIysCysValys 349
DB 1240 GACAAGTTTCTCCCTTATCATTTATCTGTGATGACCTGTCCGGAAGGCCAAGGTGATAA 1299
QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369
DB 1300 GCTGAATTCGAGAAGAGCTGGTTTACTATATAAGCCCGATGTGCTCTGATTGGCTTT 1359
QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu 389
DB 1360 ATTGGAAGATTGGACTATCAAAAAGGCATGTGATTAATTAACCTTGCCATTCCAGATCTC 1419
QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyr 409
DB 1420 ATCGCGGACAATTAATTCATGCTGTGATCTGTGTGACCCAGGTTTGAAGGATGG 1479
QY 410 MetArgSerThrGluSerIlePheIysAspIysPheArgGlyTyrPheValGlyPheSerVal 429
DB 1480 ATGAGATCCACAGATCAGGCTACAGGATAAATTCGTGGATGGTTGGATTAGTGT 1539
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
DB 1540 CCAGTTTCCCGCCGAAATAACTGCAGGTTGCGATATATTTGTTGATGCCATCCAGATTCCGAA 1599
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 1659
DB 1600 CTTGTGGCTCAATCAGCTATATCTGATATGCAATATGTTACAGTCCCTGTGTTTATGGA 1659
QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489
DB 1660 ACTGGAGGCTCAGAGATACAGTGGAGAAATTTAAACCGTTTGTCTGAGAAAGGAGAGCAG 1719
QY 490 GlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509
DB 1720 GGTACAGGTTGGGCAATTCCTCGCCACTAACCAATTTGAAAAAATGCTGTGGGCAATTCGGAT 1779
QY 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529
DB 1780 GGCAATTCGACATACAGGGAACACAGTCTCTTTGGGAGGGTCTTAATGAACCGAGGCAT 1839
QY 530 ValIysArgLeuHisValGlyProCysArg 539
DB 1840 GTCAAGCGACTTATACATGGGACCATGCCGC 1869
```

Alignment Scores:  
Pred. No.: 0 Length: 1881  
Score: 2525.50 Matches: 475  
Percent Similarity: 85.8% Conservative: 31  
Best Local Similarity: 80.5% Mismatches: 33  
Query Match: 87.3% Indels: 51  
DB: 52 Gaps: 3

US-10-628-525A-21 (1-539) x US-10-533-176-141 (1-1881)

QY 1 CysValAlaGluLeuSerArgGlu-----8  
DB 100 TCGTGGCGAGCTGACGAGGAGCGGTGGGTGGCGGAGCGCGCTGGCACCGCGCGCG 159  
QY 8 -----8  
DB 160 CTGCTGAAGCAGCGGCTCTCGCGACCTCTCTCGTGGCGAGCTGCGACCGCGCGCC 219  
QY 9 -----AapLeuGly-----11  
DB 220 ACGCAGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGGCGGAGCTCGCGGCGGAG 279  
QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAapLeuValValAla 29  
DB 280 ATCGAGCCCGATCTAGAGGCTCTCAGAGAATTCATCGACAAACAATTTTGTGGCT 339  
QY 30 SerGluGlnAapSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49  
DB 340 AGTGAGCAGGAGCTGAGATCATGATGTGAGGAGCAAGCTCAAGCTAAGTAACACGC 399  
QY 50 SerIleValPheValThrGlyLysGluLysProTyrAlaLysSerGlyLysGlyAap 69  
DB 400 AGCGTGTCTTGTAAACCGGTGAAGCTTCTCTATGCAAGTCAGGTGAGTACAGAT 459  
QY 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89  
DB 460 GTTGTGTGTTCTGTCATGTCATGCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 519  
QY 90 ProArgTyrLeuAanGlyThrSerAapLysAanTyrAlaAanAlaPheTyrThrGluLys 109  
DB 520 CCGAGATACATGAACGGGCTTGAACAAAATTTTGAACCGATTTTACATGAGAG 579  
QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
DB 580 CACATTAAGATTCATGCTTGGCGGAGAACATGAAGTTACTTTTTCACGAGTATAG 639  
QY 130 AapSerValAapTrpValPheValAapHisProSerTyrHisArgProGlyAanLeuTyr 149  
DB 640 GATTCGTGTGATGGGTGTGTGTGATCATCCCTCATATCATAGACCTGGAATTTGTAT 699  
QY 150 GlyAapLysPheGlyAlaPheGlyAapAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
DB 700 GGAGATAATTTTGTGCTTTGGGATATCATGTCAGATACACATCTCTGCTGCTATGC 759  
QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyTyrIleTyrGlyLysGlnAanCysMet 189  
DB 760 GCGTGTGAAGCCCATTAATTTCTGAACCTGGGAGATATATCTATGACAGAAATGCATG 819  
QY 190 PheValValAanAapTrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209  
DB 820 TTTGTGTGATGATTTGGCATGCGAGTCTTGTGCCAGCTCTCTGCTGCAAAATATAGA 879  
QY 210 ProTyrGlyValTyrLysAapSerArgSerIleLeuValIleHisAanLeuAlaHisGln 229  
DB 880 CCATATGGTGTACAGGATGCGCGAGTCTTGTCTATCATATCTATGACATCATG 939  
QY 230 GlyValGluProAlaSerThrTyrProAapLeuGlyLeuProGluTyrTyrGlyAla 249  
DB 940 GGTGTGGAGCTGCCAGTACATATCTGACCTGGGATTTGCCACCTGAATGTATGAGCA 999  
QY 250 LeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAapLysGlyGluAlaVal 269

DB 1000 TTAGAATGGGTGTTCAGAGTGGGCAAGCGGCATCCCTTGCAGAGGGTGAAGCAGTC 1059  
QY 270 AsnPheLeuLysGlyAlaValThrAlaAapArgIleValThrValSerLysGlyTyr 289  
DB 1060 AATTTTTTAAAGCGCAGTGTGACAGCAGATCGAATTGTGACTGTGACCGAGGGTAT 1119  
QY 290 SerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAanGluLeuLeuSerSerArg 309  
DB 1120 TCATGGGAGGTCAACTGCTGAAGGTGGCAAGGCCTCAATGAGCTCTTAAGCTCCCG 1179  
QY 310 LysSerValLeuAanGlyIleValAanGlyIleAapIleAanAapTrpAanProAlaThr 329  
DB 1180 AAGAGTGTATTTGAATGGAATTTGAATGGAATTTGAATGGAATTTGAATGGAATTTGA 1239  
QY 330 AapLysCysIleProCysHisTyrSerValAapLeuSerGlyLysAlaLysCysLys 349  
DB 1240 GACAGTTCCTCTTATCATATTTCTGTTGATGACCTGCCGGAAGGCAAGTGTAAA 1299  
QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAapValProLeuIleGlyPhe 369  
DB 1300 GCTGAATTTGCAAGGAGCTGGGTTTACCTATAAGGCCGATGTGCTCTGATTGGCTTT 1359  
QY 370 IleGlyArgLeuAapTyrGlnLysGlyIleAapLeuIleGlnLeuIleIleProAapLeu 389  
DB 1360 ATTGGAAGATTGGACTATCAAAAGGCAATTTGATTAATTAATTTGATTTCCAGATCTC 1419  
QY 390 MetArgCysLeuAapValGlnPheValMetLeuGlySerGlyAapProGluLeuAapTyr 409  
DB 1420 ATCGGGGACATATTTCAATTCGTCTGTTGGATCTGGTGACCCAGGTTTTGAAGGATGG 1479  
QY 410 MetArgSerThrGluSerIlePheLysAapLysPheArgGlyTrpValGlyPheSerVal 429  
DB 1480 ATGAGATCCACAGAAATCAGGGTACAGGATAAATTTCTGATGGGTTGGATTTAGTGT 1539  
QY 430 ProValSerHisArgIleThrAlaGlyCysAapIleLeuMetProSerArgPheGlu 449  
DB 1540 CCAGTTTCCACCGAATAATCTGAGGTTGCGATATATTTGATGATCCATCCAGATTCGAA 1599  
QY 450 ProCysGlyLeuAanGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
DB 1600 CTTTGGGCTCATCATGCTATATGCTATGCAATATGATGATGCTGTTGTTTCATGGA 1659  
QY 470 ThrGlyGlyLeuArgAapThrValGluAanPheAanPheGlyGlyGluAanGlyGluGln 489  
DB 1660 ACTGGAGGCTCAGAGATACAGTGGAGAAATTTTAAACCGTTTCTGAGAAAGGAGAGCAG 1719  
QY 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAanMetPheValAapIleAlaAan 509  
DB 1720 GSTACAGGTTGGGCTTCTGCGCACTTAACCAATTTGAAAAAATCTGTTGGGCAATTCGGGAT 1779  
QY 510 CysAanIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAanGluAlaArgHis 529  
DB 1780 GGCAATTTGACATACAGGAGACAGGATCTCTCTTGGAGGGTCTTAATGAGCGAGCAT 1839  
QY 530 ValLysArgLeuHisValGlyProCysArg 539  
DB 1840 GTCAAGCGCTTTATCATGCGACCATGCCGC 1869

## RESULT 27

US-09-654-617-385863  
; Sequence 385863, Application US/09654617  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/654,617  
; CURRENT FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 385863  
; LENGTH: 2606  
; TYPE: DNA  
; ORGANISM: Oryza sativa



US-09-654-617-385863

Alignment Scores:

Pred. No.: 0 Length: 2606  
Score: 2525.50 Matches: 475  
Percent Similarity: 85.8% Conservative: 31  
Best Local Similarity: 80.5% Mismatches: 33  
Query Match: 87.3% Indels: 51  
DB: 29 Gaps: 3

US-10-628-525A-21 (1-539) x US-09-654-617-385863 (1-2606)

QY 1 CysValAlaGluLeuSerArgGlu-----8  
DB 238 TCGTGGCGGAGCTGAGCAGGACGGTGGTGGCGCCACGGCCGCTGGCAGCGGCGCG 297  
QY 8 -----8  
DB 298 CTGGTGAAGCAGCGGCTCTCGCGACCTTCTCTGTCGCGACGCTCGACGCCACCGCGGCC 357  
QY 9 -----AspLeuGly-----11  
DB 358 AGCGAGTCCCGCGCGCGCGCGACCCCGCGCGCTTCCCGGACTCCCGCGTGGGGAG 417  
QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
DB 418 ATCGAGCCGATCTAGAAGGTCTCAGAGAATTCATCGACAAACAATTTTGTGGCT 477  
QY 30 SerGluInAspSerGluIleValValGlyGluGlnAlaArgAlaLysValThrGln 49  
DB 478 AGTGAGCAGGAGTCTGAGATCATGGATGTGAAGGAGCAAGCTCAAGCTAAAGTAACACGC 537  
QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69  
DB 538 ACGGTGCTTTGTAAACCGGTGAAGCTTCTCTATGCAAGTCAGGTGGACTAGAGAT 597  
QY 70 ValCysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValMet 89  
DB 598 GTTGTGGTTCATGCCAATGCTCTGCTCTCGTGGTCATCGTGTGATGTTGTAATG 657  
QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109  
DB 658 CCGAGATACATGAACGGGCGCTTGAACAAAAATTTTGCAAGCGCATTTTACACTGAGAAG 717  
QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
DB 718 CACATTAGATTCCATGCTTGGCGGAGAACATGAAGTTACTTTTTTCCAGGATATAGG 777  
QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149  
DB 778 GATTCGTGTTGATGGTGTGTTGTTGATCATCCCTCATATCATAGACCTGGAAATTTGTAT 837  
QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
DB 838 GGAGATAAATTTTGGTGTCTTGGCGATATACAGTTGAGATACACATCTCTGTGTATGCG 897  
QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMet 189  
DB 898 GCGTGTGAAGCCCCATTAATTTTGAACCTGGGAGATATATCTATGACAGAAATGCGATG 957  
QY 190 PheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyrArg 209  
DB 958 TTTGTTGTGAATGATGGCATGCCAGTCTTGTGGCAGTCTTCTTGTGCAAAATATAGA 1017  
QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229  
DB 1018 CCATATGGTGTGTTACAGGATGCCGAGTGTCTTGTGTCATACATAATCTAGCATCATAG 1077  
QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProProGluTrpTyrGlyAla 249  
DB 1078 GGTGTGGAGCCTCCAGATACATATCTGACCTGGGATGCGACCTGAAATGGTATGAGCA 1137  
QY 250 LeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaVal 269

DB 1138 TTAGAATGGTGTCTTCCAGAGTGGCAGCGCGCATGCCCTTGACAGAGGTGAGGCAGTC 1197  
QY 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
DB 1198 AATTTTTTAAAGGCGCAGTGTGACAGCAGATCGAATTTGTACTGTCCAGCCAGGGGTAT 1257  
QY 290 SerTrpGluValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuSerSerArg 309  
DB 1258 TCATGGAGGTCAACAATGCTGAAGGTGGCAAGGCTCAATGAGCTCTTAAGCTCCCGG 1317  
QY 310 LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThr 329  
DB 1318 AAGAGTGTATTGAATGGAATTTGAATGGAATTTGAATTTGAATTTGAATTTGAATTTGA 1377  
QY 330 AspLysCysIleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLys 349  
DB 1378 GACAAAGTTTCTCCCTTATCATTTATTTGTTGATGACCTGTCGCGAAAGCCCAAGTGTAA 1437  
QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369  
DB 1438 GCTGAATTCGAGAGAGCTGGGTTTACCTATAAGGCCCGGATGGCTCTGATTGGCTTT 1497  
QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu 389  
DB 1498 ATTGGAAGATTGGACTATCAAAAGGCAATTTGATCTAATTAATTAATTTGCCATTCAGATCTC 1557  
QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409  
DB 1558 ATGCGGCGCAATTTCAATTTGCTCATGCTGATGCTGTTGATGCTGTTGATGCTGTTG 1617  
QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerVal 429  
DB 1618 ATGAGATCCACAGAATCAGGCTACAGGAGGATAAATTTCTGTTGATGCTGTTGATGCTG 1677  
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
DB 1678 CCAGTTTCCCGCAAGTAATTCAGGCTGGGATATATTTGTTGATGCTGATGCTGATGCTG 1737  
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValHisAla 469  
DB 1738 CTTGTGGCTCAATCAGCTATATGCTATGCAATATGTTGATGCTGCTGCTGCTGCTGCTG 1797  
QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489  
DB 1798 ACTGAGGCTCAGAGATACAGTGGAGAAATTTTAACCCGTTTGTGCTGAGAAAGAGAGCAG 1857  
QY 490 GlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
DB 1858 GGTACAGGCTGGGCTTCTCGCCACTAACCATTGAAAAAATGCTGTGGGCTTGGGAT 1917  
QY 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
DB 1918 GGCATTTTCGACATACAGGGAACACAGTCTCTTTGGGAGGCTCTAATGAAGCGGCAT 1977  
QY 530 ValLysArgLeuHisValGlyProCysArg 539  
DB 1978 GTCAAGGACCTTATACATGGACCATGCGCG 2007

RESULT 28

US-09-684-016-385863  
; Sequence 385863, Application US/09684016  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 38-21(15097)D  
; CURRENT APPLICATION NUMBER: US/09/684,016  
; CURRENT FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; NUMBER OF SEQ ID NOS: 463173  
; SEQ ID NO 385863





APPLICANT: Chen, Wenquiong  
APPLICANT: Katagiri, Fumiaki  
APPLICANT: Xie, Zhiyi  
APPLICANT: Tao, Yi  
APPLICANT: Zou, Guangzhou  
APPLICANT: Cooper, Bret  
TITLE OF INVENTION: PLANT GENES INVOLVED IN DEFENSE AGAINST  
FILE REFERENCE: 1360.003US2  
CURRENT APPLICATION NUMBER: US/09/887,272A  
PRIOR FILING DATE: 2001-06-23  
PRIOR APPLICATION NUMBER: 60/213,634  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: 60/214,926  
PRIOR FILING DATE: 2000-06-23  
PRIOR APPLICATION NUMBER: 60/261,320  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 60/264,353  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/273,879  
PRIOR FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: 09/887,271  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 6813  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3846  
LENGTH: 1926  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-887-272A-3846

## Alignment Scores:

Pred. No.: 0 Length: 1926  
Score: 2511.50 Matches: 476  
Percent Similarity: 85.9% Conservative: 31  
Best Local Similarity: 80.7% Mismatches: 32  
Query Match: 86.8% Indels: 52  
DB: 34 Gaps: 3

US-10-628-525A-21 (1-539) x US-09-887-272A-3846 (1-1926)

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Qy 8 -----8
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Qy 9 -----AspLeuGly-----11
Db 220 ACGCAGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAG 279
Qy 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29
Db 280 ATCGAGCCCGATCTAGAAAGGTCTCAGAGAAGATTCATCGACAAAACAATTTTGGGCT 339
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Db 340 AGTGAGCAGGAGTCTGAGATCATGGATGTGAAGGAGCAAGCTCAAGCTAAAGTAACAGC 399
Qy 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69
Db 400 ACGGTGTCTTGTAAACCGGTGAGCTTCTCTTATGCAAGTCAGGTGAGCTAGAGAT 459
Qy 70 ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMet 89
Db 460 GTTTGGGTTCACGTGCAATGCTCTTCTCTGCTTGGTGGTCTATGCTGATGTTGTAATG 519
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Db 700 GGAGATAAATTTTGGTGTCTTTGGCGATATATAGTTTCAGATACACATCTCTGCTATGCG 759
Qy 170 AlaCysGluAlaProLeuIleLeuGluGlyGlyTyrIleTyrGlyGlnAsnCysMet 189
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Qy 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289
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Qy 450 ProCysGlyLeuAsnGluLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
Db 1600 CCTTGTGGCCTCAATCAGCTATATGCAATATGGTACAGTGCCTGTTGTTATGGA 1659
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; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12110  
; LENGTH: 2623  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AKI09458  
; DATABASE ENTRY DATE: 2002-08-28  
US-10-449-902-12110  
Alignment Scores:  
Pred. No.: 0 Length: 2623  
Score: 2511.50 Matches: 476  
Percent Similarity: 85.9% Conservative: 31  
Best Local Similarity: 80.7% Mismatches: 32  
Query Match: 86.8% Indels: 52  
DB: 51 Gaps: 3  
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Qy 8 -----8  
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Qy 9 -----AspLeuGly-----11  
Db 412 ACCGAGTGGCGAG 471  
Qy 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
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Qy 30 SerGluAsnSerGluIleValValGlyLeuGlnAlaArgAlaLysValThrGln 49  
Db 532 AGTGACGAGGAGTCTGAGATCATGGATGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 591  
Qy 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp 69

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GenCore version 5.1.7  
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Run on: April 1, 2006, 21:21:57 ; Search time 1008.01 Seconds  
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1603.719 Million cell updates/sec

Title: US-10-628-525A-21

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2525.5	87.3	1881	7	US-10-542-516-9
3	2525.5	87.3	1881	7	US-10-533-232A-307
4	1130.5	39.1	2423	8	US-11-330-822-52
5	1050.5	36.3	3066	12	US-60-757-216-1

6	1050.5	36.3	3066	12	US-60-757-810-1	Sequence 1, Appli
7	1012	35.0	558	10	US-11-227-183A-16489	Sequence 16489, A
8	993	34.3	555	10	US-11-227-183A-16488	Sequence 16488, A
9	978.5	33.8	2007	8	US-11-330-822-54	Sequence 54, Appl
10	838	29.0	1915	8	US-11-330-822-50	Sequence 50, Appl
11	802.5	27.7	598	10	US-11-292-078-969	Sequence 969, App
12	789	27.3	1882	1	PCT-US05-47111-476	Sequence 476, App
13	789	27.3	1882	12	US-60-752-355-476	Sequence 1373, Ap
14	739.5	25.6	2160266	7	US-10-513-024-1373	Sequence 6913, Ap
15	732	25.3	1431	11	US-11-348-414-6913	Sequence 32824, A
16	704	24.3	411	8	US-11-353-150-32824	Sequence 3028, Ap
17	673	23.3	407	8	US-11-329-388-3028	Sequence 11, Appl
18	633	21.9	1434	8	US-11-275-569-11	Sequence 9, Appli
19	634.5	21.6	1409	8	US-11-298-234A-9	Sequence 29117, A
20	597	20.6	374	10	US-11-227-183A-29117	Sequence 17004, A
21	590.5	20.4	635	8	US-11-330-364-17004	Sequence 36, Appl
22	587	20.3	1488	8	US-11-330-822-36	Sequence 66579, A
23	567	19.6	334	8	US-11-353-150-66579	Sequence 11887, A
24	537.5	18.6	1434	7	US-10-953-349-11887	Sequence 5, Appli
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39	380	13.1	11870	8	US-11-298-234A-18	Sequence 18, Appl
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48	334	11.5	278	10	US-11-227-183A-21291	Sequence 21291, A
49	334	11.5	638	7	US-10-953-349-37494	Sequence 37494, A
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51	329	11.4	560	8	US-11-329-388-9900	Sequence 9900, Ap
52	328.5	11.4	580	8	US-11-329-388-5264	Sequence 5264, Ap
53	326	11.3	578	10	US-11-292-078-9340	Sequence 9340, Ap
54	321	11.1	512	8	US-11-330-082-11484	Sequence 11484, A
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56	315	10.9	484	8	US-11-329-388-13004	Sequence 13004, A
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58	312	10.8	798	12	US-60-658-984A-15009	Sequence 15009, A
59	310	10.7	433	8	US-11-329-388-2698	Sequence 2698, Ap
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71	284	9.8	625	8	US-11-329-388-8047	Sequence 8047, Ap
72	282	9.7	649	8	US-11-329-388-8036	Sequence 8036, Ap
73	278	9.6	552	10	US-11-227-183A-20735	Sequence 20735, A
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75	271	9.4	536	8	US-11-329-388-6734	Sequence 6734, Ap
76	270.5	9.4	265	10	US-11-227-183A-13663	Sequence 13663, A
77	268.5	9.3	405	8	US-11-331-019-35306	Sequence 35306, A
78	268.5	9.3	452	8	US-11-353-150-71513	Sequence 71513, A

79 268 9.3 429 10 US-11-314-834-4133  
80 266.5 9.2 420 10 US-11-314-834-3119  
81 264 9.1 464 8 US-11-239-610A-35712  
82 264 9.1 498 8 US-11-330-082-9628  
83 262 9.1 430 8 US-11-239-625A-1691  
84 260.5 9.0 413 10 US-11-227-183A-22990  
85 259.5 9.0 473 10 US-11-227-183A-1156  
86 252 8.7 427 10 US-11-301-327-5271  
87 252 8.7 431 8 US-11-239-610A-8262  
88 250.5 8.7 382 8 US-11-331-019-17873  
89 249.5 8.6 362 8 US-11-239-610A-30183  
90 248 8.6 334 8 US-11-239-625A-2653  
91 248 8.6 269 10 US-11-227-183A-27339  
92 247 8.5 422 10 US-11-227-183A-28996  
93 246.5 8.5 628 10 US-11-292-078-11621  
94 244 8.4 380 8 US-11-331-019-46251  
95 244 8.4 433 8 US-11-353-150-32061  
96 243 8.4 435 10 US-11-314-834-3542  
97 242.5 8.4 340 10 US-11-227-183A-19092  
98 242 8.4 413 8 US-11-239-610A-45292  
99 239 8.3 428 10 US-11-301-327-1905  
100 236 8.2 387 10 US-11-301-327-2362  
101 236 8.2 396 8 US-11-331-019-37401  
102 235.5 8.1 532 10 US-11-292-078-14525  
103 234.5 8.1 352 8 US-11-331-019-47745  
104 234.5 8.1 660 1 PCT-US06-07642-13179  
105 234.5 8.1 660 12 US-60-658-984A-13179  
106 232.5 8.0 373 10 US-11-227-183A-2220  
107 232 8.0 11870 8 US-11-298-234A-18  
108 227.5 7.9 430 10 US-11-227-183A-32219  
109 227.5 7.9 11997 8 US-11-298-234A-29  
110 226 7.8 439 10 US-11-314-834-4822  
111 225 7.8 453 8 US-11-331-019-38804  
112 224 7.7 428 8 US-11-330-082-17895  
113 219.5 7.6 490 10 US-11-313-816-11617  
114 218.5 7.6 480 8 US-11-329-388-5012  
115 218 7.5 330 10 US-11-227-183A-29478  
116 217 7.5 519 8 US-11-329-388-6579  
117 216.5 7.5 379 8 US-11-331-019-45179  
118 216 7.5 380 10 US-11-227-183A-26498  
119 216 7.5 409 8 US-11-239-610A-35665  
120 215.5 7.4 548 8 US-11-329-388-10543  
121 215.5 7.4 572 8 US-11-329-388-8692  
122 215 7.4 270 8 US-11-330-082-254  
123 214.5 7.4 563 8 US-11-329-388-6551  
124 213.5 7.4 542 10 US-11-292-078-2668  
125 211.5 7.3 620 10 US-11-292-078-12124  
126 211 7.3 384 10 US-11-314-834-1227  
127 211 7.3 430 8 US-11-352-295-1103  
128 210 7.3 410 8 US-11-239-610A-35764  
129 209.5 7.2 634 8 US-11-329-388-11949  
130 208.5 7.2 394 8 US-11-352-295-4508  
131 208.5 7.2 405 10 US-11-301-327-5668  
132 208 7.2 375 8 US-11-329-388-1930  
133 205.5 7.1 441 10 US-11-301-327-2428  
134 204.5 7.1 552 8 US-11-329-388-6691  
135 203.5 7.0 446 8 US-11-353-150-59176  
136 201.5 7.0 393 10 US-11-227-183A-26063  
137 199 6.9 407 8 US-11-239-610A-7504  
138 198 6.8 330 10 US-11-227-183A-31596  
139 196 6.8 363 8 US-11-239-610A-38736  
140 195.5 6.8 292 8 US-11-239-610A-33195  
141 195 6.7 592 8 US-11-330-364-14379  
142 194.5 6.7 364 8 US-11-239-625A-3356  
143 194.5 6.7 377 8 US-11-331-019-38891  
144 193 6.7 381 8 US-11-239-610A-48144  
145 192.5 6.7 388 8 US-11-239-625A-944  
146 192 6.6 462 10 US-11-227-183A-17333  
147 191.5 6.6 377 8 US-11-227-183A-21493  
148 191.5 6.6 459 8 US-11-329-388-9415  
149 191 6.6 379 10 US-11-227-183A-24493  
150 191 6.6 567 1 PCT-US06-07642-21971

ALIGNMENTS

RESULT 1

US-11-330-822-56  
; Sequence 56, Application US/11330822  
; GENERAL INFORMATION:  
; APPLICANT: GUAN HANPING  
; APPLICANT: KEELING, PETER L.  
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN  
; FILE REFERENCE: 15053-04  
; CURRENT APPLICATION NUMBER: US/11/330,822  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: PCT/US98/06660  
; PRIOR FILING DATE: 1998-04-03  
; PRIOR APPLICATION NUMBER: 60/042,939  
; PRIOR FILING DATE: 1997-04-04  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 56  
; LENGTH: 1749  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1749)  
US-11-330-822-56

Alignment Scores:

Pred. No.:	4,82e-287	Length:	1749
Score:	2861.00	Matches:	539
Percent Similarity:	92.5%	Conservative:	0
Best Local Similarity:	92.5%	Mismatches:	0
Query Match:	98.9%	Indels:	44
DB:	8	Gaps:	1

US-10-628-525A-21 (1-539) x US-11-330-822-56 (1-1749)

Qy	1	CysValAlaGluLeuSerArgGlu	-----	-----	8
Db	1	TCGCTCGCGGAGCTGAGCAGGGGGGGCGCGCGCGCGCTGCCACCGCGCTGCTG			60
Qy	8	-----	-----	-----	8
Db	61	GGCGCCCGCTCGTGCCTCGCGCGCTTCCTCGCGCGCGCGCGCGCGCGCGCGCA			120
Qy	9	-----	-----	-----	16
Db	121	TCGACGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCTCGGTCGCAACCTGAAGG			180
Qy	17	IleAlaGluGlySerIleAspThrValValAlaSerGluGlnAspSerGluIle			36
Db	181	ATTGCTGAAGTTCATCGATAACACAGTAGTTGTGGCAAGTTCGAGATTCTGAGATT			240
Qy	37	ValValGlyLysGluAlaArgAlaLysValThrGlnSerIleValPheValThrGly			56
Db	241	GTGGTTGGAAAGCAGCAGCTCGAGCTAAGTAACAAAGCATTTGTTTGTAAACCGGC			300
Qy	57	GluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspValCysGlySerLeuProVal			76
Db	301	GAAGCTCTCTTATGCAAGTCTGGGGGTCTAGGAGATGTTTGTGGTTCATTGCCAGTT			360
Qy	77	AlaLeuAlaAlaArgGlyHisArgValMetValValMetProArgTyrLeuAsnGlyThr			96
Db	361	GCTCTTGCTGCTCGTGGTTCACCGCTGATGTTGTAAATGCCAGATATTTAAATGTACC			420
Qy	97	SerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLysHisIleArgIleProCysPhe			116
Db	421	TCCGATAGAGATATGCAATGCAATTTTACACAGAAACACATTCGGATTTCATGCTTT			480
Qy	117	GlyGlyGluHisGluValThrPhePheHisGluTyrArgAspSerValAspTrpValPhe			136

Db 481 GCGGTGAACATGAAGTTACCTTCTTCATGAGTATAGAGATTTCAGTTGAGTGGTGT 540  
Qy 137 ValAspHisProSerTyrHisArgProGlyAenLeuTyrGlyAspLysPheGlyAlaPhe 155  
Db 541 GTTGATCATCTCTCATATACAGACCTGGAAATTTATATGAGATAGATTGGTGTCTTT 600  
Qy 157 GlyAspAenGlnPheArgTyrThrLeuLeuCyStyAlaAlaCyGluAlaProLeuIle 176  
Db 601 GGTGATATCAGTTTCAGATACACACTCTTTGCTATGCTGCATGTGAGGCTCTTTGATC 660  
Qy 177 LeuGluLeuGlyGlyTyrIleTyrGlnAenCysMetPheValValAsnAspTyrHis 196  
Db 661 CTTCGAATGGGAGATATATTATGGACAGAAATGGCATTTGTTGTCAATGATGGCAT 720  
Qy 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
Db 721 GCCAGTCTAGTGCAGTCTCTTCTGTCGCAAAATATAGACCATATGCTGTTTATAAGAC 780  
Qy 217 SerArgSerIleLeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerThr 236  
Db 781 TCCCGCAGCATCTTGTAAATACATAATTAGCACATCAGGGTGTAGAGCCTGCACAGACA 840  
Qy 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTyrValPheProGlu 256  
Db 841 TATCTGACCTTGGTGGCCACTGAATGATGGAGCTCTGGAGTGGGTATTCCTCGAA 900  
Qy 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAenPheLeuLysGlyAlaVal 276  
Db 901 TGGCGCAGGAGGATGCCCTTGACAGGGTGAGCAGTTAAATTTTGAAGGTGCAGTT 960  
Qy 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
Db 961 GTGACACGATCGAATCGTGACTGTGTAAGGGTTATTCTGGGGAGGTGCACAACTGCT 1020  
Qy 297 GluGlyGlnGlyLeuAenGluLeuLeuSerSerArgLysSerValLeuAenGlyIle 316  
Db 1021 GAAGGTGACAGGCTCTCAATGAGCTTTAAGCTCCAGAAAGAGTGTATTAAACGGAT 1080  
Qy 317 ValAsnGlyIleAspIleAenAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
Db 1081 GTAAATGGAATTGACATTAATGATGGAACCTGCCACAGACAAATGTATCCCTGTGAT 1140  
Qy 337 TyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeu 356  
Db 1141 TATCTGTGTATCACTCTCTGGAAGGCCAAATGTAAGGTGCATTTGCAGAGAGAGCTG 1200  
Qy 357 GlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln 376  
Db 1201 GGTTCACCTATAGGCTGATGTTCTCTGATTTGCTTTTATGGAAGGTGGATATCAG 1260  
Qy 377 LysGlyIleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPhe 396  
Db 1261 AAAGCATTTGATCTCACTTCACTATCATACAGATCTCATCGGGAAGATGTTCAATTT 1320  
Qy 397 ValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGluSerIle 416  
Db 1321 GTCATCTTGGATCTGGTACCCAGAGCTTGAAGATGGATGGATGAGATCTACAGATCGATC 1380  
Qy 417 PheLysAspLysPheArgGlyTyrValGlyPheSerValProValSerHisArgIleThr 436  
Db 1381 TTCAGAGTAATTTCTGTGATGGGTGGATTTAGTTGTTCCAGTTTCCACCCGGAATACT 1440  
Qy 437 AlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAenGlnLeu 456  
Db 1441 GCCGGCTGCGATATATTGTTAATGCCATCCAGATTCGAACCTTGTGCTCTCAATCAGCTA 1500  
Qy 457 TyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThr 476  
Db 1501 TATGCTATGCAATGAGCAGTCTCTGTTGTCATGCAACTGGGGGCTCTAGAGATACC 1560  
Qy 477 ValGluAsnPheAsnProPheGlyGluAenGlyGluGlnGlyThrGlyTrpAlaPheAla 496  
Db 1561 GTGGAGACTTCAACCTTTCTGTTGAGAAATGGAGACAGGGTACAGGGTGGGATTCGCA 1620

Qy 497 ProLeuThrThrGluAenMetPheValAspIleAlaAenCysAenIleTyrIleGlnGly 516  
Db 1621 CCCCTAACACACAGAAACATGTTTGTGGACATTTGGGAACTGCAATATCTACATACAGGA 1680  
Qy 517 ThrGlnValLeuLeuGlyArgAlaAenGluAlaAargHisValLysArgLeuHisValGly 536  
Db 1681 ACACAAGTCTCTCTGGGAGGGCTAATGAAGCGAGGCATGTCAAAAGACTTCACGTGGGA 1740  
Qy 537 ProCysArg 539  
Db 1741 CCATGCCG 1749  
RESULT 2  
US-10-542-516-9  
; Sequence 9, Application US/10542516  
; GENERAL INFORMATION:  
; APPLICANT: Heim, Ute  
; APPLICANT: Herbers, Karin  
; APPLICANT: Sonnewald, Uwe  
; APPLICANT: Gluckmann, Eric  
; TITLE OF INVENTION: Expression cassette with promoters of starch synthesis 3 for the  
; TITLE OF INVENTION: expression of nucleic acids in plant tissue containing starch  
; FILE REFERENCE: 13173-00015-US  
; CURRENT APPLICATION NUMBER: US/10/542,516  
; CURRENT FILING DATE: 2005-07-18  
; PRIOR APPLICATION NUMBER: PCT/EP2004/000241  
; PRIOR FILING DATE: 2004-01-15  
; PRIOR APPLICATION NUMBER: DE 103 02 324.0  
; PRIOR FILING DATE: 2003-01-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9  
; LENGTH: 1881  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1878)  
; OTHER INFORMATION: coding for SSS3  
US-10-542-516-9

Alignment Scores:  
Pred. No.: 4,56e-252 Length: 1881  
Score: 2525.50 Matches: 475  
Percent Similarity: 85.8% Conservative: 31  
Best Local Similarity: 80.5% Mismatches: 33  
Query Match: 87.3% Indels: 51  
DB: Gaps: 3

US-10-628-525A-21 (1-539) x US-10-542-516-9 (1-1881)

Qy 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 100 TCGTGGCGGAGCTGAGCAGGACGCTGGTGGTGGCGCACGGCCGCTGGCAGCGGCGCG 159  
Qy 8 ----- 8  
Db 160 CTGGTGAACGACCGGCTCTGCGGACCTTCCTGTCGCCGACGTCGAGCCGCCGCCGCC 219  
Qy 9 -----AspLeuGly----- 11  
Db 220 ACCGAGTCGCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTCGGGAGTCCCGGAG 279  
Qy 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
Db 280 ATCGAGCCCGATCTAGAAGGTCTCAGAGAAGATTCATCGACAAACAAATTTTGTGCT 339  
Qy 30 SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln 49  
Db 340 AGTGAGGAGGATCTGAGATCATGGATGTGAAGAGCAAGCTCAAGCTAAGTAACACGC 399  
Qy 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69

Db 400 AGCGTGTCTTTGTAACCGGTGAAGCTTCTCTTTATGCAAGGTCAAGTGGAGCTAGGAGAT 459  
QY 70 ValCysGlySerLeuProValAlaLeuAlaAalaArgGlyHisArgValMetValMet 89  
Db 460 GTTGTGGTTCATGTCGAATTCGTCTTCGTCTTCGTGGTTCATGCTGTGATGTTGTAATG 519  
QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109  
Db 520 CCGAGATACATGACGGGGCCTTGAACAAATTTTGCAAGCATTTTACACTGAGAAG 579  
QY 110 HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129  
Db 580 CACATTAAGATCCATGCTTGGCGGAGAACATGAAGTTACTTTTTTCCAGATATAGG 639  
QY 130 AspSerValAspTyrValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149  
Db 640 GATTCCTGTGTGGTGTGTGTGATCATCCCTCATATCATAGACCTCGAAATTTGTAT 699  
QY 150 GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169  
Db 700 GGAGATAATTTGGTCTTTGGCGATATCACTTCAGATACACATCTCTGCTGCTATGCG 759  
QY 170 AlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMet 189  
Db 760 GCGTGTGAAGCCCATTAATTTCTGAACCTGGGAGGATATATCTATGGACAGAAATGCAATG 819  
QY 190 PheValValAsnAspTyrHisIleSerLeuValProValLeuLeuAlaIleTyrArg 209  
Db 820 TTTGTTGTGAATGATGGATCCAGTCTGTGGCCAGTCTCTTCTGCTGCAAAATATAGA 879  
QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229  
Db 880 CCATATGGTGTACAGGATGCCCGAGTGTCTTGTCATCATATATCTAGCACATCAG 939  
QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyrGlyAla 249  
Db 940 GGTGTGGAGCCTGCCAGTACATATCTGACCTGGGATTCGCCACCTGAATGGTATGGAGCA 999  
QY 250 LeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGluAlaVal 269  
Db 1000 TTAGAAATGGGTGTTCACAGATGGGCAAGCGGCATGCCCTTGACAAAGGCTGAGCGAGTC 1059  
QY 270 AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr 289  
Db 1060 AATTTTTTAAAGCGCAGTGTGTGACGAGATCGAATTTGTACTGTACGCCAGGGGTAT 1119  
QY 290 SerTyrGluValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArg 309  
Db 1120 TCATGGGAGGTCAACCTGCTGAAGTGGCAAGGCTCAATGAGCTCTTAAGCTCCCGG 1179  
QY 310 LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnProAlaThr 329  
Db 1180 AAGAGTGTATGAATGGAATGTTAAATGGAATTGACATTAATGATTTGGAACCCATCCACA 1239  
QY 330 AspLysCysIleProCysHisTyrSerValAspLeuSerGlyLysAlaLysCysLys 349  
Db 1240 GACAAGTTTCTCCCTATCATTTATCTGTGTGATGACCTGTCCGGAAGGCCAAGTGTAA 1299  
QY 350 GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe 369  
Db 1300 GCTGAATTCAGAGGAGCTGGGTTTACCTATAAGGCCGATGTGCTCTGATTTGGCTTT 1359  
QY 370 IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu 389  
Db 1360 ATTGAAGATTTGGACTATCAAAAGGCATTTGATCTAAATTAATTAATTTGCCATTCATC 1419  
QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTyr 409  
Db 1420 ATGCGGGACAATATTCATTTCTGTCATGCTTGGATCTGGTGACCCAGGTTTGAAGATGG 1479  
QY 410 MetArgSerThrGluSerIlePheLysAspLysPheArgGlyTyrValGlyPheSerVal 429

Db 1480 ATGAGATCCACAGAATCAGGGTACAGGGATAAAATTTCTGTGGATGGGTTTGGATTTAGTGT 1539  
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449  
Db 1540 CCAGTTTCCACCGCAATAACTGACAGGTTTCGATATATTTGTTGATGCCATCCAGATTCGAA 1599  
QY 450 ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469  
Db 1600 CTTTGTGGCTCAATCAGCTATATGCTATGCAATATGGTACAGTGCCTGTTGTTCAATGA 1659  
QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489  
Db 1660 ACTGGAGGCTCAGAGATACAGTGGAGAAATTTAAACCGTTTGTCTGAGAAAGGAGAGCAG 1719  
QY 490 GlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509  
Db 1720 GGTACAGGTTGGGCATTTCTCGCCACTTAACCATTTGAAAAAATGCTGTGGGCATTTGCCGAT 1779  
QY 510 CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529  
Db 1780 GGCAATTTTCGATACAGGGAACACAGTCTCTTTGGAGGGTCTAATGAAGCGAGGCAT 1839  
QY 530 VallysArgLeuHisValGlyProCysArg 539  
Db 1840 GTCAAGCGACTTTACATGGGACCATGCCGC 1869  
RESULT 3  
US-10-533-232A-307  
; Sequence 307, Application US/10533232A  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Bret  
; TITLE OF INVENTION: CELL PROLIFERATION-RELATED POLYPEPTIDES AND USES THEREFOR  
; FILE REFERENCE: 1392-10-19-2  
; CURRENT APPLICATION NUMBER: US/10/533,232A  
; PRIOR FILING DATE: 2005-04-29  
; PRIOR APPLICATION NUMBER: US 60/436,565  
; NUMBER OF SEQ ID NOS: 349  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 307  
; LENGTH: 1881  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1881)  
US-10-533-232A-307  
Alignment Scores:  
Pred. No.: 4,568-252 Length: 1881  
Score: 2525.50 Matches: 475  
Percent Similarity: 85.8% Conservative: 31  
Best Local Similarity: 80.5% Mismatches: 33  
Query Match: 87.3% Indels: 51  
DB: 7 Gaps: 3  
US-10-628-525A-21 (1-539) x US-10-533-232A-307 (1-1881)  
QY 1 CysValAlaGluLeuSerArgGlu----- 8  
Db 100 TCGTGGCGGAGCTGAGCAGGAGCGGTGGTGGCGCAGCGCGCGTGGCACCGCGCGCG 159  
QY 8 ----- 8  
Db 160 CTGGTGAAGCAGCGCGTCTGCGGACCTTCTGCTGGCGACGCTGACGCGCCCGGCC 219  
QY 9 -----AspLeuGly----- 11  
Db 220 AGCAGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGGCGGAGTCCCGCGTGGGGAG 279  
QY 12 LeuGluPro-----GluGlyIleAlaGluGlySerIleAspAsnThrValValAla 29  
Db 280 ATCGAGCCCGATCTAGAAGGTCTCAGAAAGATTCATCGAACAACCAATTTTGTGGCT 339



Qy	30	SerGluGlnAspSerGluIleValValGlyLysGluGlnAlaArgAlaLysValThrGln	49
Db	340	AGTGAGCAGGAGTCTGAGATCATGGATGTGAAGGAGCAAGCTCAAGCTAAAGTAGTAACACGC	399
Qy	50	SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp	69
Db	400	AGCGTTGTCTTTGTAACCGGTGAAGCTTCTCTTATGCAAGTCAGGTGGACTAGGAGAT	459
Qy	70	ValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValValMet	89
Db	460	GTTTGTGGTTCACCTGCCAAATGCTCTTGCTCTTCGTGTGTCATCGTGTGATGGTTGTAATG	519
Qy	90	ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys	109
Db	520	CCGAGATACATGAACGGGGCTTGAACAAAATTTTGCNAACGCAATTTTACCTAGAGAAG	579
Qy	110	HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlyTyrArg	129
Db	580	CACATTAAAGATTCCATGCTTTGGCGGAGAACATGAAGTTACTTTTTTTCACGAGTATAGG	639
Qy	130	AspSerValAspTTPValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr	149
Db	640	GATTCTGTGTGATTGGGTGTTTGTGATCATCCCTCATATCATAGACCTGGAAAATTTGTAT	699
Qy	150	GlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla	169
Db	700	GGAGATAAATTTTGGTGTCTTTTGGCGGATTAATCAGTTTCAGATACACACTCCCTGTGTATGCG	759
Qy	170	AlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMet	189
Db	760	GGGTGTGAAGCCCCCATTAATCTTGAATCGGAGGATATATCTATGGACAGAAATGCATG	819
Qy	190	PheValValAsnAspTTPHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArg	209
Db	820	TTTTGTGTGAATGATGTGCATGCCAGTCTTGTGCGAGTCTCTTCTGTGCAAAATATAGA	879
Qy	210	ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln	229
Db	880	CCATATGGTGTTTAAGGGATGCCCGCAGTGTTCTTGTCTACATAATATCTAGACACATCAG	939
Qy	230	GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTTPtTyrGlyAla	249
Db	940	GGTGTGAGCGCTGCCAGTACATATCTTGACTGGGATTCGCCACTGAATGGTATGGAGCA	999
Qy	250	LeuGluTTPValPheProGluTTPAlaArgArgHisAlaLeuAspLysGlyGluAlaVal	269
Db	1000	TTAGAATGGGTGTATTCCAGAGTGGCGAAGCGCGCATGCCCTTGTCAAGGGGTGAGCGATC	1059
Qy	270	AsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyr	289
Db	1060	AAATTTTAAAGCGCAGTTGTGACAGCAGATCGAATTTGACTGTGACCGCAGGGGTAT	1119
Qy	290	SerTTPGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArg	309
Db	1120	TCATGGGAGGTCCACACTGCTGAAGGTGGCGAAGCCCTCAATGAGCTCTTAAAGTCCCGG	1179
Qy	310	LysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTTPAsnProAlaThr	329
Db	1180	AAGAGTGTATTGAATGGAAATGTAAATGGAATTGACATTAATGATTGGAACCCCATCCACA	1239
Qy	330	AspLysCysIleProCysHisTyrSerValAspAsnLeuSerGlyLysAlaLysCysLys	349
Db	1240	GACAAAGTTTCTCCCTTATCATTTCTTGTGTGATGACTGTCCGGAAGGCCAAGTGTAAA	1299
Qy	350	GlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPhe	369
Db	1300	GCTGAATTGCAGAGGAGCTGGGTTTACCTATAGGCCCGATGTGCCCTCTGATTTGGCTTT	1359
Qy	370	IleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleIleProAspLeu	389
Db	1360	ATTGGAAGATTGGACTATCAAAAGGCGATGATCTAATTAACTTTGCAATTCAGATCTC	1419

```

QY 390 MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409
Db 1420 ATGGCGGACCAATATTCAATTCGTTCATCTCTGGATCTGGTACCACCGGTTTTGAAGGATGG 1479
QY 410 MetArgSerThrGluSerIlePheLeuAspLysPheArgGlyTrpValGlyPheSerVal 429
Db 1480 ATGAGATCCACAGAAATCAGGTACAGGGATAAATTTCTGTGATGGTTGGATTAGTGTT 1539
QY 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuMetProSerArgPheGlu 449
Db 1540 CCAGTTCCTCCACCGAAATAATCGCAGGTTCGATATATTGTTGATGCCATCCAGATTCGAA 1599
QY 450 ProCysGlyLeuAsnGlnLeuThrAlaMetGlnTrpGlyThrValProValValHisAla 469
Db 1600 CTTTGTGGCTCTCAATCAGCTATATGCTATGCAATATGTAATGTAAGTGCCTGTTTTCATGGA 1659
QY 470 ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489
Db 1660 ACTGGAGGCTCAGAGATACAGTGGAGAAATTTAACCCGTTTCTGAAAGAGAGAGCAG 1719
QY 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn 509
Db 1720 GGTACAGGTGGGCAATTCGCCCACTAACCAATGTAAGAAAATGCTGTGGCATTCGGAT 1779
QY 510 CysAsnIleTyrlleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArgHis 529
Db 1780 GGCAATTCGACATACAGGGAACACAAAGTCCTCTTGGGAGGGTCTAATGAAGCGAGGCAT 1839
QY 530 VallyArgLeuHisValGlyProCysArg 539
Db 1840 GTCAAGCGACTTTTACATGGGACCAATGCCG 1869

RESULT 4
US-11-330-822-52
; Sequence 52, Application US/11330822
; GENERAL INFORMATION:
; APPLICANT: GUAN, HANPING
; APPLICANT: KEELING, PETER L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; TITLE OF INVENTION: HOSTS
; FILE REFERENCE: 15053-04
; CURRENT APPLICATION NUMBER: US/11/330,822
; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 2423
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2094)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2107)..(2304)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2308)..(2421)
US-11-330-822-52

Alignment Scores:
Pred. No.: 1,13e-106 Length: 2423
Score: 1130.50 Matches: 254
Percent Similarity: 57.2% Conservative: 64
Best Local Similarity: 45.7% Mismatches: 159
Query Match: 39.1% Indels: 80
DB: 8 Gaps: 11

US-10-628-525A-21 (1-539) x US-11-330-822-52 (1-2423)

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Qy	3	AlaGluLeuSerArgGluAppLeuGlyLeuGluProGluGlyIleAlaGluGlySerIle	22
Db	565	GCTCCTTATGACAGGAGGAT-----AATGAACCTGGCCCTTTGGCTGGCCCTAAATGTG	618
Qy	23	AspAenThrValValAlaSerGluClnAspSerGluIleValValGlyLysGluCln	42
Db	619	ATGAACCTGCTGGTGGCTTCT-----	642
Qy	43	AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla	62
Db	643	-----GAAATGCTCCTTCTTCGC	660
Qy	63	LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAalaArgGly	82
Db	661	AAGACAGTGGCCTTGAGATGTCTGGTGGCTTTGCTTAAGGCTCTGGCGAGGAGGA	720
Qy	83	HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAenTyrAla	102
Db	721	CACCGTGTATGGTGGTATACCAAGATAT-----GGAGAGTATGCC	762
Qy	103	AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluVal	122
Db	763	GAAGCCCGGATTTAGGTGTAAGGAGACGTTACAAGGTAGCTGCAGGATTTCAGAAATT	822
Qy	123	ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyr	142
Db	823	ACTTATTTTCACTCTTACATTGATGGAGTTGATTTTGTATTCTGTAGAAGCCCTCCCTTC	882
Qy	143	--HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPhe	161
Db	883	CGGCACCGGCACATAATATTATGGG-----GGAGAAGATTGGATATTTTGAAG	933
Qy	162	ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGly	181
Db	934	CGCATGATTTTGTCTCAAGCGCGCTGTTGAGGTTCCATGGTATGCTCCATGTGGCGGT	993
Qy	182	TyrIleTyrGlyGln---AsnCysMetPheValValAsnAspTrpHisAlaSerLeuVal	200
Db	994	ACTGTCTATGGTGTATGGCACTTAGTTTTCATTGCTAATGATTGGCATACCGCACTTCG	1053
Qy	201	ProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIle	220
Db	1054	CCTGTCTATCTAAAGGCTATTACCGGGACATAGTGTGTGATGCAGTATGCTCGCTCTGTG	1113
Qy	221	LeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeu	240
Db	1114	CTTGTGATACACAACATTGCTCATCGGTCGTGGCCCTGTAGACGACTTCGTCAATTTT	1173
Qy	241	GlyLeuProProGluTyrTyrGlyAlaLeuGluTyrPheProGluTyrAlaArgArg	260
Db	1174	GACTTGGCT-----GAA	1185
Qy	261	HisAlaLeuAspLys-----GlyGluAlaValAsnPheLeu	272
Db	1186	CATCATCGACCACTTCAACTGTATGACACAACTGGTGGGATCACAGCACTTTT	1245
Qy	273	LysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu	292
Db	1246	GCTCGGGGTGAAGACGGCAGACCGGGTGTGACCGTTAGCAATGCTACATGTGGGAG	1305
Qy	293	ValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal	312
Db	1306	CTGAAGACTTCGGAAGGCGGGTGGGGCTTCACGACATCATAAACACAGAACGACTGGAAG	1365
Qy	313	LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys	332
Db	1366	CTCAGGGCATCGTGAACGCATCGACATGAGCGAGTGGAAACCCCGCTGTGC	1419
Qy	333	IleProCysHisTyrSerValAspAspLeu-----Ser	343
Db	1420	-----GTGCACCTTCCATCCGACGACTACACCAACTACAGTTTCGAGAGCGCTGGA	1473

Qy	344	GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProAsp	363
Db	1474	GGCAAGCGGCAAGTCAAGCGCGGCTTCAGACGGCAGCTGGGCGCTGCAGGTCGCGACGAC	1533
Qy	364	ValProLeuLeuGlyPheIleGlyArgLeuAspTyrlnLysGlyIleAspLeuIleGln	383
Db	1534	GTGCCACTGATCGGTTTCATCGCGCGCTGGACACCAAGAGCGGTGGACATCATCGCC	1593
Qy	384	LeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp	403
Db	1594	GACGCGATCCACTGGATCGCGGGCGAGGACGTGCAGCTCTGTGCTGGGACACCGGCGG	1653
Qy	404	ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly	423
Db	1654	GCCGACCTCGAGGACATGCTCGCGCGCTTCGAGTCGGAGCACAGCGCAAGGTGCGCGCG	1713
Qy	424	TrpValGlyPheSerValProValSerHisArgIleThrIleGlyCysAspIleLeuLeu	443
Db	1714	TGGGTGGGTTCTCGGTGGCCCTTGGCGCACCGCATCACGGCGGGCGCGGACATCCTGCTG	1773
Qy	444	MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTrpAlaMetGlnTyrlnGlyThr	463
Db	1774	ATGCCGTGCGGGTTCGAGCGCTGGGGGCTGACACAGCTCTACGCCATGGCGTACGGGACC	1833
Qy	464	ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProphe	483
Db	1834	GTGCCCGTGTGTGCAGCGCGTGGGGGCTCCGGGACACGGTGGCGCGTTCGACCCGCTTC	1893
Qy	484	GlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMet	503
Db	1894	AACGACACC-----GGGCTCGGTTGGAGCTTCGACCGCGCGGAGCGAACCAGGATG	1944
Qy	504	PheValAspIleAlaAsnCysAsnIleTyrlleGlnGlyThrGlnValLeuLeuGlyArg	523
Db	1945	ATGACGCGCTCTCGCACTCCCT-CACCAGTACCGGAACCTACAGGAGAGCTGGCGCGC	2003
Qy	524	AlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg	539
Db	2004	CTGCAGGCGCGCGCATGCGCGGAGGACCTCAGCTGGGACCCAGCGCGC	2051
RESULT 5			
US-60-757-216-1			
; Sequence 1, Application US/60757216			
; GENERAL INFORMATION:			
; APPLICANT: Claus Proberg,			
; APPLICANT: Ralf-Christian Schmidt			
; TITLE OF INVENTION: Rice starches with improved quality			
; FILE REFERENCE: BCS 05-5011-US Provisional			
; CURRENT APPLICATION NUMBER: US/60757, 216			
; CURRENT FILING DATE: 2006-01-06			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 1			
; LENGTH: 3006			
; TYPE: DNA			
; ORGANISM: Triticum aestivum			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (227)..(2623)			
; OTHER INFORMATION:			
; FEATURE:			
; NAME/KEY: Region1			
; LOCATION: (1190)..(1279)			
; OTHER INFORMATION:			
; FEATURE:			
; NAME/KEY: Region2			
; LOCATION: (1493)..(1612)			
; OTHER INFORMATION:			
; FEATURE:			
; NAME/KEY: Region3			
; LOCATION: (2147)..(2350)			
; OTHER INFORMATION:			
; PUBLICATION INFORMATION:			

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; TITLE: Nucleic acid molecules encoding enzymes from
; TITLE: wheat which are involved in starch synthesis
; DATABASE ACCESSION NUMBER: Derwent/AAV01528
; DATABASE ENTRY DATE: 1998-05-21
; PATENT DOCUMENT NUMBER: WO 97 45545
; PATENT FILING DATE: 1997-05-28
; PUBLICATION DATE: 1997-12-04
; RELEVANT RESIDUES: (1)..(2825)

```

**Alignment Scores:**

Pred. No.:	3,33e-98	Length:	3006
Score:	1050.50	Matches:	230
Percent Similarity:	60.4%	Conservative:	70
Best Local Similarity:	46.3%	Mismatches:	170
Query Match:	36.3%	Indels:	28
DB:	12	Gaps:	8

US-10-628-525A-21 (1-539) x US-60-757-216-1 (1-3006)

QY	50	SerileValPheValThrGlyuAlaSerProTyrAlaLysSerGlyGlyLeuGlyAsp	69
DB	1151	AAAGTGGTCTCGTGGCTGCTAGTGTCTCCCTGGTCAAAACAGGTGCTCGGAGAT	1210
QY	70	ValCysGlySerLeuProValAlaLeuAlaAaArgGlyHisArgValMetValMet	89
DB	1211	GTTCGGGTGCTCTGCCAAGGCTTTGGCAAGAGAGACATCGTGTATATGGTTGGTA	1270
QY	90	ProArgTyrLeuAenGlyThrSerAspLysAenTyrAlaAenAlaPheTyrThrGluLys	109
DB	1271	CCAAAGGTAT-----GGGGCATATGAAGAGCCCTACGATCGCGAGTC	1312
QY	110	HisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg	129
DB	1313	CGAAATACTACAAGGCTGCTGACAGGATATCGAGTGAATTATTTCCATGCTTATATC	1372
QY	130	AspSerValAspTrpValPheValAspHisProSerTyr---HisArgProGlyAsnLeu	148
DB	1373	GATGGAGTTGATTTGTGTTTCATTGACGCTCTCTCTCCGACACCGTCAGGAAGACATT	1432
QY	149	TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr	168
DB	1433	TATGGG-----GCCACGACAGCAAAATTATGAAGCGCATGATTTTGTTCGCAAG	1483
QY	169	AlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln---Asn	187
DB	1484	CGCGCTGTTCAGGTTCCATGGCACAGTTCCTATCGCGGGGTGCTCCCTTATGGGATGCAAAAT	1543
QY	188	CysMetPheValValAenAspTrpHisAlaSerLeuValProValLeuLeuAlaLys	207
DB	1544	CTGCTGTTTATTCGAATGATGGACACGGCACTCCTCGCTGCTATCTGAAAGCATAT	1603
QY	208	TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAla	227
DB	1604	TACAGGACCATGTTTGATCGAGTACATCGTCTCATTTATGTGTATACATAACATCGCT	1663
QY	228	HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluIuTyrTyr	247
DB	1664	CACCAAGGCGGTGGCCCTGTAGATGAATTCCCGTTCCACGAGTTGCTTGAGCACTACCTG	1723
QY	248	GlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGlu	267
DB	1724	-----GAAACATTCAGACTGTACGACCCCGTGGGTGGTGAA	1759
QY	268	AlaValAasnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSerLys	287
DB	1760	CAGGCCAACTACTTCGCGCGCGGCTTGAAGATGGCGGACCAAGGTTGCTGGTGTAGCCCC	1819
QY	288	GlyTyrSerTrpGluValThrAlaGluGlyGlnGlyLeuAenGlnLeuLeuSer	307
DB	1820	GGGTACCTCTGGAGCTGAAGACGGTGGAGGGCGGCTGGGGGCTTCACGACATCATACGG	1879
QY	308	SerArgLysSerValLeuAenGlyIleValAenGlyIleAspIleAenAspTrpAenPro	327

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; LOCATION: (1493)..(1612)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: Region3
; LOCATION: (2147)..(2350)
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; TITLE: Nucleic acid molecules encoding enzymes from wheat which are
; TITLE: Involved in starch synthesis
; DATABASE ACCESSION NUMBER: D9745545
; DATABASE ENTRY DATE: 1998-05-21
; PATENT DOCUMENT NUMBER: WO 97 45545
; PATENT FILING DATE: 1997-05-28
; PUBLICATION DATE: 1997-12-04
; RELEVANT RESIDUES: (1)..(2825)
US-60-757-810-1

Alignment Scores:
Pred. No.: 3,33e-98 Length: 3006
Score: 1050.50 Matches: 230
Percent Similarity: 60.4% Conservative: 70
Best Local Similarity: 46.3% Mismatches: 170
Query Match: 36.3% Indels: 28
DB: 12 Gaps: 8

US-10-628-525A-21 (1-539) x US-60-757-810-1 (1-3006)
QY 50 SerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69
DB 1151 AACGGTGGTTCGTGGCTGCTGAGTGTCTCCCTGGTGCACAAACAGGTGGTCTGGGAGAT 1210
QY 70 ValCysGlySerLeuProValAlaLeuAlaAArgGlyHisArgValMetValMet 89
DB 1211 GTTGGGGTGTCTGCCCAAGCTTTGGCAAGAGAGACATCGTGTATGTTGTGGTA 1270
QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109
DB 1271 CCAAGGTAT-----GGGGACTATGAAGAGCCTACGATGTCGGAGTC 1312
QY 110 HisIleArgIleProCysPheGlyGlyGluHisGlyValThrPhePheHisGlyTyrArg 129
DB 1313 CGAAATACTACAGGCTGCTGGACGAGTATGGAAGTGAATATTTCCATCTTATATC 1372
QY 130 AspSerValAspTyrValPheValAspHisProSerTyr---HisArgProGlyAsnLeu 148
DB 1373 GATGGNGTTGATTTGTTCATTAGCGCTCTCTTCCGACACCGTCAGGAACAT 1432
QY 149 TyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyr 168
DB 1433 TATGGG-----GGCAGCAGACAGGAATATTATGAAGCGCATGATTTTGTCTGCAAG 1483
QY 169 AlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGln---Asn 187
DB 1484 GCCGTGTTGGAGTTCATCGGCAGCTTCATCGCGGGTCCCTTATGGGATGGAAT 1543
QY 188 CysMetPheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAlaLys 207
DB 1544 CTGGTGTATTGCAATGATTGGACACGGCAGCTCTGCTGCTATCTGAAGCATAT 1603
QY 208 TyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAla 227
DB 1604 TACAGGACCATGTTGATGTCAGTACATCGTCCATGATGATGATGATGATGATGATGAT 1663
QY 228 HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTyr 247
DB 1664 CACCAAGGCGCGGCGCTGTAGATGAATTCCTGTCACCGAGTGTGCTGAGCACTACCTG 1723
QY 248 GlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLysGlyGlu 267
DB 1724 -----GACACTTCAGACTGTACGACCCCGTGGTGGTGGTA 1759
QY 268 AlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrValSerLys 287
DB 1759 -----GACACTTCAGACTGTACGACCCCGTGGTGGTGGTA 1759

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DB 1760 CACGCCAACTACTTCGCGCGCGCTGAAGATGGCGGACACGAGTTGTCTGTGTAGSCCCC 1819
QY 288 GlyTyrSerTyrGluValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSer 307
DB 1820 GGGTACCTGTGGAGCTGAAGACGGTGGAGGCGCTGGGGCTTCACGACATCATACGG 1879
QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTyrAsnPro 327
DB 1880 CAGAACGACTGGAAGACCGCGGCGATCTCAACGGCATCGACACATGAGTGGAGACCC 1939
QY 328 AlaThrAspLysCysIlePro-----CysHisTyrSerValAspAspLeu--- 342
DB 1940 GAGGTGGAGCGCCACCTCAAGTCGCGACGCTACACCACTTCTCCTGAGGACGCTGGAC 1999
QY 343 SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362
DB 2000 TCCGCAAGCGGCGAGTCAAGAGGCGCTGCGAGCGGAGCTGGGCTGCGAGTCCGCGCC 2059
QY 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIle 382
DB 2060 GACGTGCGGCTGCTGCGCTTCTATCGCGCGCTGGAGCGGCGAGAGGCTGGAGATCATC 2119
QY 383 GlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402
DB 2120 GCGGACGCGCATGCCCTGGATCGTGAGCCAGGACGTCAGCTGTGTATGCTGGGACCGGG 2179
QY 403 AspProGluLeuGluAspTyrMetArgSerThrGluSerIlePheLysAspLysPheArg 422
DB 2180 CGCCACGACCTGGAGAGCATGCTGCAGCATCTTCGAGCGGAGCACCACGACAAAGTGCGC 2239
QY 423 GlyTyrValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442
DB 2240 GGGTGGTGGGTTCTCGTGGCTTGGCGGACCGGATCATCGCGGGGCGGACGCGCTC 2299
QY 443 LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGly 462
DB 2300 CTCATGCCCTCCGGTTCGAGCGGCGGCTGGAACAGCTCTACGCCATGCCCTACGCGC 2359
QY 463 ThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnPro 482
DB 2360 ACCGTCGCGCTGTCGACGCGCTGCGCGGCTTCAGGACACCGCTGCCGCGCTGACCC 2419
QY 483 PheGlyGluAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsn 502
DB 2420 TTCACCACTCC-----GGGTCGCTGGAGCTTCGACCGCGCGGCGGCGCACAG 2470
QY 503 MetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGly 522
DB 2471 CTGATCGAGGCGCTCGGCACTGCTCCT-CCGCACTTACCGAGACTTCAAGGAGAGCTGGAG 2529
QY 523 ArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyProCysArg 539
DB 2530 GGCCCTCCAGGACCGCGCATGTCTCAGGACTTTCAGTGGGAGACGCGCGC 2580

RESULT 7
US-11-227-183A-16489
; Sequence 16489, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 16489
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:

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OTHER INFORMATION: Clone ID: LIB3150-035-Q1-N1-F10.F2  
US-11-227-183A-16489

Alignment Scores:		
Pred. No.:	2,686-95	558
Score:	1012.00	182
Percent Similarity:	100.0%	0
Best Local Similarity:	100.0%	0
Query Match:	35.0%	0
DB:	10	0
Length:		
Matches:		
Conservative:		
Mismatches:		
Indels:		
Gaps:		

US-10-628-525A-21 (1-539) x US-11-227-183A-16489 (1-558)

Qy	68	GlyAspValCysGlySerLeuProValAlaLeuAlaAaArgGlyHisArgValMetVal	87
Db	12	GGAGATGTTTGTGGTTCAATGCCAGTCTCTTGTCTGTGTGTACCGGTGTGATGGTT	71
Qy	88	ValMetProArgTyrLeuAsnGlyThrSerAspIysAsnTyrAlaAsnAlaPheTyrThr	107
Db	72	GTAAATGCCACAGATATTAAATGGTACCTCCCATAGAATATTATGCAAATGCATTTTACACA	131
Qy	108	GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu	127
Db	132	GAANAACACATTCGAGATTCATGCTTTGGCGGTGAACATGAAGTTACTCTTCTCCATGAG	191
Qy	128	TyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsn	147
Db	192	TATAGAGATTTCAGTTGACTGGGGTGTGTTGTGATCATCCCTCATATACACAGACCTGGAAAT	251
Qy	148	LeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCys	167
Db	252	TTATATGAGAGATAAGTTTGGTGTCTTTTGGTGATTAATCAGTTTCAGATACACACTCCITTCG	311
Qy	168	TyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGlyGlnAsn	187
Db	312	TATGCTGCATGTAGGCTCCITTTGATCCTTGAAATGGAGGATATAATTATGACAGAAAT	371
Qy	198	CysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLys	207
Db	372	TGCATGTTTGTGTCAATGATTGGCATGGCCAGTCTAGTGGCAGTCTCTTCCTGTCGAAA	431
Qy	208	TyrArgProTyrGlyValTyrIysAspSerArgSerIleLeuValIleHisAsnLeuAla	227
Db	432	TATAGACCATATGGTGTATTAAAGATCCCGCAGCATCTCTGTGTAATACATAATTTAGCA	491
Qy	228	HisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTyrTrpTyr	247
Db	492	CATCAGGGTGTAGAGCCTGCAGACACATATCCTGACCTTGGGTTCACACTGATGGTAT	551
Qy	248	GlyAla	249
Db	552	GGAGCT	557

## RESULT 8

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US-11-227-183A-16488
; Sequence 16488, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalquidi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 16488
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: unsure at all n locations

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; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-035-Q1-N1-F10.F1
US-11-227-183A-16488

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[illegible]

US-10-628-525A-21 (1-539) x US-11-227-183A-16488 (1-555)

Qy	66	GlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgVal	85
Db	1	GGTACTAGTNTNTNTGTTGGTTTCATTGCCAGTTGCTCTTGCTGCTGCTGGTCACCGTGA	60
Qy	86	MetValValMetProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPhe	105
Db	61	TAGGTGTGAATGCCCAGATATTTAAATGGTACCTCCGATTAAGAAATTAATGCAAAATGCATTT	120
Qy	106	TyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePhe	125
Db	121	TACACAGAAACACATTCGATTCGATCTTTGGCGGTGAACATGAAGTTACTCTTCTTC	180
Qy	126	HisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgPro	145
Db	181	CATGAGTATAGAGATTTCAGTTTCAGTGGGTGTTTGTTCATCATCCCTCATATCACAGACCT	240
Qy	146	GlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeu	165
Db	241	GGAAATTTATATGGAGATTAAGTTTGGTGCTTTTGGTGATAATCAGTTTCAGATACACACTC	300
Qy	166	LeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluGlyGlyTyrIleTyrGly	185
Db	301	CTTTGCTATGCTGCATGTGAGGCTCCTTTGATCTCTGAAATGGGAGGATATATTATATGGA	360
Qy	186	GlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAla	205
Db	361	CAGAAATTCATGTTGTTGTCAATGATGGCATGGCCAGTCTAGTGGCCAGTCTCTTGCT	420
Qy	206	AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn	225
Db	421	GCNAAATATAGACCATATGGTGTTTATAAGACTCCCGCAGCATTTCTGTAAATACATAAT	480
Qy	226	LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu	245
Db	481	TTAGCACATCAGSGGTAGAGCCTGCAGGCACATATCTGACCTTGGGTGGCCACCTGAA	540
Qy	246	TrpTyrGlyAlaLeu	250
Db	541	TCGGTATGGAGCTCTG	555

## RESULT 9

```

US-11-330-822-54
; Sequence 54, Application US/11330822
; GENERAL INFORMATION:
; APPLICANT: GUAN, HANPING
; APPLICANT: KEELING, PETER L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; TITLE OF INVENTION: HOSTS
; FILE REFERENCE: 15053-04
; CURRENT APPLICATION NUMBER: US/11/330.822
; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 2007

```

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/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(2007)
/ US-11-330-822-54

Alignment Scores:
Pred. No.: 5 67e-91 Length: 2007
Score: 978.50 Matches: 217
Percent Similarity: 59.2% Conservative: 76
Best Local Similarity: 43.8% Mismatches: 174
Query Match: 33.8% Indels: 29
DB: 8 Gaps: 9

US-10-628-525A-21 (1-539) x US-11-330-822-54 (1-2007)

QY 50 SerileValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAsp 69
Db 544 AACGTGATCGTGGTGGCTGCTGAATGTTCTCCATGGTGCAGAAACAGGTGGTCTTGGAGAT 603
QY 70 ValCysGlySerLeuProValAlaLeuAlaAArgGlyHisArgValMetValValMet 89
Db 604 GTTGTGGAGCTTTACCCAGGCTTTAGCGAGAAGAGGACATCGTGTATTATGTTGTGATA 663
QY 90 ProArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThrGluLys 109
Db 664 CCNAGTAT-----GGGGACTATGTGAAGCCCTTTCATATGGGAATC 705
QY 110 HisileArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyrArg 129
Db 706 CGGAATACTACAAAGCTCGAGGACAGGACCTAGAAGTGAATTAATTCATGCAATTATT 765
QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLeuTyr 149
Db 766 GATGGAGTCGACTTGTGTTCATTGATGCTCTTTCCGGCACCCGTCAGATGACATATAT 825
QY 150 GlyAspLysPheGlyValaPheGlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAla 169
Db 826 GGG-----GGAGTAGGAGGAGGAATCATGAGCGCATGATTTTGTTCAGGTT 876
QY 170 AlaCysGluAlaProLeuLeuLeuGluLeuGlyTyrIleTyrGlyGln---AsnCys 188
Db 877 GCTGTGAGTTCTTGGCACGCTCCATCGCGTGGTGTGTGTACGGAGATGGAATTTG 936
QY 189 MetPheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaLysTyr 208
Db 937 GTGTTTCATTCGCAATTTGGCACACATGCACCTCTGCCTGTTTATCTGAAGGCATATTAC 996
QY 209 ArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHis 228
Db 997 AGAGACCATGGTTAATGAGTACACTCGCTCGCTCTGCTATACATACATCGGCCAC 1056
QY 229 GlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyrGly 248
Db 1057 CAGGCGCGGTGCTGTATCAATTCCTCGTACATGAGCTTCTGTAACACTAACCTTCAA 1116
QY 249 AlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLysGlyGluAla 268
Db 1117 CATTTTCGAGCTACGATCCCGTC-----GGTGGCGAGGAC 1152
QY 269 ValAsnPheLeuLysGlyAlaValVal---ThrAlaAspArgIleValThrValSerLys 287
Db 1153 GCCAATCTTTGGCCGCTGTGTTCTGAAGATGGCAGACCGGTGGTGTACTGTACGCCG 1212
QY 288 GlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuSer 307
Db 1213 GGCTACCTGTGGAGCTGAAGACAGTGAAGCGGCTGGGGCTCCACGACATCCGT 1272
QY 308 SerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnPro 327
Db 1273 TCTAACGACTGAAGATCAATGGCATTCGTGAACGATCGACCAACAGGAGTGAACCC 1332
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QY 328 AlaThrAspLysCysIlePro-----CysHisTyrSerValaAspLeu--- 342
Db 1333 AAGTGGACGTGCACCTCGGGTCGACGGCTACACCACTACTCTCTCGACACCTCGAC 1392
QY 343 SerGlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362
Db 1393 GCTGGAAGCGGCAGTCAAGCGCCCTGCGACGGGAGCGTGGCTGCGAAGTGGCGAC 1452
QY 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeu 382
Db 1453 GACGTGCCGCTGCTCGGCTTCATCGGGCTTCGTGATGGACAGAGGGCGGTGACATCAT 1512
QY 383 GlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402
Db 1513 GGGGACGGATGCGGTGATCGCGGGGAGGACGTGCGAGTGTGTGTGCTGGGCACCGGC 1572
QY 403 AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422
Db 1573 CCACCTGACCTGGAACGAATGCTGCAGCACTTTGGAGCGGAGCATCCCAACAAGGTGCGC 1632
QY 423 GlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442
Db 1633 GGGTGGGTGGGTTCCTGCTCTAATGTGTGCATCGCATCACCGCGGCGGCCACCGCTG 1692
QY 443 LeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGly 462
Db 1693 GTGATGCCCTCCGCTTTCGCCGC---GGGCTGAACCAAGCTCTACGCGATGCATACGGC 1749
QY 463 ThrValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnPro 482
Db 1750 ACCGTCCCTGTGTGCACCGCGTGGCGGGCTCAGGGACACCGTGGCGCGCTTCGACCCG 1809
QY 483 PheGlyGluAsnGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsn 502
Db 1810 TTC-----GGCGACGCGCGGCTCGGGTGGACTTTTGACCGCGCGGAGCCAAACAAG 1860
QY 503 MetPheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuGly 522
Db 1861 CTGATCAGGTGCTCAGCCACTGCT-CGACACGTACCGAAACTACGAGGAGAGTGGNA 1919
QY 523 ArgAlaAsnGluAlaArgHisValLysArgLeuHisValGlyPro 537
Db 1920 GAGTCTCCAGGCGCGCGCATGTGCGAGAACCTCAGCTGGGACCA 1964

RESULT 10
US-11-330-822-50
; Sequence 50, Application US/11330822
; GENERAL INFORMATION:
; APPLICANT: GUAN, HANPING
; APPLICANT: KEELING, PETER L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; TITLE OF INVENTION: HOSTS
; FILE REFERENCE: 15053-04
; CURRENT APPLICATION NUMBER: US/11/330,822
; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 50
; LENGTH: 1915
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1815)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1819)..(1914)
US-11-330-822-50
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## Alignment Scores:

Pred. No.: 2,24e-76 Length: 1915  
 Score: 838.00 Matches: 200  
 Percent Similarity: 54.3% Conservative: 86  
 Best Local Similarity: 38.0% Mismatches: 174  
 Query Match: 29.0% Indels: 68  
 DB: 8 Gaps: 15

US-10-628-525A-21 (1-539) x US-11-330-822-50 (1-1915)

```

Qy 40 LysGluGlnAlaArg-----AlaLysValThr 48
Db 169 CAGCAGCAGCGCGCGCGCGCGCGCGTCCCGTCGCTCGTGTGGCGCAGCGCGCGC 228
Qy 49 GlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGly 68
Db 229 ATGAACGCTGCTCTGTCGCGCGCGCGCGCGCGTGGAGCAAGACCGCGCGCTCGGC 288
Qy 69 AspValCysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValVal 88
Db 289 GAGTCTCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348
Qy 89 MetProArgTyrLeuAenGlyThrSerAspLysAsnTyrAlaAenAlaPheTyrThrGlu 108
Db 349 TCTCCCGCTAC-----GACCAGTACAGGACGCGCTCGGACACCGC 390
Qy 109 LysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluTyr 128
Db 391 GTCGTGTCCGAGATCAAGATGGGAGACCGGTACGAGACGCTCAGGTCTTCTCCACTGCTAC 450
Qy 129 ArgAspSerValAspTrpValPheValAspHisProSerTyr-----142
Db 451 AAGCGGAGTGGACCGCGGTGCTGTGACCCACCTGTTCTCTGGAGAGGGTTTGGGGA 510
Qy 143 HisArgProGlyAenLysGlyAspLysPheGlyAla---PheGlyAspAenGlnPhe 161
Db 511 AAGACCGAGGAGAGATCTACGGCGCTGTCGTGGACGACTACAGGACACACAGCTG 570
Qy 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuLeuLeuGlyGly 181
Db 571 CGGTTTCAGCTGTATGCCAGGCGACACTTGAAGCTCCAGGATCCTGAGCCTCAACAC 630
Qy 182 -----TyrIle-----TyrGlyGlnAsnCysMetPheValValAenAspTrpHis 196
Db 631 AACCCATACTTCTCCGACCATACGGGAGGAGCGTGTGTCGTGCAACGACTGGCAC 690
Qy 197 AlaSerLeuValProValLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216
Db 691 ACCGGCCCTCTCTCGTCTACTCAAGAGCACTACCGTCCCGCGCATCTACAGGAC 750
Qy 217 SerArgSerIleLeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerThr 236
Db 751 GCAAGACCGCTTCTGCTATCCACAACTCTCTACCGCGCGGTTCGCTTCTCCGAC 810
Qy 237 TyrProAspLeuGlyLeuProGluTyrTyrGlyAlaLeuGluTrpValPheProGlu 256
Db 811 TACCCGAGCTGAACCTCCCGGAGAGATTCAAGTCTGCTTCGATTTCATC-----861
Qy 257 TrpAlaArgHisAlaLeuAenLys-----GlyGluAlaValAenPheLeuLys 273
Db 862 -----GACCGCTACGAGAGCGCGTGGAGCGCGGAGATCACTGGATGAAG 909
Qy 274 GlyAlaValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu---292
Db 910 GCGGAGATCTCGAGGCGGACAGGCTCTCACCGTCCAGCCCTACTACCGGAGGCTC 969
Qy 293 ValThrThrAlaGluGlyGlnGlyLeuAenGluLeuSerSerArgLysSerVal 312
Db 970 ATCTCCGGCATCGCCAGGGGCTCGAGCTCGAACATCATG-----CGCCTCACCGGC 1023
Qy 313 LeuAenGlyIleValAenGlyIleAenPheAenAspTrpAenProAlaThrAspLysCys 332
Db 1024 ATCACCGCATCGTCAACGGCATGACGTCAGGAGTGGAGCCCGCAGGAGCAAGTAC 1083

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Qy 333 IleProCysHisTyrSerValAspAsp---LeuSerGlyLysAlaLysCysLysGlyVala 351
Db 1084 ATCGCGTGAAGTACGACGCTGTCGACGCGCGTGGAGCGCGCTGAACNAGGAGCG 1143
Qy 352 LeuGlnLysGlnLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGly 371
Db 1144 CTGACGCGGAGGTTCGGGCTTCGGGTCCCGGTGACCGAACAATCCCGTGTGGGCTTCATCGGC 1203
Qy 372 ArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIleLeuProAspLeuMetArg 391
Db 1204 AGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1263
Qy 392 -----GluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp 409
Db 1264 ATGGTGGAGGAGCTGTCAGATCGTTCCTGCGGACGCGGCAAGAGAGTTCGAGCGCATG 1323
Qy 410 MetArgSerThrGlnSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerVal 429
Db 1324 CTCTAGCGCGCGGAGGAGAGAGTTCGAGGACAGGTGCGCGCGCTCAAGTTCAACGCG 1383
Qy 430 ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu 449
Db 1384 GCCTGGCGGACCAATCATGTGCGCGCGCGCGCTGCTCGCCCTACCGAGCGCTTCGAG 1443
Qy 450 ProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla 469
Db 1444 CCCTGGCGCTCATCCAGCTGCGAGGGATGCGATACGGAAGCGCTCGCGCTCGCTCC 1503
Qy 470 ThrGlyGlyLeuArgAspThrValGluAenPheAenProPheGlyGluAenGlyGluGln 489
Db 1504 ACCGTGGAGCTGCTGACACCATCATC-----GAAGGC 1536
Qy 490 GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAenMetPheValAenPheAlaAen 509
Db 1537 AGACCGGTTTCAATGCGCGCGCTCAGCGTGCAC-----1572
Qy 510 CysAenIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAenGluAlaArgHis 529
Db 1573 TGTAACTGCTGGA-GCCGCG-----GGAGCTCAAGAGGTGGCCACCAC 1616
Qy 530 ValLysArgLeuHisValGly 536
Db 1617 ATTGACGCGCGCATCAAGGT 1637

```

RESULT 11  
 US-11-292-078-969  
 ; Sequence 969, Application US/11292078  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deikman, Jill  
 ; APPLICANT: Feng, Paul C.C.  
 ; APPLICANT: Fincher, Karen L.  
 ; APPLICANT: Ziegler, Todd E.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE OF INVENTION: Plants  
 ; FILE REFERENCE: 16517.346 - 38-21(52274)C  
 ; CURRENT APPLICATION NUMBER: US/11/292,078  
 ; CURRENT FILING DATE: 2005-12-02  
 ; PRIOR APPLICATION NUMBER: US 10/021,323  
 ; PRIOR FILING DATE: 2001-12-12  
 ; PRIOR APPLICATION NUMBER: US 60/255,619  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 17880  
 ; SEQ ID NO 969  
 ; LENGTH: 598  
 ; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3825-016-Q1-K6-D4  
 US-11-292-078-969

Alignment Scores:  
 Pred. No.: 1.92e-73 Length: 598







Db 1588 GGTTCGTCATCGAGTCGGAACCTGTTGAT 1620

RESULT 14

US-10-513-024-1373

; Sequence 1373, Application US/10513024

; GENERAL INFORMATION:

; APPLICANT: CHIRON SRL

; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH

; APPLICANT: TELFORD John

; APPLICANT: MASIGNANI Vega

; APPLICANT: MARGARIT Y ROS Immaculada

; APPLICANT: GRANDI Guido

; APPLICANT: FRASER Claire

; APPLICANT: TETTELIN Hervé

; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B

; FILE REFERENCE: P030497W0

; CURRENT APPLICATION NUMBER: US/10/513, 024

; CURRENT FILING DATE: 2004-11-01

; PRIOR APPLICATION NUMBER: GB-0210128.5

; PRIOR FILING DATE: 2002-05-02

; NUMBER OF SEQ ID NOS: 1373

; SOFTWARE: SeqWin99, version 1.03

; SEQ ID NO 1373

; LENGTH: 2160266

; TYPE: DNA

; ORGANISM: Streptococcus pyogenes

US-10-513-024-1373

Alignment Scores:

Pred. No.:	1.62e-61	Length:	2160266
Score:	739.50	Matches:	183
Percent Similarity:	54.4%	Conservative:	94
Best Local Similarity:	36.0%	Mismatches:	160
Query Match:	25.6%	Indels:	73
DB:	7	Gaps:	15

US-10-628-525A-21 (1-539) x US-10-513-024-1373 (1-2160266)

QY 17 IleAlaGluGly---SerIleAspAenThrValVal-----ValAlaSer 30

Db 857475 ATCGGAGAGGGGCAACCACTTAAATCTATTATTGACAAATGCGTTAAGGTTGCATCC 857534

QY 31 -----GluGlnAepSerGluIleValValGlyLys-----GluGln 42

Db 857535 CGAGTTACATTGAAGGTAGTTAGATAAACCGTTAGTCAATTCCTAAATTTTCAGAGATT 857594

QY 43 AlaArgAlaLysValThrGlnSerIleValPheValThrGlyGluAlaSerProTyrAla 62

Db 857595 AATGA-GGATATTATACAAATGAAATAATGTTGTCGGCAGAGGGTCTCCCTTTGCT 857653

QY 63 LysSerGlyGlyLeuGlyAspValCysGlySerLeuProValAlaLeuAlaAlaArgGly 82

Db 857654 AAACAGGGTGGTTGGAGATGTGATGCGCACTCCCAAAATCACTTAGTAAAGGTT 857713

QY 83 HisArgValMetValValMetProArgTyrLeuAsnGlyThrSerAspLysAenTyrAla 102

Db 857714 CATGATGTCGCTGTTGTCATGCCATATTAT-----GATATGGTAGACCAAAATTTGGA 857767

QY 103 AenAla-----PheTyrThrGluLysHisIleArgIleProCysPhe 116

Db 857768 GACCAAAATAGAAAACCTCATGTATTCTATACA----- 857800

QY 117 GlyGlyGluHisGluValThrPhePheHisGluTyr-----Arg 129

Db 857801 -----GATGTTGGCTGGCGTCATCAATATGTAGGAGTTAAGAGACTTTCTCAA 857848

QY 130 AspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAenLeuTyr 149

Db 857849 GATAATGTTACGTTCTACTTTATGATATCAATATTATTTTATAGAGGTCATGTCAT 857908

QY 150 GlyAspLysPheGlyAlaPheGlyAspAenGlnPheArgTyrThrLeuLeuCysTyrAla 169

Db 857909 CGTGAT-----TGGGATGATGGGAGCGTTTGTCTATTATTCCAATTAGCT 857953

QY 170 AlaCysGluAlaProIleLeuGluLeuGlyGlyTyrIleTyrClyGlnAenCysMet 189

Db 857954 GCTTTTAGAG-----TTGATGGAGAAAATCGATTTTATTATCCCGAT-----GTC 857995

QY 190 PheValValAsnAspTrpHisAlaSerLeuValProValLeuLeuAlaAlaLysTyrArg 209

Db 857996 TTACAGCTCCATGATTATCATACAGCAATGATTCCTTCTTATTTGAAAGAGAGTACCAC 858055

QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAenLeuAlaHisGln 229

Db 858056 TGGATTCCAGCGCTATAATAATAAAGAGCAGATTTTACTATTACCAATATGCAATTTCAA 858115

QY 230 GlyValGluProAlaSerThrTyrProAspLeu---GlyLeuProGluTrpTyr--- 247

Db 858116 GGGCAGTTGGTCCGAAATGTTAGAGATTATTGAGAGTTGGCGCTCAGAGATATGAA 858175

QY 248 ---GlyAlaLeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAspLysGly 266

Db 858176 GATGGNACTCTTAGATGG----- 858196

QY 267 GluAlaValAsnPheLeuLysGlyAlaValValThrAlaAspArgIleValThrValSer 286

Db 858197 AATTGCTTTAATTGGATGAAGCAGCAATCTTTACTCAGATAGAGTACAACGGTATCA 858256

QY 287 LysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeu 306

Db 858257 CCAAGCTACGCAATGAAATAAAACTCCAGAAATTTGGTAAAGGTTAGATCAAAATATG 858316

QY 307 SerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAenAspTrpAen 326

Db 858317 CGTATGGAAGCAGGCAAAATTTATCTGGAATTTGAATGTTGATAGCGATTTGTTAAAT 858376

QY 327 ProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLysSerGlyLysAla 346

Db 858377 CCAGAAACAGATGCTTTTGTCCATATCATTTTCAAAAAGCAACTTAGAGGCAAAAT 858436

QY 347 LysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366

Db 858437 AAAATAAGTTGGCTTTTACAGGAAATTTGGGCTTACCTCAAGATAAAANTATGACATTA 858496

QY 367 IleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGlnLeuIle 386

Db 858497 ATTGCTATTGTTTTCAGACTTACCGATCAAAAGGATTTGATATTATTGCTTCTGAAATG 858556

QY 387 ProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeu 406

Db 858557 GACAAATATGCTTCAACAAGATATTCAAAATGGTTATTTTAGGAACAGGCTATCACCATTT 858616

QY 407 GluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGlyTrpValGly 426

Db 858617 GAAGAAACGTTCTCTTATTTTGTCTAGTCGTACCTCGTAAATACTATCTGCTAATATTACT 858676

QY 427 PheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSer 446

Db 858677 TTTGACTTAAGATTAGCGCAACAGATTTATGCGGCTTCAGATATCTTCATGATGCCAGT 858736

QY 447 ArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProVal 466

Db 858737 GCTTTTGAACCTTGTGGTCTCTCGCAGATGATGGCTATCAGATATCGTAGCTTGGCTTG 858796

QY 467 ValHisAlaThrGlyGlyLeuArgAspThrValGluAenPheAsnPropGlyGluAen 486

Db 858797 GTACATGAAGTTGGAGGATTAAGATATCTGTGGTAGCCCTTCATCAATTTGATGTAGT 858856

QY 487 GlyGluGlnGlyThrGlyTrpAlaPhe 495

Db 858857 -----GGTACAGGTTTTCATT 858874

RESULT 15

US-11-348-413-6913

; Sequence 6913, Application US/11348413

; GENERAL INFORMATION:

; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; APPLICANT: Murphy, Ellen  
 ; APPLICANT: Olmsted, Stephen  
 ; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES  
 ; FILE REFERENCE: 031896-084100 (AM 101724)  
 ; CURRENT APPLICATION NUMBER: US/11/348,413  
 ; CURRENT FILING DATE: 2006-02-07  
 ; PRIOR APPLICATION NUMBER: PCT/US05/035471  
 ; PRIOR FILING DATE: 2005-10-05  
 ; PRIOR APPLICATION NUMBER: US 11/243,445  
 ; PRIOR FILING DATE: 2005-10-05  
 ; PRIOR APPLICATION NUMBER: US 60/615,573  
 ; PRIOR FILING DATE: 2004-10-05  
 ; NUMBER OF SEQ ID NOS: 1276209  
 ; SEQ ID NO 6913  
 ; LENGTH: 1431  
 ; TYPE: DNA  
 ; ORGANISM: Streptococcus agalactiae  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(1431)  
 ; OTHER INFORMATION: WANO1UL07; ORF; 0000011100000; Cluster contains WANO1PJHM  
 ; OTHER INFORMATION: :SAG0856:giga-glycogen synthase:2603.NC\_004116.1  
 ; US-11-348-413-6913

## Alignment Scores:

Pred. No.: 1,57e-65 Length: 1431  
 Score: 732.00 Matches: 169  
 Percent Similarity: 55.5% Conservative: 87  
 Best Local Similarity: 36.7% Mismatches: 147  
 Query Match: 25.3% Indels: 58  
 DB: 11 Gaps: 11

US-10-628-525A-21 (1-539) x US-11-348-413-6913 (1-1431)

QY 51 IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspVal 70  
 DB 7 ATAAATGTTGTTGGCGAGAGGTGCTCCCTTTGCTTAAACACAGGTGGTTGGGAGATGTG 66  
 QY 71 CysGlySerLeuProValAlaLeuAlaAlaArgGlyHisArgValMetValMetPro 90  
 DB 67 ATTGGGGCACTCCCAAAATCACTTAGTAAAGGTCATGATGCTGTTGTTCATGCCA 126  
 QY 91 ArgTyrLeuAsnGlyThrSerAspLysAsnTyrAlaAsnAla 104  
 DB 127 TATTAT-----GATATGTTAGACCAAAATTTGGAGACCAATAGAAACCTCATGTAT 180  
 QY 105 PheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhe 124  
 DB 181 TTCTATACA-----GATGTTGGCTGG 201  
 QY 125 PheHisGluTyr-----ArgAspSerValAspTrpValPheVal 137  
 DB 202 CGTCATCAATATGATAGAGTTAAGAGACTTCTCAAGATAAATGTTACGTTCTACTTTATT 261  
 QY 138 AspHisProSerTyrHisArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGly 157  
 DB 262 GATAATCAATATTATTTTATAGAGTTCATGCTATGGTGTAT-----TGG 306  
 QY 158 AspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeu 177  
 DB 307 GATGATGGGGAGCGGTTTTCCTTATTCCAAATAGCTGCTTAGAG-----TTGATG 357  
 QY 178 GluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAla 197  
 DB 358 GAGAAATCAATTTTATTCGGAT-----GTCTTACGCTCCATGATTATATACA 408  
 QY 198 SerLeuValProValLeuAlaLysTyrArgProTyrGlyValTyrLysAspSer 217  
 DB 409 GCAATGATTCCTTCTTATTGAAAGAGAGATACCACTGGATTCCAGCCCTATAATAATA 468  
 QY 218 ArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyr 237

DB 469 AGARCAAGTTTTTTACTATTCAATAATTTGAATTTCAAGGGCAGTTTGGTCCAGAAATGTTA 528  
 QY 238 ProAspLeu---GlyLeuProProGluTyrPhe-----GlyAlaLeuGluTyrPheValPhe 254  
 DB 529 GGAGATTTATTTGGAGTTGGCGCTGAGAGATATGAAGATGGAATCTTTAGATGG----- 582  
 QY 255 ProGluTrpAlaArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGly 274  
 DB 583 -----AATAATTTGTTCTTAATTTGGATGAAAGCA 609  
 QY 275 AlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThr 294  
 DB 610 GCAATTTCTTTACTCAGATAGATGCAACCGGTATCCCAAGCTACGCAAAATGAATAAAA 669  
 QY 295 ThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsn 314  
 DB 670 ACTCCAGAAATTTGGTAAGGTTTAGATCAAAATTTGCGTATGGAAGCAGGCAAAATATCT 729  
 QY 315 GlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIlePro 334  
 DB 730 GGAATTTGTAATGTTATTGAYACGGATTTGTTAAATCCAGAAACAGATGCTTTTGGCCA 789  
 QY 335 CysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLys 354  
 DB 790 TATCATTTTTCRAAAAGCAACTTAGAGGGCAAAATTTAAAAATTAAGTTGGCTTTACAGAA 849  
 QY 355 GluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGlyArgLeuAsp 374  
 DB 850 AATTTGGGCTTACCTCAAGATAAAATGTACCAATTAATTTGGTATTGTTTCCAGCATACC 909  
 QY 375 TyrGlnLysGlyIleAspLeuGlnLeuIleProAspLeuMetArgGluAspVal 394  
 DB 910 GATCAAAAAGGATTTGATATTATTTGCTTCTGAATTCGACACATATGCTTCAACAAGATATT 969  
 QY 395 GlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMetArgSerThrGlu 414  
 DB 970 CAAATGGTTATTTTAGAAACAGGCTATCACCATTTTGAAGAAACGTTCTCTTATTTTGTCT 1029  
 QY 415 SerIlePheLeuAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArg 434  
 DB 1030 AGTCGTTACCTTGAAAAACTATCTGCTAATATATCTTTTGACTTAAGATTAGCGCAACAG 1089  
 QY 435 IleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsn 454  
 DB 1090 ATTTATGGCGCTTCAGATATCTTCATGATGCCAGTGCTTTTGAACCTTGTGCTCTCTCG 1149  
 QY 455 GlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArg 474  
 DB 1150 CAGATGATGGCTATGAGATATGATGCTTGGCTTGGTACATGAAAGTTGGAGGATTAAAA 1209  
 QY 475 AspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGlnGlyThrGlyTrpAla 494  
 DB 1210 GATACTGTGGTAGCCTTCAATTTGATGGTAGT-----GGTACAGGTTTTTCA 1260  
 QY 495 Phe 495  
 DB 1261 TTT 1263

## RESULT 16

US-11-353-150-32824  
 ; Sequence 32824, Application US/11353150  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andersen, Scott E.  
 ; APPLICANT: Conner, Timothy W.  
 ; APPLICANT: Lalgudi, Raghunath V.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 16517.365 - 38-21(15459)D/US  
 ; CURRENT APPLICATION NUMBER: US/11/353,150  
 ; CURRENT FILING DATE: 2006-02-14  
 ; PRIOR APPLICATION NUMBER: 09/565,386  
 ; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: 60/132,860  
 ; PRIOR FILING DATE: 1999-05-07  
 ; NUMBER OF SEQ ID NOS: 83523  
 ; SEQ ID NO 32824

```

; LENGTH: 411
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:

```

Alignment Scores:	1.96E-63	Length:	411
Pred. No.:	Score:	Matches:	131
	704.00	Conservative:	1
Percent Similarity:	97.1%	Mismatches:	4
Best Local Similarity:	96.3%	Indels:	0
Query Match:	24.3%	Gaps:	0
DB:	8		

US-10-628-525A-21 (1-539) x US-11-353-150-32824 (1-411)

390	MetArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrp	409
QY		
Db		
2	ATCGCGGAAGATGTTCAATTTGTCATGCTTGGATCTGGTGACCCAGAGACTTGAAGAGTGG	61
QY		
Db		
410	MetArgSerThrGluSerIlePheIysAspIysPheArgGlyTrpValGlyPheSerVal	429
QY		
Db		
62	ATGAGATCTACAGAGTCGATCTTCAAGGATATAATTTCTGGATGGGTGGATTAGTGGTT	121
QY		
Db		
430	ProValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGlu	449
QY		
Db		
122	CCAGTTTCCACCGAATACCTGCCGGTTCGATATATTGTTATGCCATCCAGATTCGAA	181
QY		
Db		
450	ProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAla	469
QY		
Db		
182	CCTTGTGGTCTCAATCAGCTATATGCTATGCAAGTATGSCACAGTTCCTGTTGCCATGCA	241
QY		
Db		
470	ThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln	489
QY		
Db		
242	ACTGGGGGCTTTAGAGNATCCGGTGAGAACTTCAACCCCTTTCGGTGAGAAATGGAGAGCAG	301
QY		
Db		
490	GlyThrGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsn	509
QY		
Db		
302	GGTACAGGGTGGGCATTTCGACCCCTTACCACAGGAAAAACATGTTGTGGACATTGCGAAC	361
QY		
Db		
510	CysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsn	525
QY		
Db		
362	TGCAATATCTCATACAGGAACAACAGTCTCTCTGGGAGGGGCTAAT	409
QY		
Db		

```

RESULT 17
US-11-329-388-3028
; Sequence 3028, Application US/11329388
; GENERAL INFORMATION:
; APPLICANT: Andersen,
; APPLICANT: Andersen, Scott E.
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Mole
; TITLE OF INVENTION: Plance
; FILE REFERENCE: 16517.357 - 38-21 (155)
; CURRENT APPLICATION NUMBER: US/11329
; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: 09/553,094

```

Alignment Scores:	Length:	407
Pred. No.:	3.26e-60	

Score:	673.00	Matches:	121
Percent Similarity:	94.8%	Conservative:	6
Best Local Similarity:	90.3%	Mismatches:	7
Query Match:	23.3%	Indels:	0
DB:	8	Gaps:	0

US-10-628-525A-21 (1-539) x US-11-329-388-3028 (1-407)

104	AlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThr	123
1	GCATTTTACACAGAAAAACACATTCGGATTCCATGCTTTTGGCGTGAAACGCTGAAGTTACC	60
124	PhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSerTyrHis	143
61	TTCTTCCATGAGCTCGAGATTCAGTTGACGGGTGTTTGTGCATCATGCTCATATCAC	120
144	ArgProGlyAsnLeuTyrGlyAspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr	163
121	ACACCTGGGAATATATATGGAGATAAGTTCGGTGCTTTTGGTGATCATCAGTTTCAGATAC	180
164	ThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIle	183
181	ACACCTCCTTTGCTATGCTGTCATGTGAGGCTCCTTTGCACCTTCGAATCGGGAGGATATATT	240
184	TyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeu	203
241	TATGACACGACATAGCAGATGTTTGTGTCAATGATTGGCATGCCACTCTAGTGCCAGTACTT	300
204	LeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIle	223
301	CTTGCTGCAAAATATAGACCATATATGGCGTTTATAAAGACTCCCGCAGCATCTCTGTGTATA	360
224	HisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyr	237
361	CATAATTTTATCACATCAAGGTGTACAGCCTGCAAGCACATAT	402

```

RESULT 18
US-11-275-569-11
; Sequence 11, Application US/11275569
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co., Inc.
; TITLE OF INVENTION: METHOD FOR PRODUCING
; TITLE OF INVENTION: ENTEROBACTERIACEAE F
; FILE REFERENCE: C440-C5323
; CURRENT APPLICATION NUMBER: US/11/275,569
; CURRENT FILING DATE: 2006-01-17
; PRIOR APPLICATION NUMBER: RU2005101110
; PRIOR FILING DATE: 2005-01-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1434
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1434)
US-11-275-569-11

```

Alignment Scores:		
Pred. No.:	3.18e-55	Length:
Score:	633.00	Matches:
Percent Similarity:	51.4%	Conservative:
Best Local Similarity:	34.6%	Mismatches:
Query Match:	21.3%	Indels:
DB:	8	Gaps:
		10
		1434

US-10-628-525A-21 (1-539) x US-11-275-569-11 (1-1434)

Qy	51	I	e	v	a	l	P	h	e	V	a	l	T	h	r	G	l	y	G	l	u	A	l	a	S	e	r	P	r	o	T	y	r	A	l	a	l	y	S	e	r	C	l	y	G	l	y	L	e	u	G	l	y	A	s	p	V	a	l	70
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
Db	7	G	T	T	T	A	C	A	T	G	T	T	C	A	G	A	G	A	T	G	T	T	C	C	G	T	G	C	T	T	A	A	A	A	C	C	G	G	C	G	T	C	T	G	G	T	G	A	T	G	T	66								

QY 71 CysGlySerLeuProValAlaLeuAlaAalaArgGlyHisArgValMetValValMetPro 90  
Db 67 ATGGGGGATATACCGGAGCAAAATGCGAGCGGCTTGACGCTCGCGTACTGTTGCCT 126  
QY 91 ArgTyr-----LeuAenGlyThrSerAspLysAenTyrAlaAenAlaPheTyrThr 107  
Db 127 GCATTTCCGATATTCGCGGTGGGTGACCGATGCGCAGGTATATCC----- 174  
QY 108 GluLysHisIleArgIleProCysPheGlyGluHisGluValThrPhePheHisGlu 127  
Db 175 -----CGTCGTATACCTTCGCCGGA-----CATATCAGCGTGTGTTCGGT 216  
QY 128 TyrArgAspSerValAspTrpValPheValAspHisProSer-----TyrHisArgProGly 146  
Db 217 CATTACACAGGGGTGGCATTTACCTGATTGACCGCGCATCTCTATGATCGTCGCGGA 276  
QY 147 AsnLeuTyrGlyAsp---LysPheGlyAlaPheGlyAspAenGlnPheArgTyrThrLeu 165  
Db 277 AGCCCGTATCAGCATACCACTTATTGCTATACCGACACGATGTTGGTTCGCTG 336  
QY 166 LeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyTyrIleTyrGly 185  
Db 337 CTGGGCTGGTGGGCGAGAA-----ATGCCAGCGGCTTGACCCATTCTCG 384  
QY 186 GlnAenCysMetPheValValAenAspTrpHisAlaSerLeuValProValLeuLeuAla 205  
Db 385 CGTCTGATGTGTGTGTCGCGACGATGCGCATGCGGCTTCGCGCTGCTATCTGGG 444  
QY 206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAen 225  
Db 445 GCGGCGGCGGCTCG-----GCGAAGTCGTGTTTACTGTGCACAAAC 486  
QY 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu 245  
Db 487 CTGGCCTATCAGGCATGTTTATGTCATCATCATGATGATGATGATGATGATGATG 540  
QY 246 TrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgHisAlaLeuAspLys 265  
Db 541 -----TGGTCATTC-----TTTAATATTCATGGCTGGAATTC 573  
QY 266 GlyGluAlaValAenPheLeuLysGlyAlaValValThrAlaAspArgIleValThrVal 285  
Db 574 AACGGACAATCTCTTCTGAAGCGGCTGTACTATGCTATGCTATGCTATGCTATG 633  
QY 286 SerLysGlyTyrSerTrpGluValThrAlaGluGlyGlyGlnGlyLeuAenGluLeu 305  
Db 634 AGTCCAACTACGCTCGGAGATCACCGAACCGCAGTTTTCCTACGTTATGGAAGTCTG 693  
QY 306 LeuSerSer-----ArgLysSerValLeuAenGlyIleValAenGlyIleAspIleAen 323  
Db 694 TTGCAACACGCTACCGTGAAGGCGCTCTTCGCGGTACTGAACCGCGTGCAGCAAA 753  
QY 324 AspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSer 343  
Db 754 ATCTGAGTCCAGACGAGCTTACTGTGGCTCGCTGCTGCTGCTGCTGCTGCTGCTG 813  
QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363  
Db 814 GATAAAGCGGAAATAAGCGCAGTTACAAATCGCAATCGGCTTAAGCTTGACGATAA 873  
QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspLeuIleGln 383  
Db 874 GTGCGCTTTTTCGATGTGTGAGCGCTCTGACCGACGAGAAAGTCTCGACCTGTG 933  
QY 384 LeuIleProAspLeuMetArgLysValPheValGlnPheValMetLeuGlySerGlyAsp 403  
Db 934 GAAGCCTTACCGGCTCTCTGAGCAGGCGGCGGAGCTGCGCTACTCGCGCGGCGGAT 993  
QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423  
Db 994 CCGGTGCTCAGGAGGTTTCTTGGCGGCGGAGGATATCCCGGTGAGTGGCGGTT 1053  
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeuLeu 443

Db 1054 CAGATTGGCTATCACCAGACATTTTCGCATTCGATATATGCGCGCGGACGTCATCTG 1113  
QY 444 MetProSerArgPheGluProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGlyThr 463  
Db 1114 GTGCCACCGGCTTTTACCGCGCTTAAACCAACTTTATGATTTGAAGTACGGTACG 1173  
QY 464 ValProValValHisAlaThrGlyLeuArgAspThrValGluAen 479  
Db 1174 CTGCCGTAGTGGCGGCGACCGGTGGCTTGTGATACGGTTTCTGAC 1221  
RESULT 19  
US-11-298-234A-9  
; Sequence 9, Application US/11298234A  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fenggao  
; APPLICANT: Hauge, Brian M.  
; APPLICANT: Oggero, Christopher M.  
; TITLE OF INVENTION: Methods for Ligation Independent Cloning of DNA  
; FILE REFERENCE: 53344  
; CURRENT APPLICATION NUMBER: US/11/298,234A  
; PRIOR FILING DATE: 2005-12-09  
; PRIOR APPLICATION NUMBER: 60634779  
; PRIOR FILING DATE: 2004-12-09  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 9  
; LENGTH: 1409  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-11-298-234A-9  
Alignment Scores:  
Pred. No.: 2,38e-54 Length: 1409  
Score: 624.50 Matches: 142  
Percent Similarity: 55.8% Conservative: 68  
Best Local Similarity: 38.4% Mismatches: 117  
Query Match: 21.6% Indels: 43  
DB: 8 Gaps: 11  
US-10-628-525A-21 (1-539) x US-11-298-234A-9 (1-1409)  
QY 40 LysGluGlnAlaArg-----AlaLysValThr 48  
Db 343 CAGCAGCAGCG 402  
QY 49 GlnSerIleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGly 68  
Db 403 ATGAACGTCTCTTCTGCG 462  
QY 69 AspValCysGlySerLeuProValAlaLeuAlaAalaArgGlyHisArgValMetValVal 88  
Db 463 GACGTCTCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 522  
QY 89 MetProArgTyrLeuAenGlyThrSerAspLysAenTyrAlaAenAlaPheTyrThrGlu 108  
Db 523 TCTCCCGCTAC-----GACAGTACAGGACGCTTGGACACGAGCAGC 564  
QY 109 LysHisIleArgIleProCysPheGlyGluHisGluValThrPhePheHisGluTyr 128  
Db 565 GTGCTGTCGAGATCAAGATGGGAGACGGGTACGAGACGCTTCTTCCATGCTTAC 624  
QY 129 ArgAspSerValAspTrpValPheValAspHisProSerTyr----- 142  
Db 625 AAGCGCGGAGTGGACCGGCTGTTCGTTGACCAACCGCTGCTTCTGAGAGGGTGGGGA 684  
QY 143 HisArgProGlyAsnLeuTyrGlyAspLysPheGlyAla---PheGlyAspAenGlnPhe 161  
Db 685 AAGACCGGAGGAGACATCTACCGGCTGCTGCGTGGAAACGAGCTACAGGACACGAGCTG 744  
QY 162 ArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGlyGly 181  
Db 745 CGGTTTCAGCTCTATGCCAGCGACCTTGAAGCTTCAAGGATCTGTAGGCTTCAACAC 804

QY 182 -----TyrIle-----TyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196  
DB 805 AACCCATACTTCTCCGACCATACCGGGAGAGCTGCTGCTGCTGCAACGACGTCGCAC 864  
QY 197 AlaSerLeuValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
DB 865 ACCGGCCCTCTCTCGGCTACCTCTACAGACAACTACCACTCCACGCACTACAGGAC 924  
QY 217 SerArgSerIleLeuValIleHisLeuAlaHisGlnGlyValGluProAlaSerThr 236  
DB 925 GCAAGACCGCTTCTGCACTCACAACTCTCTACAGGCGGCTGTCCTTCTCCGAC 984  
QY 237 TyrProAspLeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGlu 256  
DB 985 TACCGGAGCTGAACCTCCCGGAGAGATTCAAGTCGCTCTTCGATTTCATC----- 1035  
QY 257 TrpAlaArgHisAlaLeuAspLys-----GlyGluAlaValAsnPheLeuLys 273  
DB 1036 -----GACGGCTACGAGAAGCCGCTGGAAGCGCGGAAGATCAACTCGATGAAG 1083  
QY 274 GlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu--- 292  
DB 1084 GCGGGATCTCGAGCGCAGAGGCTCTCAACGTCAGCCCTACTACCCGAGAGCTC 1143  
QY 293 ValThrThrAlaGluGlyGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312  
DB 1144 ATCTCCGGCATCGCCAGGGCTCGGAGCTCGACATCATG-----CGCTCACCGGC 1197  
QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332  
DB 1198 ATCAGCGGCATGCTCAACGCGCATGACGTGACGTGAGGACCCAGCAGGAGCAAGTAC 1257  
QY 333 IleProCysHisTyrSerValAspAsp---LeuSerGlyLysAlaLysCysLysGlyAla 351  
DB 1258 ATCGCGGTGAAGTACAGCTGTCGACGCGCGTGGAGGCCAAGCGCTGAACAGGAGCG 1317  
QY 352 LeuGlnLysGluLeuGlyLeuProIleArgProAspValProLeuIleGlyPheIleGly 371  
DB 1318 CTGAGCGGAGGTGCGGGCTCCGGTGGACCGAATCCCGCTGGTGGCTTCATCGGC 1377  
QY 372 ArgLeuAspTyrGlnLysGlyIleAspLeu 381  
DB 1378 AGGCTGGAAGACAGAAAGGCCCGCAGCTC 1407

## RESULT 20

US-11-227-183A-29117  
; Sequence 29117, Application US/11227183A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalgudi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT APPLICATION NUMBER: US/11/227,183A  
; PRIOR FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 29117  
; LENGTH: 374  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3180-041-P2-M2-H8  
US-11-227-183A-29117

Alignment Scores:  
Pred. No.: 2,348-52 Length: 374  
Score: 597.00 Matches: 120  
Percent Similarity: 96.0% Conservative: 0  
Best Local Similarity: 96.0% Mismatches: 3

Query Match: 20.6% Indels: 2  
DB: 10 Gaps: 0  
US-10-628-525A-21 (1-539) x US-11-227-183A-29117 (1-374)  
QY 263 LeuAspLysGlyGluAlaValAsnPheLeu-LysGlyAlaValValThrAlaAspArgIle 282  
DB 3 CTTGACAAAGGCTGAGGACAGTTAAATTTGTGGGAAAGTGCAGTTGTGCACAGCGATCNAAT 62  
QY 282 eValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlnGlyLe 302  
DB 63 CGTGACTGTGACAGAGGTATTTCGTGGAGGTCAACTGCTGAAGGTGGACAGGCGCT 122  
QY 302 uAsnGlnLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyLe 322  
DB 123 CAATGAGCTCTTAAAGTCCAGAAAGAGTGTATTAAACGGAATGTAAATGGAAATTGACAT 182  
QY 322 eAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLe 342  
DB 183 TAATGATTGGAACCTGCCACAGACAAATGTATCCCTGTCTATTCTCTTTGATGACCT 242  
QY 342 uSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPr 362  
DB 243 CTCTGAAAGGCCAAATGTAAAGGTGCATTGCGAAGGAGCTGGGTTTACCTATTAAGGCC 302  
QY 362 cAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGln-LysGlyIleAspLeuI 382  
DB 303 TGATGTTCTCTGATTGGCTTTATTGGAAGGTGGATTATCAAAAGGCGCATTGATCTCA 362  
QY 382 LeGlnLeuIle 385  
DB 363 TTCAACTTATT 373

## RESULT 21

US-11-330-364-17004  
; Sequence 17004, Application US/11330364  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Dubois, Patrice  
; APPLICANT: Mahadeo, Debbie A.  
; APPLICANT: Masucci, James D.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 16517.352 - 38-21(51721)C/US  
; CURRENT APPLICATION NUMBER: US/11/330,364  
; PRIOR FILING DATE: 2006-01-12  
; PRIOR APPLICATION NUMBER: US 09/696,664  
; PRIOR FILING DATE: 2000-10-25  
; PRIOR APPLICATION NUMBER: US 60/161,619  
; PRIOR FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 17472  
; SEQ ID NO 17004  
; LENGTH: 635  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3279-215-Q6-K1-C2  
US-11-330-364-17004

Alignment Scores:  
Pred. No.: 2,478-51 Length: 635  
Score: 590.50 Matches: 114  
Percent Similarity: 98.3% Conservative: 0  
Best Local Similarity: 98.3% Mismatches: 1  
Query Match: 20.4% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-21 (1-539) x US-11-330-364-17004 (1-635)  
QY 424 TrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 443  
DB 20 TGG---GGATTAGTGTTCAGTTCCTCCAGTTCCTCCAGCAATAACTGCGGCTGCGATATATTGTTA 76

QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463  
 Db 77 ATGCCATCCAGATTGGAACCTTGTGGTCTCAATCAGCTATATGCTATGCTATGGCACA 136  
 QY 464 ValProValValHisAlaThrGlyGlyLeuArgAspThrValGluAsnPheAsnProPhe 483  
 Db 137 GTTCTGTGTTCATGCACTGGGGGCTTAGAGATACCGTGGAGAACTTCAACCCCTTC 196  
 QY 484 GlyLeuAsnGlyGluGlnGlyThrGlyTyrAlaPheAlaProLeuThrThrGluAsnMet 503  
 Db 197 GGTGAGAAATGAGAGCAGGCTACAGGTGGGCATTCGACCCCTTAACACAGAAACATG 256  
 QY 504 PheValAspIleAlaAsnCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArg 523  
 Db 257 TT-GTGGACATTGCAACTGCAATATCTACATACAGGGAACACAGAGTCTCTCTGGGAAG 315  
 QY 524 AlaAsnGluAlaArgHisValValArgLeuHisValGlyProCysArg 539  
 Db 316 GCTAATGACGAGGCATGTCAAAAGACTTTCACGTGGGACCATGCCGC 363  
 RESULT 22  
 US-11-330-822-36  
 ; Sequence 36, Application US/11330822  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GUAN, HANPING  
 ; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN  
 ; FILE REFERENCES: 15053-04  
 ; CURRENT APPLICATION NUMBER: US/11/330,822  
 ; CURRENT FILING DATE: 2006-01-11  
 ; PRIOR APPLICATION NUMBER: PCT/US98/06660  
 ; PRIOR FILING DATE: 1998-04-03  
 ; PRIOR APPLICATION NUMBER: 60/042,939  
 ; PRIOR FILING DATE: 1997-04-04  
 ; NUMBER OF SEQ ID NOS: 86  
 ; SOFTWARE: PatentIn Ver. 3.3  
 ; SEQ ID NO 36  
 ; LENGTH: 1488  
 ; TYPE: DNA  
 ; ORGANISM: Escherichia coli  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1431)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1435)..(1488)  
 US-11-330-822-36  
 Alignment Scores:  
 Pred. No.: 2,07e-50 Length: 1488  
 Score: 587.00 Matches: 152  
 Percent Similarity: 47.5% Conservative: 66  
 Best Local Similarity: 33.1% Mismatches: 195  
 Query Match: 20.3% Indels: 46  
 DB: 8 Gaps: 12  
 US-10-628-525A-21 (1-539) x US-11-330-822-36 (1-1488)  
 QY 51 IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyGlyLeuGlyAspVal 70  
 Db 7 GTTTTACATGTATGTTTCAGAGATGTTCCCGCTCTTAAACCCGCGCTCTGGGTGATGTT 66  
 QY 71 CysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValValMetPro 90  
 Db 67 ATTGGGGCATTACCCGACGACCAAAATCGCAGCGGTTGACCGCTCGGTACTGTGTCCT 126  
 QY 91 ArgTyr-----LeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyrThr 107  
 Db 127 GCATTTCCGACATTCGCGCGTGGCGGACCGATGCGCAGGTAGTAGTCCCGTCTGTGATACC 186  
 QY 108 GluLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGlu 127

Db 187 -----TCGCGCGGCACATATCACGCTGTTGTCGGTCA 219  
 QY 128 TyrArgAspSerValAspTyrValPheValAspHisProSer---TyrHisArgProGly 146  
 Db 220 TAC---AACGGGTGGCATTTACCTGATTGACGGCCGCATCTCTATGATCGTCCGGGA 276  
 QY 147 AsnLeuTyrGlyAsp---LysPheGlyAlaPheGlyAspAsnGlnPheArgTyrThrLeu 165  
 Db 277 AGTCCGTATCACGATACCAACTATTATTGTCATACCGACCAACGTAATTGCGCTTTGCGCTG 336  
 QY 166 LeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyGlyTyrIleTyrGly 185  
 Db 337 CTGGGTGGGTGGGGCAGAA-----ATGCCACGCGGCTTGACCAATTCTCG 384  
 QY 186 GlnAsnCysMetPheValValAsnAspTyrHisAlaSerLeuValProValLeuLeuAla 205  
 Db 385 CGTCTGATGTGTGTGATCGGCACGACTGCGATGCGGCTTGCGCTGCTGCTGCTGCG 444  
 QY 206 AlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsn 225  
 Db 445 GCGCGCGGCGTCCG-----GCGAAGTCGCTGTTTACTGTGCAAC 486  
 QY 226 LeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGlu 245  
 Db 487 CTAGCCTATCAAGGCATGTTTATGCACATCACATGAATGCATCCAAATTGCCA----- 540  
 QY 246 TrpTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeuAspLys 265  
 Db 541 -----TGGTCATTC-----TTTAATATTATGCGCTGGAATTC 573  
 QY 266 GlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleValThrVal 285  
 Db 574 AACGGCAAAATCTCTTCTGAAGCGCGTCTGCTACTATGCGCATCACATTACGGCGT 633  
 QY 286 SerLysGlyTyrSerTrpGluValThrAlaGluGlyGlnGlyLeuAsnGluLeu 305  
 Db 634 AGTCCAACTACGCTCGGAGATCACCGAACCGCAGTTTGCCTTACGCTATGGAAGTCTG 693  
 QY 306 LeuSerSer-----ArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323  
 Db 694 TTGCAACGCGTCACCGCAGAGCGCTCTTCGCGGTACCGAACGCGGTGACGAGAAA 753  
 QY 324 AspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAspLeuSer 343  
 Db 754 ATCTGGAGTCCAGAGACGCACTTACTGTTGGCTCGCTGCTTACACCCGCGATCGTTGGA 813  
 QY 344 GlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgProAsp 363  
 Db 814 GATAAAGCGGAAATAAGCGCCAGTCAAAATCGCAATCGGATCCCAAGGTTGACGATAA 873  
 QY 364 ValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspIleGln 383  
 Db 874 GTGCCCTTTTTCAGTGTGTGAGCGCTCTGACCGCAGAAAGGTCTCGATTGCGGTGCTG 933  
 QY 384 LeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGlyAsp 403  
 Db 934 GAAGCTCACCGGTTCTTCGAGGACGCGGCGGCGCTACTCGCGCGGCGGAT 993  
 QY 404 ProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArgGly 423  
 Db 994 CCGGTGCTCGACGAAGGTTTCTTCGCGCGGCGAGCGGAATATCCCGGTGAGTGGCGGTT 1053  
 QY 424 TrpValGlyPheSerValProValSerHisAspIleThrAlaGlyCysAspIleLeuLeu 443  
 Db 1054 CAGATTGGCTATCAAGAACATTTTCGATCGCATTCGATTCGCGCGCGCGGCGGCGGCTTCG 1113  
 QY 444 MetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyrAlaMetGlnTyrGlyThr 463  
 Db 1114 GTGCCAGCGGTTTCAACCGTGGCTTAAACGCACTTTATGGATCGAAGTACGATACG 1173  
 QY 464 ValProValHisAlaThrGlyGlyLeuArgAspThrVal-----Glu 478

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Db 1174 CTGCCGTTAGTCGACGACCGCGTGGCTTGCTGATACGAGTTTCTGACTGTTCTCTCCGAG 1233
QY 479 AsnPheAsnProPheGlyGluAangly-----GluglnGlyThrGlyTrpAla 494
Db 1234 AACCTTGCAGATGGCGTCCCAATGGGTTTACTTTCGAAGATAGTAATCCCTGGTGCG 1290

RESULT 23
US-11-353-150-66579
; SEQUENCE 66579, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 66579
; LENGTH: 334
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3076-030-Q1-K1-F4
US-11-353-150-66579

Alignment Scores:
Pred. No.: 2,62e-49 Length: 334
Score: 567.00 Matches: 107
Percent Similarity: 98.2% Conservative: 2
Best Local Similarity: 96.4% Mismatches: 2
Query Match: 19.6% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-21 (1-539) x US-11-353-150-66579 (1-334)
QY 351 AlaLeuGlnLysGluLeuGlyLeuProLeuArgProAspValProLeuIleGlyPheIle 370
Db 1 GCATTTGCAGAGAGCTGGGTTTACTATAAGCCCTGATGTTCTCTGATTCGCTTTAGT 60
QY 371 GlyArgLeuAspTyrGlnLysGlyLeuAspLeuIleGlnLeuIleProAspLeuMet 390
Db 61 GGAGGTGTGGATTATCGGAAGGCAATTGATCTCACTTCACTTATCATACCAGATCTCATG 120
QY 391 ArgGluAspValGlnPheValMetLeuGlySerGlyAspProGluLeuGluAspTrpMet 410
Db 121 CGGGAAGATGTTCAATTTGTCTATGTTGATCTGTGACCCAGAGCTTGAAGATTGGATG 180
QY 411 ArgSerThrGluSerIlePheLysPheLysPheArgGlyTrpValGlyPheSerValPro 430
Db 181 AGATCTACAGAGTCGATCTTCAAGATAAATTTCTGGATGGGTTGGATTTAGTTTCCA 240
QY 431 ValSerHisArgIleThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluPro 450
Db 241 GTTTCCTCCCGAATAACTGCGCGGCTGCGGATATATTGTTAATGCCATCCAGATTCGAACCT 300
QY 451 CysGlyLeuAsnGlnLeuTyrAlaMetGlnTyr 461
Db 301 TGTGCTCTCAATCAGCTATATGCTATGCAGTAT 333

RESULT 24
US-10-953-349-11887
; SEQUENCE 11887, Application US/10953349
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2

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; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 11887
; LENGTH: 1434
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (93)..(93)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (195)..(195)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1302)..(1302)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1314)..(1314)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1320)..(1320)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1327)..(1327)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1347)..(1347)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1369)..(1369)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1392)..(1392)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1407)..(1407)
; OTHER INFORMATION: n is a, c, g, or t
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-11887

Alignment Scores:
Pred. No.: 2,78e-45 Length: 1434
Score: 537.50 Matches: 131
Percent Similarity: 57.3% Conservative: 61
Best Local Similarity: 39.1% Mismatches: 117
Query Match: 18.6% Indels: 27
DB: 7 Gaps: 8

US-10-628-525A-21 (1-539) x US-10-953-349-11887 (1-1434)
QY 210 ProTyrGlyValTyrLysAspSerArgSerIleLeuValIleHisAsnLeuAlaHisGln 229
Db 3 CCAGGGGCATCTATATGAATGCCGGGTGTTTTTGTATCCACACATTCCTTACCAC 62
QY 230 GlyValGluProAlaSerThrTyrProAspLeuGlyLeuProGluTrpTyrGlyAla 249
Db 63 GGAAGATTGGATTCGCCGACTTCACCTTTAAATCTCCAGACCACTTTAAGAGCTCC 122
QY 250 LeuGluTrpValPheProGluTrpAlaArgHisAlaLeuAsp---LysGlyGluAla 268

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Db 123 TTTGACTTAT-----GATGGCATGTTAAACCAAGTGGTGGAGGAAA 167
Qy 269 ValAenPheLeuTySGLyAlaValThrAlaAspArgIleValThrValSerLySGLy 288
Db 168 ATCAATTGGTGAAGCTGAGCTATATANAATCATGTTTGTGATACTGTTAGCCCAAN 227
Qy 289 TyrSerTrpGlu---ValThrAlaGluGlyGlnGlyLeuAenGluLeuSer 307
Db 228 TATGCTAAAGAACTGGTGTGAGTCCAGACAGAGAGTGGAAATGGACACATCCTT--- 284
Qy 308 SerArgLys-----SerValLeuAenGlyIleValAenGlyIleAenAsn 323
Db 285 ---CGCAAAATTGATGATGCTGTTGTTGGAAATTTGGAATGGCATGGATGTTTCAG 341
Qy 324 AspTrpAenProLathrAspLysCysIleProCysHisTyrSerValAspAsp---Leu 342
Db 342 GAGTGGAAATCCAACTGACCAATATATAGTGTCAAAATACGATGTTTCAACAGATTTG 401
Qy 343 SerGlyLysAlaLysCysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362
Db 402 GAAGCAAGAGCTCTTTTGAAGAAGCCCTCCAGACGAGAGTGGATTGCGGTGACAGA 461
Qy 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAenLeu 382
Db 462 AATATCTCTTATGTTTATGTTGTTGAGCTTGAAGAGCAAAAGGTTCTGATATCTT 521
Qy 383 GlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402
Db 522 GCAGAAGCTATTCCCAATTTATCAGGAGAAATGTTGAGTGGTGGCTTGGACAGGA 581
Qy 403 AspProGluLeuGluAspTrpMetArgSerThrGluSerIlePheLysAspLysPheArg 422
Db 582 AAAAAACAAATGTAAGAAACAACTACAGGAATTTGAAATATCATACCTGACAGGCCA 641
Qy 423 GlyTrpValGlyPheSerValProValSerHisArgIleThrAlaGlyCysAspIleLeu 442
Db 642 GAGTGGCAAAATTCATGTTCCCTAGCCCAATGATGATATTCCTGGAGCTGATTTTATA 701
Qy 443 LeuMetProSerArgPheGluProCysGlyLeuAenGlnLeuTyrAlaMetGlnTyrGly 462
Db 702 TTGGTCTTAGCAGATTTGAGCTTGTGCTCTCATTCAGTTACAGCTATGCTATGGA 761
Qy 463 ThrValProValValHisAlaThrGlyLeuArgAspThrValGluAenPheAenPro 482
Db 762 TCTGTACCAATTTGTTCCCTCAACAGGTGATTTAGTTGACACTGCCAAA----- 809
Qy 483 PheGlyGluAenGlyGluGlnGlyThrGlyTrpAlaPheAlaProLeuThrThrGluAen 502
Db 810 -----GAGGTTTCACTGGATTTTCAGATGGTGGCTTTCAGTGTGTAATGT 854
Qy 503 MetPheValAspIleAlaAenCysAenIleTyrIleGlnGlyThrGln-----Val 519
Db 855 GATGCTGTGATCCAGCTGA-TGTGATGCTATAGCAAGACGTGTCAAAGGCGCCCTTGC 913
Qy 520 LeuLeuGlyArgAlaAenGluAlaArgHisValLysArgLeuHis 534
Db 914 AGTCTAGGAATCCAGCTTTTACAGAAATATAAAGAACTGCAT 958
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## RESULT 25

US-10-542-516-5

; Sequence 5, Application US/10542516

; GENERAL INFORMATION:

; APPLICANT: Heim, Ute

; APPLICANT: Herbers, Karin

; APPLICANT: Sonnewald, Uwe

; APPLICANT: Glickmann, Eric

; TITLE OF INVENTION: Expression cassette with promoters of starch synthesis 3 for the

; FILE OF INVENTION: expression of nucleic acids in plant tissue containing starch

; FILE REFERENCE: 13173-00015-US

; CURRENT APPLICATION NUMBER: US/10/542,516

; CURRENT FILING DATE: 2005-07-18

; PRIOR APPLICATION NUMBER: PCT/EP2004/000241

; PRIOR FILING DATE: 2004-01-15

; PRIOR APPLICATION NUMBER: DE 103 02 324.0

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 5

; LENGTH: 3693

; TYPE: DNA

; ORGANISM: Solanum tuberosum

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(3690)

; OTHER INFORMATION: coding for SSS3

US-10-542-516-5

## Alignment Scores:

Pred. No.:	2,01e-42	Length:	3693
Score:	516.00	Matches:	150
Percent Similarity:	48.0%	Conservative:	69
Best Local Similarity:	32.9%	Mismatches:	145
Query Match:	17.8%	Indels:	92
DB:	7	Gaps:	17

US-10-628-525A-21 (1-539) x US-10-542-516-5 (1-3693)

Qy	51	IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAapVal	70
Db	2344	ATTGTCCATATTCTCTCGAATATGGACCAATTTGCAAGGTGGAGGCCTTGGTGA	2403
Qy	71	CysGlySerLeuProValAlaLeuAlaArgGlyHisArgValMetValMetPro	90
Db	2404	GTTACTAGTCTTTCCCGTCTGTTCAAGATTAAACCAATAATGTGGATATTATCTT	2463
Qy	91	ArgTyr-----LeuAenGlyThrSerAsp-----LysAenTyrAla	102
Db	2464	AAGTATGACTGTTTGAAGATGAATAATGGAAGGACTTTTCGGTTTCACAAAACTAC	2520
Qy	103	AsnAlaPheTyrThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu	122
Db	2521	-----TTTTGGGGTGGGACTGAAATA	2541
Qy	123	ThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer	142
Db	2542	AAAGTATGTTTGGAAAGGTGGAAGGTCTCTCGGTCTATTATTTTGGAG-----	2589
Qy	143	HisArgProGlyAen---LeuTyr-----GlyAspLysPheGlyAlaPheGlyAap	159
Db	2590	-----CCTCAAAACGGGTATTTCGAAAGGGTGGCTCTATGGTTGTAGCAATGATG	2643
Qy	160	GlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGlu	179
Db	2644	GAA---CGATTGGTTCCTCTGTCTCAGCGGCTTTGGAG-----TTTCTTCTGCAA	2691
Qy	180	GlyGlyTyrIleTyrGlyGlnAenCysMetPheValValAsnAspTrpHisAlaSer	199
Db	2692	GGTGGATTT-----AGTCCGGATATCATTTCATTCGATGATGGTCTAGTGCTCT	2742
Qy	200	ValProValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArg	219
Db	2743	GTTCCTGGCTCTTTAAGGAACAATATACACTATGGTCTAAGCAAAA---TCTCGTATA	2799
Qy	220	IleLeuValIleHisAenLeuAlaHisGlnGlyValGluProAlaSerThrTyrPro	239
Db	2800	GTCTTCACGATACATACTTGA-----TTTGGGCA-----	2823
Qy	240	LeuGlyLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArg	259
Db	2824	-----TTTGGGCA-----	2832
Qy	260	ArgHisAlaLeuAspLysGlyGluAlaValAenPheLeuLysGlyAlaValValThr	279
Db	2833	-----GATCTCTTGGGAGACCAATGATACGCA	2862

QY 280 AspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGly 299  
 DB 2863 GACAAAGCTACAACTTTACCACTTACTACAGAGGTGTCTGGA----- 2910  
 QY 300 GlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGly 319  
 DB 2911 -----AACCTGTAATTGGCGCTCACCTTACCAAGTTCCATGCTATAGTAAAGG 2961  
 QY 320 IleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerVal 339  
 DB 2962 ATGACCCAGATATTGGGATCTTTAAACGATAAAGTTCAATCCGATTCGATACACTCA 3021  
 QY 340 AspAsp---LeuSerGlyLysAlaLysCysLysGlyValAlaLeuGlnLysGluLeu 358  
 DB 3022 GAAACGTTGTTCAAGGCAAAACAGCAGCCAGGAAGCTTTGAGCGAAACTTGGACTG 3081  
 QY 359 ProIleArgProAspValProIleGlyPheIleGlyArgLeuAspTyrGlnLysGly 378  
 DB 3082 AAA---CAGGCTGACCTTCTTGGTAGGAATTATCACCCTTAACCTACCAAGAAAGA 3138  
 QY 379 IleAspLeuIleGlnLeuIleProAspLeuMetArgGluAspValGlnPheValMet 398  
 DB 3139 ATCCACCTCTAAACATGCTATTGGCGCCTTGGAAACGGAACGACAGTAGTCTTG 3198  
 QY 399 LeuGlySerGly---AspProGluLeuGlu-----AspTrpMetArgSerThr 413  
 DB 3199 CTGGTCTCTGCTGATCTAGGTACAAACGATTTGTAAATTTGGCAATCAATG 3258  
 QY 414 GluSerIlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHis 433  
 DB 3259 CACTCCAAATAAATGACCGCAGCAGCTCTGTCTAAATATGACGAGCAGCTTCTCTAC 3318  
 QY 434 ArgIleThrAlaGlyCysAspIleLeuMetProSerArgPheGluProCysGlyLeu 453  
 DB 3319 CTGATATATGCTGGGCTGCTATTATTCTAGTTCCTTCAATATTGAGCCATGTGGACTA 3378  
 QY 454 AsnGlnLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyLeu 473  
 DB 3379 ACACAACTTACCGCTATGAGATATGTTCAATTCAGTCTGCTGTAATAACTGGAGACTT 3438  
 QY 474 ArgAspThrValGluAsnPheAsnProPheGlyGluAsnGlyGluGln 489  
 DB 3439 TATGATCTGTATTGATGTTGACCATGACCAAGAGAGACGACCAACAG 3486  
 RESULT 26  
 US-10-542-516-15  
 ; Sequence 15, Application US/10542516  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heim, Ute  
 ; APPLICANT: Herbers, Karin  
 ; APPLICANT: Sonnwald, Uwe  
 ; APPLICANT: Glickmann, Eric  
 ; TITLE OF INVENTION: Expression cassette with promoters of starch synthesis 3 for the  
 ; FILE REFERENCE: 13173-00015-US  
 ; CURRENT APPLICATION NUMBER: US/10/542,516  
 ; CURRENT FILING DATE: 2005-07-18  
 ; PRIOR APPLICATION NUMBER: PCT/EP2004/000241  
 ; PRIOR FILING DATE: 2004-01-15  
 ; PRIOR APPLICATION NUMBER: DE 103 02 324.0  
 ; PRIOR FILING DATE: 2003-01-20  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 15  
 ; LENGTH: 3444  
 ; TYPE: DNA  
 ; ORGANISM: Vigna unguiculata  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(3441)  
 ; OTHER INFORMATION: coding for sss3  
 US-10-542-516-15

Alignment Scores:  
 Pred. No.: 4,08e-41 Length: 3444  
 Score: 503.00 Matches: 143  
 Percent Similarity: 47.7% Conservative: 70  
 Best Local Similarity: 32.0% Mismatches: 136  
 Query Match: 17.4% Indels: 98  
 DB: 7 Gaps: 16  
 US-10-628-525A-21 (1-539) x US-10-542-516-15 (1-3444)  
 QY 51 IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAspVal 70  
 DB 2095 ATTTGTTTATATGCTGTTGAGATGCCCCCAATTGCAAGTTGGAGGCTTGGTGATGT 2154  
 QY 71 CysGlySerLeuProValAlaLeuAlaalaArgGlyHisArgValMetValMetPro 90  
 DB 2155 GTTACTAGTCTTTCCGAGCTGTTCAAGATTATAATCATTAATGTGGATATCATTTCTTCCA 2214  
 QY 91 ArgTyr-----LeuAsnGlyThrSerAspLysAsnTyrAlaAsnAlaPheTyr 106  
 DB 2215 AATATGACTGCTTGAACCTTAGCAATGTAAAGGACTTGCATTTTCACAAAAGCTATTATTC 2274  
 QY 107 -----ThrGluLysHisIleArgIleProCysPheGlyGlyGluHisGlu----- 121  
 DB 2275 TGGAGTGGGACTGAA-----ATAAAGTATGGCACGGAAGGTCGAGGGCCTC 2322  
 QY 122 ValThrPhePheHisGluTyrArgAspSerValAspTrpValPheValAspHisProSer 141  
 DB 2323 TCGGTCTACTTTTGGAGCCTCAGAATGGATTATTTTGGGTG----- 2364  
 QY 142 TyrHisArgProGlyAsnLeuTyrGly-----AspLysPheGlyAlaPhe 156  
 DB 2365 -----GGCTGTATATGCTGTCGCAAAATGATGCAGAGAGATTGGTTTTTT 2412  
 QY 157 GlyAspAsnGlnPheArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIle 176  
 DB 2413 -----TGCCATGCGCTCTTGAA-----TTTCTA 2436  
 QY 177 LeuGluLeuGlyGlyTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHis 196  
 DB 2437 CTCCAAAATGGAAGTCATCCTGATATCATCCACTGC-----CATGACTGGTGC 2484  
 QY 197 AlaSerLeuValProValLeuLeuAlaLysTyrArgProTyrGlyValTyrLysAsp 216  
 DB 2485 AGTGCTCCAGTTGCTGCTATTTAAAGACAGTATACATTATGGCTTAGTAG--- 2541  
 QY 217 SerArgSerIleLeuValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThr 236  
 DB 2542 GCTCGAGTTGTTCTTCAAAATTCATAACCTTGAA----- 2574  
 QY 237 TyrProAspLeuGlyLeuProGluTyrGlyAlaLeuGluTyrValPheProGlu 256  
 DB 2575 -----TTTGTGTC----- 2583  
 QY 257 TrpAlaArgArgHisAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaVal 276  
 DB 2584 -----AATCTCATTTGGAAGAGCTATG 2604  
 QY 277 ValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGluValThrAla 296  
 DB 2605 GCATACGCTGACAGGCTACAACTGCTCTCCCACTTATTCAGGAGAGATTGCTGG--- 2661  
 QY 297 GluGlyGlyGlnGlyLeuAsnGluLeuSerSerArgLysSerValLeuAsnGlyIle 316  
 DB 2662 -----AATCATGCGTTGCTACTCATCTTCAAGTTTCATGCTATATA 2703  
 QY 317 ValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHis 336  
 DB 2704 ATAAATGGAATCGACCCAGATATATGGACCCATTAATGATTAATCTCTCTGTACCA 2763  
 QY 337 TyrSerValAspAsp---LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGlu 355  
 DB 2764 TACACAGCAGAAAATGTTGTTGAAGGAAAAGAGCGTCCAAAGGAGCCTTACAAACAAAG 2823



Db 1915 -----TGGGGAGGAAGT---GAAATAAAAGTTTGGCAT 1944  
QY 127 GluTyrArgAspSerValAspTrpValPheValAsp---HisProSerTyrHisArgPro 145  
Db 1945 GGAAGAGTAGAAGGCTTTCGGTTTACTTCTTAGATCCCAAAATGGATGTTTTCAGCGA 2004  
QY 146 GlyAsnLeuTyrGly-----AspLysPheGlyAlaPheGlyAspAsnGlnPheArgTyr 163  
Db 2005 GGATGGTTTACGGTTGTCAGATGATGACGAGAGATTCGGT----- 2046  
QY 164 ThrLeuLeuCyTyrAlaAlaCysGluAlaProLeuLeuLeuGluLeuGlyTyrIle 183  
Db 2047 ---TTCTTCTGTCATGCGGCTCTTGAA-----TTTCTTCTCCAAGGAGTTTCCATCCA 2097  
QY 184 TyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValProValLeu 203  
Db 2098 GACATTCTTCACTGT-----CATGCTGGTCTAGTGTCCGGTTTCATGGTTA 2145  
QY 204 LeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLeuValIle 223  
Db 2146 TTCAAGGATCATACACAGTACGGTTTAATTA---ACCGTATTGCTTTCACAAAT 2202  
QY 224 HisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuGlyLeuPro 243  
Db 2203 CATAATTTGGAA----- 2214  
QY 244 ProGluTyrTyrGlyAlaLeuGluTyrValPheProGluTyrAlaArgArgHisAlaLeu 263  
Db 2215 ---TTTGGAGCG----- 2223  
QY 264 AspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspArgIleVal 283  
Db 2224 -----AATGCCATTGGTAAGCAATGACATTTGCAGACAAAGCCACA 2265  
QY 284 ThrValSerLysGlyTyrSerTrpGluValThrThrAlaGluGlyGlyGlnGlyLeuAsn 303  
Db 2266 ACGGTTTACCACAACTATGCTAAGCAAGTTGCTGCA-----AAC 2304  
QY 304 GluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAspIleAsn 323  
Db 2305 TCTGTAATCTCGCACATTTATACAAATTTACGGAATTTATAAACGGGATTCACCCAGAT 2364  
QY 324 AspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValAspAsp---Leu 342  
Db 2365 ATATGGATCCATATAACGATAACTTTATTCCTGACCTTATCTTACAGAACGTTGTA 2424  
QY 343 SerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuGlyLeuProIleArgPro 362  
Db 2425 GAAAGCAAAAGACGACCAAGGAAGAAATTCGCAAAACAGGCTTGGACTAAAG---AGTGCC 2481  
QY 363 AspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAspIle 382  
Db 2482 GATTTTCAGTAGTAGGAATTAATACGGCTTTAAACACACAGAGGGAATACATTTGATC 2541  
QY 383 GlnLeuIleProAspLeuMetArgGluAspValGlnPheValMetLeuGlySerGly 402  
Db 2542 AAGCAGCTATTGTCGTACCTTGGACCGAATGCAGAGTGTCTTATAGTTTACGCT 2601  
QY 403 ---AspProGluLeuGlu---AspTrpMetArgSerThrGluSerIlePheLys----- 418  
Db 2602 CCAGATCTCGGATCCAAATGATTTGTAACTTTGGCAACCAATATCATCTTCTCAT 2661  
QY 419 ---AspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgIleThrAla 437  
Db 2662 GGTGACCGGCTCGGCTTGTCTTAACCTACGATGAACCTCTTTCATTTGATTTATGCT 2721  
QY 438 GlyCysAspIleLeuMetProSerArgPheGluProCysGlyLeuAsnGlnLeuTyr 457  
Db 2722 GGGGCTGACTTATTTCTGTACCGTCGATATTGAGCCATGTGGACTGACACAGCTCAT 2781  
QY 458 AlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAspThrVal 477  
Db 2782 GCCATGAGATACGGGCTGTTCTCTGTTGTAGAAAAAAGTGGAGGACTCTTTGATACGGTT 2841

QY 478 GluAsnPheAsnProPheGlyGluAsnGlyGlu-----GlnGlyThrGlyTyr 493  
Db 2842 TTTGATGTTGACCACGATATAAGAAAGGGCACAAGCTCAAGTTCTAGAACCTAATGGTTTC 2901  
QY 494 AlaPhe-----AlaProLeuThrThrGluAsnMetPheValAspIleAla-As 509  
Db 2902 AGTTTCGACGGAGCTGATGCTCT-----GGTGTGATTTATGCTCTC 2943  
QY 509 nCysAsnIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAlaArg-- 528  
Db 2944 AATAGGGCGATATCGCGTGGTACGATGCTAGAGAGTGGTTTAACTCGCTGTGCAAGACG 3003  
QY 529 -----HisValLysArgLeuHisVal 535  
Db 3004 GTGATGGAGCAAGACTGGTGCATGGAACCGTCTCGACATTG 3043

RESULT 29  
US-11-329-388-1791  
; Sequence 1791, Application US/11329388  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US  
; CURRENT APPLICATION NUMBER: US/11/329,388  
; PRIOR FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: 09/553,094  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18831  
; SEQ ID NO 1791  
; LENGTH: 289  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(289)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3061-040-Q1-K1-H2  
US-11-329-388-1791

Alignment Scores:  
Pred. No.: 6, 28e-40 Length: 289  
Score: 476.00 Matches: 91  
Percent Similarity: 97.9% Conservative: 1  
Best Local Similarity: 96.8% Mismatches: 2  
Query Match: 16.5% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-21 (1-539) x US-11-329-388-1791 (1-289)

QY 273 LysGlyAlaValValThrAlaAspArgIleValThrValSerLysGlyTyrSerTrpGlu 292  
Db 7 CGTGGGCGAGTTGTGACAGCATATCGAATCGTACTGTCAAGGGTTATTTCATGGGAG 66  
QY 293 ValThrThrAlaGluGlyGlnGlyLeuAsnGluLeuLeuSerSerArgLysSerVal 312  
Db 67 GTCACAACTGCTGAAGGTGGACAGGGCTCAATAGCTCTTAAAGCTCCAGAAAGAGTGA 126  
QY 313 LeuAsnGlyIleValAsnGlyIleAspIleAsnAspTrpAsnProAlaThrAspLysCys 332  
Db 127 TTAACCGAATTTGAATGGAATTGACATTAATGATTGGACCTCCACACACAAATGT 186  
QY 333 IleProCysHisTyrSerValAspAspLeuSerGlyLysAlaLysCysLysGlyAlaLeu 352  
Db 187 ATCCCTGCTATTATCTGTGATGACCTCTCTGAAAGGCCAAATGTAAGGTGCATTG 246  
QY 353 GlnLysGluLeuGlyLeuProIleArgProAspValProLeu 366  
Db 247 CAGAAGGAGCTGGGTTTACCTATTAAGGCCTGATGTTCTCTG 288

RESULT 30

## US-10-542-516-17

; Sequence 17, Application US/10542516  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heim, Ute  
 ; APPLICANT: Herbers, Karin  
 ; APPLICANT: Sonnewald, Uwe  
 ; APPLICANT: Gluckmann, Eric  
 ; TITLE OF INVENTION: Expression cassette with promoters of starch synthesis 3 for the  
 ; FILE REFERENCE: expression of nucleic acids in plant tissue containing starch  
 ; CURRENT FILING DATE: 2005-07-18  
 ; PRIOR APPLICATION NUMBER: US/10/542,516  
 ; PRIOR FILING DATE: 2004-01-15  
 ; PRIOR APPLICATION NUMBER: DE 103 02 324.0  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 17  
 ; LENGTH: 5025  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(5022)  
 ; OTHER INFORMATION: coding for sss3

## US-10-542-516-17

Alignment Scores:  
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 Score: 456.50 Matches: 155  
 Percent Similarity: 45.5% Conservative: 71  
 Best Local Similarity: 31.2% Mismatches: 163  
 Query Match: 15.8% Indels: 109  
 DB: 7 Gaps: 20

## US-10-628-525A-21 (1-539) x US-10-542-516-17 (1-5025)

QY 51 IleValPheValThrGlyGluAlaSerProTyrAlaLysSerGlyLeuGlyAspVal 70  
 DB 3682 ATTGTCCACATTGCTGTGAGATGGCCCAATCGCAAGGTTGGAGGCTCTGGTGATGT 3741  
 QY 71 CysGlySerLeuProValAlaLeuAlaAArgGlyHisArgValMetValMetPro 90  
 DB 3742 GTCACATAGTCTTTCACGCTGCTGCAAGATTAGGACACAAATGTGGAGGTATTCTTCCA 3801  
 QY 91 ArgTyr-----LeuAsnGlyThrSerAspLysAsn-TyrAlaAsnAlaPheTyrThrG 108  
 DB 3802 AAGTACGGTGTGTTGAATCTAGCAATGTCAGAACTCTAC----- 3841  
 QY 108 uLysHisIleArgIleProCysPheGlyGlyGluHisGluValThrPhePheHisGluT 128  
 DB 3842 -AAATCCATCAGATTTT-TCTTGGGGTGGTCTGAA-----ATAAATGTGTG 3887  
 QY 128 rArgAspSerValAspTrpValPheValAspHisProSerTyrHisArgProGlyAsnLe 148  
 DB 3888 GCGTGGCAGTAGTCGAAGGCTTTGTGTT-----TACTTCTCGAACCTCMAAAT-- 3936  
 QY 148 uTyrGlyAspLysPheGlyAlaPheGly-----AspAsnGlnPh 161  
 DB 3937 -----GGGATGTTTGGATCGGATATGATATGCGAGGAGCATGACCG 3980  
 QY 161 eArgTyrThrLeuLeuCysTyrAlaAlaCysGluAlaProLeuIleLeuGluLeuGlyG 181  
 DB 3981 CCGATTGGCTTCTTCTGCTGCTCTAGAG-----TTTCTCTCCAAAGTGGATC 4034  
 QY 181 yTyrIleTyrGlyGlnAsnCysMetPheValValAsnAspTrpHisAlaSerLeuValPr 201  
 DB 4035 TTCTCCGAACATAATACATTGC-----CATGATTGGTCAAGTGCCTCTGTC 4082  
 QY 201 oValLeuLeuAlaAlaLysTyrArgProTyrGlyValTyrLysAspSerArgSerIleLe 221  
 DB 4083 CTGGCTACACAGGAAACTACCGGAGTCTAGCTTG-----GCNAACGCCAGCGGTGTGATT 4139

QY 221 uValIleHisAsnLeuAlaHisGlnGlyValGluProAlaSerThrTyrProAspLeuG 241  
 DB 4140 CACCATCCCAATCTT----- 4155  
 QY 241 yLeuProGluTrpTyrGlyAlaLeuGluTrpValPheProGluTrpAlaArgArgH 261  
 DB 4156 -----GAATTTGGAGCGCATCA 4172  
 QY 261 sAlaLeuAspLysGlyGluAlaValAsnPheLeuLysGlyAlaValThrAlaAspAr 281  
 DB 4173 TATT-----GGCAAGCAATGAGATAT-----TGTGATAA 4202  
 QY 281 gIleValThrValSerLysGlyTyrSerTrpGluValThrAlaGluGlyGlnG 301  
 DB 4203 AGCAACAACCTGCTCTAATACATATTCAAGGAAGTGTC-----GTCATGG 4250  
 QY 301 yLeuAsnGluLeuLeuSerSerArgLysSerValLeuAsnGlyIleValAsnGlyIleAs 321  
 DB 4251 T-----GCCATAGTTCTCTCATCTTGGGAAATTTCTATGGCAATTTCTCAATGGAATTGA 4301  
 QY 321 pIleAsnAspTrpAsnProAlaThrAspLysCysIleProCysHisTyrSerValaAspAs 341  
 DB 4302 TCCGGATATATGGATCCGTACATGACAACTTTATCCCGGTCCACTACACTTGTGAGAA 4361  
 QY 341 p---LeuSerGlyLysAlaLysCysLysGlyAlaLeuGlnLysGluLeuProI 360  
 DB 4362 TGTGGTTGAAGGCAAGAGGGCTGCTAAGAGGGCACCTGCAGCAGAGTTGGGTTCAG-- 4419  
 QY 360 eArgProAspValProLeuIleGlyPheIleGlyArgLeuAspTyrGlnLysGlyIleAs 380  
 DB 4420 -CAATTCGATGTCCTCCGTCGTAGGAATCGTCACTCGCTCAGACGCCAAAGGGGTCCCA 4478  
 QY 380 pLeuIleGlnLeuIleIleProAspLeuMetArgGluAspValGlnPheValMetLeuG 400  
 DB 4479 CTGTATCAAGCATCGATTACCGGTACACTCGAACGGAACGACAGGTGTTTGTCTGG 4538  
 QY 400 ySerGly-----AspProGluLeuGluAspTrpMetArgSerThrGluSe 415  
 DB 4539 TTCAGCGCGGACTCTCGAATCCAAAGCTGATTTTGTCAACCTGGCGAATACGCTCCACGG 4598  
 QY 415 rIlePheLysAspLysPheArgGlyTrpValGlyPheSerValProValSerHisArgI 435  
 DB 4599 CGTAAACCATGGGCAAGTGAGGCTTTCTTGACCTACGACGAGCCTCTCTCGCATCTGAT 4658  
 QY 435 eThrAlaGlyCysAspIleLeuLeuMetProSerArgPheGluProCysGlyLeuAsnG 455  
 DB 4659 ATACGCTGGCTCTGACTTCTGCTCCATCTATATTGTAGCCTTGGCGCTAACTCA 4718  
 QY 455 nLeuTyrAlaMetGlnTyrGlyThrValProValValHisAlaThrGlyGlyLeuArgAs 475  
 DB 4719 GCTCGTCGCATGCGGTATGGAAACCATCCCGATTGTCCGCAAGACTGGAGGCTCTTCGA 4778  
 QY 475 pThrValGluAsnPheAsnProPheGlyGlu-----AsnGlyGluGlnGlyTh 491  
 DB 4779 CACTGTCTTCGATGTGGCAATGACAAGGAACGAGCCGAGATCGAGGCTTGGAGCCCAA 4838  
 QY 491 rGlyTrpAlaPheAlaProLeuThrThrGluAsnMetPheValAspIleAlaAsnCysAs 511  
 DB 4839 CCGGTTTAGCTTT-----GACGGAGCTGATAGCAA 4868  
 QY 511 nIleTyrIleGlnGlyThrGlnValLeuLeuGlyArgAlaAsnGluAla 527  
 DB 4869 C-----GGTGTGTAGCTACGCGTGAACAGGGCGATCTCAGCT 4905

Search completed: April 2, 2006, 04:06:40  
 Job time : 1907.01 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using **same p2n model**

Run on: April 1, 2006, 04:29:01 ; Search time 1115.38 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525a-33

Perfect score: 271

Sequence: 1 MASSMLSSAAVATRTNPAQA.....SRQNLDITSIASNGRVC 56

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOCALLIGN=200 -THR\_SCORE=pcst -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcst -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss06h  
-USER=US10628525 @CGN\_1.1.4375 @runat\_31032006\_095113\_16622 -NCPUS=6 -ICPU=3  
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Database :

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2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	244.5	90.2	806	15	AY220079 Nicotiana
2	240.5	88.7	177	6	I24839 Sequence 8
3	240.5	88.7	177	6	I40228 Sequence 6

4	240.5	88.7	177	6	I72655
5	240.5	88.7	204	6	AR528363
6	240.5	88.7	225	11	ARPRECA2
7	240.5	88.7	499	6	AR205973
8	240.5	88.7	796	15	NSRUB1
9	240.5	88.7	799	15	TORUBPA
10	240.5	88.7	1314	15	PERBCS11
11	240.5	88.7	2293	15	NPRBCS8B
12	240.5	88.7	2293	15	TORBCS8B
13	240.5	88.7	2362	15	NTRUBSS
14	237.5	87.6	22574	11	CVE18556
15	234.5	86.5	1629	15	STRBCS2
16	231.5	85.4	1386	15	PERBCS2C
17	231.5	85.4	2242	15	PERBCS08
18	230.5	85.1	1027	15	TOMRBCSC
19	230.5	85.1	1341	15	LERBCS3C
20	230.5	85.1	1520	15	LERBCS3A
21	229.5	84.7	1054	15	LERBCS3B
22	229.5	84.7	4124	15	TOMRBCO
23	228.5	84.3	723	15	SLARBCS
24	228.5	84.3	1703	15	STRBCS2B
25	226	83.4	3323	15	STRBCS1
26	223.5	82.5	599	15	TOMRBCSB
27	223.5	82.5	684	6	AR428736
28	223.5	82.5	684	6	AR455412
29	223.5	82.5	684	6	AX329368
30	223.5	82.5	684	6	AX382258
31	223.5	82.5	742	15	TOMRBCSE
32	223.5	82.5	1097	15	BT013023
33	223.5	82.5	2776	15	LERBCS2
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35	215.5	79.5	2795	15	NSRUBSSU
36	212	78.2	1337	15	TOMRUBPB
37	210	77.5	546	15	POTRBCS
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57	206	76.0	1454	15	LERBCS1
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60	204.5	75.5	562	15	AY705444
61	204.5	75.5	797	15	HEVRBSS
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63	204	75.3	177	6	I06974
64	203.5	75.1	9647	15	ATATSGS
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66	200.5	74.0	1761	15	BNRBCSSW
67	200	73.8	813	15	PYRBCS
68	199.5	73.6	546	15	AY143814
69	199.5	73.6	652	15	AF410283
70	199.5	73.6	711	6	AX364024
71	199.5	73.6	711	6	AX366113
72	199.5	73.6	739	6	AX364175
73	199.5	73.6	2116	15	AY142543
74	199.5	73.6	2714	15	BNRBCS
75	198	73.1	680	15	CIPRBCS2
76	198	73.1	2671	15	CIP2RSS





DEFINITION Sequence 8 from patent US 5545816.  
ACCESSION I24839  
VERSION I24839.1 GI:1604709  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 177)  
AUTHORS Ausich,R.L., Brinkhaus,F.L., Mukharji,I., Proffitt,J., Yarger,J. and Yen,H.-C.B.  
TITLE Phytoene biosynthesis in genetically engineered hosts  
JOURNAL Patent: US 5545816-A 8 13-AUG-1996;  
FEATURES Location/Qualifiers  
source 1..177  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.23e-20 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x I24839 (1-177)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCACTGGCGCTTAAGTCAGCTGCCTCATTTCCCTGTTCAAGGAAG 120  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 3  
LOCUS I40228  
DEFINITION Sequence 6 from patent US 5618988.  
ACCESSION I40228  
VERSION I40228.1 GI:2083233  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 177)  
AUTHORS Hauptmann,R., Eschenfeldt,W.H., English,J. and Brinkhaus,F.L.  
TITLE Enhanced carotenoid accumulation in storage organs of genetically engineered plants  
JOURNAL Patent: US 5618988-A 6 08-APR-1997;  
FEATURES Location/Qualifiers  
source 1..177  
/organism="unknown"  
/mol\_type="unassigned DNA"

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Alignment Scores:  
Pred. No.: 1.23e-20 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x I40228 (1-177)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCACTGGCGCTTAAGTCAGCTGCCTCATTTCCCTGTTCAAGGAAG 120  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 4  
LOCUS I72655  
DEFINITION Sequence 12 from patent US 5684238.  
ACCESSION I72655  
VERSION I72655.1 GI:3008794  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 177)  
AUTHORS Ausich,R.L., Brinkhaus,F.L., Mukharji,I., Proffitt,J.H., Yarger,J.G. and Yen,H.-C.B.  
TITLE Biosynthesis of zeaxanthin and glycosylated zeaxanthin in genetically engineered hosts  
JOURNAL Patent: US 5684238-A 12 04-NOV-1997;  
FEATURES Location/Qualifiers  
source 1..177  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.23e-20 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x I72655 (1-177)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCACTGGCGCTTAAGTCAGCTGCCTCATTTCCCTGTTCAAGGAAG 120  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 5  
LOCUS AR528363  
DEFINITION Sequence 3 from patent US 6723895.  
ACCESSION AR528363  
VERSION AR528363.1 GI:53916426  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 204)  
AUTHORS DeBonte,L.R. and Shorrosh,B.S.  
TITLE Plants containing a cytosolic acetyl CoA-carboxylase nucleic acid  
JOURNAL Patent: US 6723895-A 3 20-APR-2004;  
FEATURES Location/Qualifiers  
source 1..204  
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/mol\_type="genomic DNA"

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Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCACTGGCGCTTAAGTCAGCTGCCTCATTTCCCTGTTCAAGGAAG 120  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 6  
LOCUS AR528363  
DEFINITION Sequence 3 from patent US 6723895.  
ACCESSION AR528363  
VERSION AR528363.1 GI:53916426  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 204)  
AUTHORS DeBonte,L.R. and Shorrosh,B.S.  
TITLE Plants containing a cytosolic acetyl CoA-carboxylase nucleic acid  
JOURNAL Patent: US 6723895-A 3 20-APR-2004;  
FEATURES Location/Qualifiers  
source 1..204  
/organism="unknown"  
/mol\_type="genomic DNA"

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCACTGGCGCTTAAGTCAGCTGCCTCATTTCCCTGTTCAAGGAAG 120  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171



SOURCE	Nicotiana sylvestris (wood tobacco)
ORGANISM	Nicotiana sylvestris
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Asterids; lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE	1 (bases 1 to 796)
AUTHORS	Pinck M., Guilley, E., Durr, A., Hoff, M., Pinck, L. and Fleck, J.
TITLE	Complete sequence of one of the mRNAs coding for the small subunit of ribulose biphosphate carboxylase of Nicotiana sylvestris
JOURNAL	Biochimie 66 (7-8), 539-545 (1984)
PUBMED	6549380
COMMENT	Data kindly reviewed (22-JUL-1985) by J. Fleck.
FEATURES	Location/Qualifiers
source	1..796

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repeat_region  
misc_feature  
repeat_region  
repeat_region  
  
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    /gb_xref="GOA:P69250"  
    /db_xref="UniProt:IPR000894"  
    /db_xref="Swiss-Prot:P69250"  
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ITSIASGRGVCQQWPVPINKKYETILSYLPDLSOQLSLSEVEYLKGNGWPCLSFE  
TEHGVTYRENNKSFGYIDGRVTWKMLPMEFCTDTQTQVLAEVBEAKAYPAQWIIRIG  
FDNRVRQCICSPFIAYKPBG"  
transit_peptide 61..231  
    /note="transit peptide (aa -57 to -1)"  
mat_peptide 232..600  
    /product="mature small subunit protein (aa 1-123)"  
repeat_region 249..257  
    /note="direct repeat 2'"  
misc_feature 601..796  
    /note="j3' untranslated region"  
polya_site 796  
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Alignment Scores:			
Pred. No.:	6.56e-20	Length:	796
Score:	240.50	Matches:	52
Percent Similarity:	96.5%	Conservative:	3
Best Local Similarity:	91.2%	Mismatches:	1
Query Match:	88.7%	Indels:	1
DB:	15	Gaps:	1

US-10-628-525A-33 (1-56) x NSRUB1 (1-796)

Qy	1	MetAlaSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla	20
		:::::	
Db	61	ATGGCTTCTCAGATTCTTTCTCTGCAGCATGTTCACCGCAAGTTGTCTCAAGCT	120
		:::::	
Qy	21	SerMetValAlaProPheThrGlyLeuLysSerIalala---PheProValSerArgLys	39
		:::::	
Db	121	AACATGGTTGCACCTTTCACTGGCCTTAAGTCAGCTGCCTCATTCCCTGTTTCAAGAAA	180
		:::::	
Qy	40	GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys	56
		:::::	
Db	181	CATAACTTGATCATCACTTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC	231

RESULT 9	
TOBRUBPA	
LOCUS	799 bp DNA linear PLN 26-MAY-1994
DEFINITION	Tobacco ribulose-1,5-bisphosphate carboxylase small subunit gene, exons 1 and 2, clone TSSU3-8.
ACCESSION	M32419
VERSION	M32419.1 GI:170327
KEYWORDS	ribulose 1,5-bisphosphate carboxylase.
SOURCE	Nicotiana tabacum (common tobacco)
ORGANISM	Nicotiana tabacum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE	O'Neal,J.K., Pokalsky,A.R., Kiehne,K.L. and Shewmaker,C.K. 1 (bases 1 to 979) Isolation of tobacco SSU genes: characterization of a transcriptionally active pseudogene
JOURNAL	Nucleic Acids Res. 15 (21), 8661-8677 (1987)
PUBMED	3684569
COMMENT	source text: Nicotiana tabacum DNA.
FEATURES	Original Location/Qualifiers
	1..979
source	

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    /protein_id="AAA34116.1"
    /db_xref="GI:170328"
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    584. .757
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    precursor"
    intron
    761. .853
    /note="ribulose-1,5-bisphosphate carboxylase small
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    /number=1
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ORIGIN	/ number=2
Alignment Scores:	
Pred. No.:	8.26e-20
Score:	240.50
Percent Similarity:	96.5%
Best Local Similarity:	91.2%
Query Match:	88.7%
DB:	15
	Gaps: 1
	Indels: 1
	Mismatches: 1
	Conservative: 3
	Matches: 52
	Length: 979

US-10-628-525A-33 (1-56) x TOBRUBPA (1-979)

Qy	1	MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla	20
		:           :	
Db	584	ATGGCTTCCTCAGTTCTTCTCTGTGCAGCAGTTGCCACCGCAGCAATGTGCTCAAGCT	643
Qy	21	SerMetValAlaProPheThrGlyLeuLySerAlaAla---PheProValSerArgLyse	39
		:	
Db	644	AACATGGTGCACTTTACTGCGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGAAG	703

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QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
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Db 704 CAAACCTTGACATCACTTCATTCGACGACACGGCGGAGAGTGCAATGC 754

RESULT 10
PERBCS11
LOCUS
DEFINITION
Petunia x hybrida rbcS gene (ssuIIA) for ribulose 1,5-bisphosphate
carboxylase small subunit.
ACCESSION
X03821
VERSION
X03821.1 GI:20492
SOURCE
ribulose biphosphate carboxylase.
ORGANISM
Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Petunia.
1 (bases 1 to 1314)
Tumer,N.E., Clark,W.G., Tabor,G.J., Hironaka,C.M., Fraley,R.T. and
Shah,D.M.
The genes encoding the small subunit of ribulose-1,5-bisphosphate
carboxylase are expressed differentially in petunia leaves
Nucleic Acids Res. 14 (8), 3325-3342 (1986)
3010233
2
Dean,C., Favreau,M., Dunsmuir,P. and Bedbrook,J.
Confirmation of the relative expression levels of the Petunia
(Mitchell) rbcS genes
Nucleic Acids Res. 15 (11), 4655-4668 (1987)
3588304
COMMENT
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/mol_type="genomic DNA"
/cultivar="Mitchell"
/db_xref="taxon:4102"
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186..193
TATA_signal
213..215
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/protein_id="CAA27445.1"
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/db_xref="UniProt/Swiss-Prot:P04715"
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456..672
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673..807
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958..>1188
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ORIGIN

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Alignment Scores:
Pred. No.: 1 15e-19 Length: 1314
Score: 240.50 Matches: 52
Percent Similarity: 94.7% Conservative: 2
Best Local Similarity: 91.2% Mismatches: 2
Query Match: 88.7% Indels: 1
DB: 15 Gaps: 1

US-10-628-525A-33 (1-56) x PERBCS11 (1-1314)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
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Db 279 ATGGCTTCTCAGTCAGTGATGCTCCTCAGTCAGTGGCAGTGGCACAAGCACCACCAATGCTGCTCAAGCC 338

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
|||||
Db 339 AGCATGGTGGACCCCTTCACCTGGCCCTCAAGTCTGAGCGCTCCCTTCCTGTTTCCAGGAAA 398

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
|||||
Db 399 CAGAACCTTGACATTCATTCCTAGCAATGGTGGAGAGATTCATGTC 449

RESULT 11
NPRBCS8B
LOCUS
DEFINITION
Nicotiana plumbaginifolia rbcS-8B gene for ribulose biphosphate
carboxylase small subunit.
X13711
ACCESSION
X13711.1 GI:19705
VERSION
X13711.1
KEYWORDS
enhancer-like sequence; rbcS gene; ribulose biphosphate
carboxylase.
SOURCE
Nicotiana plumbaginifolia (curled-leaved tobacco)
ORGANISM
Nicotiana plumbaginifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 2293)
Poulsen,C., Fluhr,R., Kauffman,J.M., Boutry,M. and Chua,N.H.
Characterization of an rbcS gene from Nicotiana plumbaginifolia and
expression of an rbcS-CAT chimeric gene in homologous and
heterologous nuclear background
Mol. Gen. Genet. 205, 193-200 (1986)
2 (bases 1 to 1130)
Poulsen,C. and Chua,N.H.
Dissection of 5' upstream sequences for selective expression of the
Nicotiana plumbaginifolia rbcS-8B gene
Mol. Gen. Genet. 214 (1), 16-23 (1988)
3226423
FEATURES
Location/Qualifiers
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complement(403..410)
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/note="SV40 enhancer core similarity"
435..892
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885..892
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911..915
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927..931
CAAT_signal
945..949
TATA_signal
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CDS
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1290..1380
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1381..1515
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1815..2171
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2167..2170
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ORIGIN
Alignment Scores:
Pred. No.:      2,13e-19      Length:      2293
Score:          240.50      Matches:      52
Percent Similarity: 96.5%      Conservative: 3
Best Local Similarity: 91.2%      Mismatches: 1
Query Match:      88.7%      Indels:      1
DB:              15          Gaps:         1

US-10-628-525A-33 (1-56) x NPRCS8B (1-2293)

QY      1  MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20
Db      1113  ATGGCTTCCTCAGTTCTTCTCTGACAGCAGTGGCCACCGCAATGTTGCTCAAGCT 1172

QY      21  SerMetValAlaProPheThrGlyLeuLySerAlaAla---PheProValSerArgLys 39
Db      1173  AACATGGTTGCACCTTTCATCTGCTTAAGTCAGCTGCCTCATCTCCTGTTTCAGGAAG 1232

QY      40  GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db      1233  CAAACCTTGACATAACTTCCATTGCCAGCAGCGGGAAGAGTGCAATGC 1283

RESULT 12
TOBRCS8B
LOCUS   N.plumbaginifolia ribulose biphosphate carboxylase (rbcS-8B) gene,
DEFINITION complete cds.
ACCESSION M36685
VERSION   M36685.1 GI:170317
KEYWORDS  ribulose biphosphate carboxylase.
SOURCE    Nicotiana plumbaginifolia (curled-leaved tobacco)
ORGANISM  Nicotiana plumbaginifolia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS   Poulsen,C., Fluhr,R., Kauffman,J.M., Boutry,M. and Chua,N.H.
TITLE     Characterization of an rbcS gene from Nicotiana plumbaginifolia and
          expression of an rbcS-CAT chimeric gene in homologous and
          heterologous nuclear background
JOURNAL   Mol. Gen. Genet. 205, 193-200 (1986)
COMMENT   Original source text: Nicotiana plumbaginifolia (library: Boutry

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ORIGIN

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     1008..1015
        /gene="rbcS 8B"
     1035..1289
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        /note="major transcription start site"
        /number=1
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        /note="minor transcription start sites"
        /number=1
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        /gene="rbcS 8B"
     CDS             join(1113..1289,1381..1515,1644..1696,1815..1992)
        /gene="rbcS 8B"
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        /protein_id="AAA34110.1"
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        /number=2
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        /note="putative"
        /number=2
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        /gene="rbcS 8B"
        /number=3
     exon            1644..1696
        /gene="rbcS 8B"
        /note="putative"
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     intron          1697..1814
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        /gene="rbcS 8B"
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        /note="5 alternative mRNA ends"
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Alignment Scores:		2.13e-19	Length:	2293
Pred. No.:		240.50	Matches:	52
Score:		96.5%	Conservative:	3
Percent Similarity:		91.2%	Mismatches:	1
Best Local Similarity:		88.7%	Indels:	1
Query Match:		15	Gaps:	1
DB:				
US-10-628-525A-33 (1-56) x TOBRBCS8B (1-2293)				
QY	1	MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla	20	
Db	1113	ATGGCTTCCTCAGTCTTCTCTGAGCAGTGCCACCGCAGCAATGTTGCTCAAGCT	1172	
QY	21	SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys	39	
Db	1173	AACATGGTTGCACCTTTCATGCTGCTTAAGTTCAGCTGCCTCATTCCTGTTTCAAGGAAG	1232	
QY	40	GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56	
Db	1233	CAAAACCTTGACATACTTCCATTGCCAGCAACGGCGAAGAGTGCAATGC	1283	
RESULT 13				
NTRUBSS				
LOCUS	2362 bp DNA linear PLN 18-APR-2005			
DEFINITION	Tobacco gene for ribulose 1,5-bisphosphate carboxylase small subunit.			
ACCESSION	X02353			
VERSION	X02353.1 GI:20023			
KEYWORDS	ribulose biphosphate carboxylase.			
SOURCE	Nicotiana tabacum (common tobacco)			
ORGANISM	Nicotiana tabacum			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.				
REFERENCE	1 (bases 1 to 2362)			
AUTHORS	Mazur, B.J. and Chui, C.F.			
TITLE	Sequence of a genomic DNA clone for the small subunit of ribulose bis-phosphate carboxylase-oxygenase from tobacco			
JOURNAL	Nucleic Acids Res. 13 (7), 2373-2386 (1985)			
PURMED	4000958			
FEATURES				
source	Location/Qualifiers			
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	46..111			
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repeat_unit	57..63			
misc_signal	/note="put. regulatory sequence"			
repeat_region	93..406			
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repeat_unit	389..454			
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misc_signal	435..442			
misc_signal	/note="put. regulatory sequence"			
misc_signal	586..592			
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misc_signal	891..896			
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promoter	955..962			
	/note="put. TATA-box"			
CDS	Join(1048..1224,1318..1452,1609..1661,1807..1984)			
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	/db_xref="GI:20024"			
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	/db_xref="UniProt/Swiss-Prot:P69249"			
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	carboxylase"			
	/EC_number="4.1.1.39"			
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misc_signal	1307..1313			
	/note="put. regulatory sequence"			
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intron	1662..1806			
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misc_feature	2145..2153			
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polyA_site	2175			
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Pred. No.:	2.21e-19	Length:	2362	
Score:	240.50	Matches:	52	
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Best Local Similarity:	91.2%	Mismatches:	1	
Query Match:	88.7%	Indels:	1	
DB:	15	Gaps:	1	
US-10-628-525A-33 (1-56) x NTRUBSS (1-2362)				
QY	1	MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla	20	
Db	1048	ATGGCTTCCTCAGTCTTCTCTGAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT	1107	
QY	21	SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys	39	
Db	1108	AACATGGTTGCACCTTTCATGCTGCTTAAGTTCAGCTGCCTCATTCCTGTTTCAAGGAAG	1167	
QY	40	GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56	
Db	1168	CAAAACCTTGACATCATTCCATTGCCAGCAACGGCGAAGAGTGCAATGC	1218	
RESULT 14				
CVE18556				
LOCUS	22574 bp DNA linear SYN 24-FEB-1999			
DEFINITION	Cloning vector pSLJ8313, T-DNA region.			
ACCESSION	Y18556			
VERSION	Y18556.1 GI:4191249			
KEYWORDS	cloning vector; T-DNA.			
SOURCE	Cloning vector pSLJ8313			
ORGANISM	Cloning vector pSLJ8313			
	Other sequences; artificial sequences; vectors.			
REFERENCE	1			
AUTHORS	Ratet, P. and Rippla, S.			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 22574)			
AUTHORS	Ratet, P.			
TITLE	Direct Submission			
JOURNAL	Submitted (21-DEC-1998) P. Ratet, Institut des Sciences Vegetales			
	(ISV), CNRS, Avenue de la Terrasse, Bat 23, 91198 Gif sur Yvette			
	cedex, FRANCE			
REMARK	Revised by author			

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COMMENT      Related sequences X00493, M32238, X03820, X79465, M25427, M19104,
X01077, X05822, M35007, A00196, V00087.
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                  /lab_host="Escherichia coli"
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                  /db_xref="taxon:358"
                  /plasmid="pTil15955"
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                  /organism="Petunia sp."
                  /mol_type="other DNA"
                  /db_xref="taxon:4104"
                  /focus
  source      2489..3703
                  /organism="Streptomyces griseolus"
                  /mol_type="other DNA"
                  /db_xref="taxon:1909"
  source      join(5273..5482,13154..14507)
                  /organism="Cauliflower mosaic virus"
                  /mol_type="other DNA"
  source      join(5483..13153,14596..15589,19205..20106)
                  /organism="Zea mays"
                  /mol_type="other DNA"
                  /db_xref="taxon:4577"
  source      join(14508..14595,16075..16146)
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  source      join(15790..16074,22003..22290)
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                  /plasmid..16698
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                  /organism="Streptomyces hygroscopicus"
                  /mol_type="other DNA"
                  /db_xref="taxon:1912"
  source      join(17944..19204,20121..21944)
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                  /mol_type="other DNA"
                  /db_xref="taxon:562"
  misc_feature 299..323
                  /note="T-DNA left border"
  misc_feature 322..22574
                  /note="T-DNA region"
  gene          891..5272
                  /gene="cytochrome P450, artificial"
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                  /note="source: rbcS gene, Petunia sp."
  CDS           2447..3703
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                  /codon_start=1
                  /transl_table=11
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                  /db_xref="GI:4191250"
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QFALPVPMVI CRLLGVVPADHEFPQDASKRLVQSDAQSAALTARNDLAGYLDGLITQ
FQTEPGAGLVGALVDQLANGIDRELLISTAMLLIAGHETASMTLSLVTLLDHP
EQTAURADRSVPGAVESLLRYLAADIAGGRVATADIEVEGHLLIRAGEGIVVNSI
ANRDGTYVEDPDALDIHRSARHHLAFGFGVHQCLGQNLARLELEVLNLMALMDRVPETLR
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  /note="source: rbcS gene, Petunia sp."
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  /product="source: suac gene, Streptomyces griseolus"
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  /note="contains polyA signal from rbcS, Petunia sp."
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  5483..13153
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source: Zea mays"
  13154..14507
  /note="source: Cauliflower mosaic virus"
  14508..14595
  /note="5' leader sequence, Tobacco mosaic virus"
  14596..20106
  /note="En/Spm transposable element, defective"
  15790..17439
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  15790..16698
  /gene="bar, artificial"
  15790..16074
  /gene="bar, artificial"
  /note="source: nopaline synthase gene, Agrobacterium
tumefaciens, plasmid pTi137"
  16147..16698
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  /protein_id="CAA77216.1"
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  /translation="MSPERPAPDIRATADMPACTIVNHVYIETSTVNRTRPQBEPQ
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GSTLYTHLLKSLEAQKFSVAVVIGLPNDPSVRMHEALGYAPRGLRAAGFKHGNWHD
VGFWQLDFSLPVPVPPRVLVPVTBI"
  16711..17439
  /note="contains polyA signal
source: octopine synthase gene, Agrobacterium tumefaciens,
plasmid pTi15955"
  17944..18954
  /note="source: Escherichia coli"
  /codon_start=1
  /transl_table=11
  /product="adenyl transferase"
  /protein_id="CAA77217.1"
  /db_xref="GI:4191252"
  /translation="NRSNRWSTLTERSGNGAVAFVMACYDCFCFQVQSMPRASKQQA
RYAVGRCMLWSSNDVTOQSRPKTKLNTMRRAVIAEVSTOLSEVVGVLEHLEPTLL
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VTIVVHDDILPWRYPAKRELQFGQWRNDILAGIFEPATIDIDLALLTKARSHVAL
PGPAABELPDPVPEQDLFEALNETLTLMNSPPDWAGDERNVLTLSRIWYSVAVTGKIA
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GK"
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intron      1391. .1510
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exon        1511. .1564
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intron      1565. .1720
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exon        1721. .>1897
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ORIGIN      2051. .2056

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Score:          231.50      Matches:      50
Percent Similarity: 93.0%      Conservative: 3
Best Local Similarity: 87.7%      Mismatches: 3
Query Match:      85.4%      Indels:      1
DB:              15      Gaps:      1

US-10-628-525A-33 (1-56) x PERBCS08 (1-2242)

QY      1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThraAsnProAlaGlnAla 20
DB      485 ATGGCTTCCTCTGTGATTTCTCTGCGAGCTGTGCTACTGACCTAATGTGGCTCAAGCT 544

QY      21 SerMetValAlaProPheThrGlyLeuLySerAla---AlaPheProValSerArgLyS 39
DB      545 AGCATGGTTGCACCTTTTAATGGTCTTAAGTCTGCTGTCTCTCTCCAGTTTCAAGCAG 604

QY      40 GlnAenLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB      605 CAAACCTTGCATCATTCCATTGCTAGCAATGGTGAAGAGTCCAATGC 655

RESULT 18
TOMRBCSC      1027 bp      DNA      linear      PLN 27-APR-1993
LOCUS      Tomato (L.esculentum) ribulose-1,5-bisphosphate
DEFINITION      carboxylase/oxygenase (RBCS) small subunit gene, clone Rbcs-3A.
ACCESSION      M13544
VERSION      M13544.1 GI:170499
KEYWORDS      ribulose 1,5-bisphosphate carboxylase/oxygenase.
SOURCE      Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE      1 (bases 1 to 1027)
AUTHORS      Pichersky,E., Bernatzky,R., Tanksley,S.D. and Cashmore,A.R.
TITLE      Evidence for selection as a mechanism in the concerted evolution of
              Lycopersicon esculentum (tomato) genes encoding the small subunit
              of ribulose-1,5-bisphosphate carboxylase/oxygenase
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 83 (11), 3880-3884 (1986)
PUBMED      3012537
COMMENT      Original source text: Tomato (L.esculentum) DNA, clone Rbcs-3A.
              Clean copy sequence for [1] kindly provided by E.Pichersky,
              31-OCT-1986.
FEATURES      Location/Qualifiers
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CDS
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            EDNVQVOCISFIAYKPSGY"
            <136..312
            /note="ribulose-1,5-bisphosphate carboxylase/ oxygenase
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            405..539
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            /note="RBCS cds intron B"
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ORIGIN      525 bp upstream of EcoRI site; chromosome 2, Rbcs-3 locus.

Alignment Scores:
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Score:          230.50      Matches:      50
Percent Similarity: 93.0%      Conservative: 3
Best Local Similarity: 87.7%      Mismatches: 3
Query Match:      85.1%      Indels:      1
DB:              15      Gaps:      1

US-10-628-525A-33 (1-56) x TOMRBCSC (1-1027)

QY      1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThraAsnProAlaGlnAla 20
DB      136 ATGGCTTTCTTCAATGATGCTCTCAGCAGCTGTGCCCGCGCAATGGTGCAAGCT 195

QY      21 SerMetValAlaProPheThrGlyLeuLySer---AlaAlaPheProValSerArgLyS 39
DB      196 AGCATGGTTGCACCTTCTCACTGGACTCAAGTCCACCGCTTCTTCCCTGTTTCAAGGAAG 255

QY      40 GlnAenLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB      256 CAAACCTTGCATTCATTCCATTGCTAGCAACGGTGAAGAGTCAGTTGC 306

RESULT 19
LERBCS3C      1341 bp      DNA      linear      PLN 10-FEB-1999
LOCUS      Tomato rbcS3C gene for ribulose 1,5-bisphosp(hate
DEFINITION      carboxylase/oxygenase small subunit.
ACCESSION      X05986
VERSION      X05986.1 GI:19337
KEYWORDS      rbcS gene; ribulose bisphosphate carboxylase.
SOURCE      Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE      1 (bases 17 to 1224)
AUTHORS      Sugita,M., Manzara,T., Pichersky,E., Cashmore,A. and Grullessen,W.
TITLE      Genomic organization, sequence analysis and expression of all five
              genes encoding the small subunit of ribulose-1,5-bisphosphate
              carboxylase/oxygenase from tomato
JOURNAL      Mol. Gen. Genet. 209 (2), 247-256 (1987)
PUBMED      3478552
COMMENT      2 (bases 1 to 1340)
              Manzara,T.
              Direct Submission
              Submitted (02-FEB-1989)
              JOURNAL
              REFERENCE      3 (bases 1 to 1341)
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AUTHORS Manzara,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-AUG-1989)  
 FEATURES  
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 122. .134  
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 139. .147  
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 174. .184  
 236. .244  
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 281. .474  
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 298. .468  
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 Score: 230.50 Matches: 50  
 Percent Similarity: 93.0% Conservative: 3  
 Best Local Similarity: 87.7% Mismatches: 3  
 Query Match: 85.1% Indels: 1  
 DB: 15 Gaps: 1  
 US-10-628-525A-33 (1-56) x LERBSC3C (1-1341)  
 QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
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 DB 298 ATGGCTTCTTCAGTAATGCTCCTCAGCAGCTGTGTCACCGGGCAATGTCACCAAGCT 357  
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 QY 21 SerMetValAlaProPheThrGlyLeuLysSer---AlaAlaPheProValSerArgLys 39  
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Db 358 AGCATGGTTGACCCCTTCACTGGACTCAAGTCCACCGCTTCTTCCCTGTTCAAGGAAG 417  
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 QY 40 GlnAenLeuAepIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56  
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 Db 418 CAAACCTTGACATTACCTTCATTGCTAGCAACGTCGAGAGAGTCAAGTTGC 468  
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RESULT 20  
 LERBSC3A 1520 bp DNA linear PLN 10-FEB-1999  
 LOCUS Tomato rbcS3A gene for ribulose 1,5-bisphosphate  
 DEFINITION carboxylase/oxygenase small subunit.  
 ACCESSION X05984  
 VERSION X05984.1 GI:19333  
 KEYWORDS rbcS gene; ribulose bisphosphate carboxylase.  
 SOURCE Lycopersicon esculentum (Solanum lycopersicum)  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamiids; Solanales; Solanales; Solanales; Lycopersicon.  
 REFERENCE 1 (bases 98 to 1442)  
 AUTHORS Sugita,M., Manzara,T., Pichersky,E., Cashmore,A. and Gruissem,W.  
 TITLE Genomic organization, sequence analysis and expression of all five  
 genes encoding the small subunit of ribulose-1,5-bisphosphate  
 carboxylase/oxygenase from tomato  
 JOURNAL Mol. Gen. Genet. 209 (2), 247-256 (1987)  
 PUBLISHED 3478552  
 REFERENCE 2 (bases 1 to 1520)  
 AUTHORS Manzara,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-FEB-1989)  
 COMMENT see x05982 - x05986.  
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 FDNVRQVCISFIAYKPEGY"  
 378. .548  
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 join(549. .554,647. .781,869. .1093)  
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 555. .646  
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 intron





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exon		734..910
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		/number=1
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intron		911..999
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exon		1000..1134
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		/product="ribulose biphosphate carboxylase"
		/number=2
		/EC_number="4.1.1.39"
intron		1135..1215
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exon		/gene="rbcS2b"
		/product="ribulose biphosphate carboxylase"
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3'UTR		1447..1703
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Score:	228.50	Matches: 49
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Best Local Similarity:	86.0%	Mismatches: 3
Query Match:	84.3%	Indels: 1
DB:	15	Gaps: 1
US-10-628-525A-33 (1-56) x STRBCS2B (1-1703)		
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20		
Db 734 ATGGCTTCTCTATAGTTCTTCAGTCTGTGGCCTCGCGCAATGGTGCACAAGCC 793		
QY 21 SerMetValAlaProPheThrGlyLeuLysSer---AlaAlaPheProValSerArgLys 39		
Db 794 AGCATGGTGGGCCCTTCACGTGACTCAAGTCCACGCCCTCTTCCCTGTTTCAAGGAAG 853		
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56		
Db 854 CAAACCTTGACATTACCTCCATTGCTAGCAATGGTGAAGAGTCAGATGC 904		
RESULT 25		
STRBCS1		
LOCUS		STRBCS1 3323 bp DNA linear PLN 09-OCT-1996
DEFINITION		S.tuberosum rbcS1 gene for ribulose-(1,5)-biphosphate carboxylase/oxygenase small subunit.
ACCESSION		X69759
VERSION		X69759.1 GI:21562
KEYWORDS		chloroplast; gene expression; gene family; photosynthesis; protein transport; rbcS1 gene.
SOURCE		Solanum tuberosum (potato)
ORGANISM		Solanum tuberosum
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.
AUTHORS		1 (bases 1 to 3323) Fritz,C.C., Wolter,F.P., Schenkemeyer,V., Herget,T. and Schreier,P.H.
TITLE		The gene family encoding the ribulose-(1,5)-biphosphate carboxylase/oxygenase (Rubisco) small subunit of potato
JOURNAL		Gene 137 (2), 271-274 (1993)
PUBMED		8299958
REFERENCE		2 (bases 1 to 1703) Schreier,P.H.
AUTHORS		Direct Submission
TITLE		Submitted (01-DEC-1992) P.H. Schreier, Bayer AG, PF-E/FU Gebaeude 6240, 5090 Leverkusen-Bayerwerk, FRG
JOURNAL		Related sequence: Fritz, C.C., Proc. Natl. Acad. Sci. 88:4458-4462 (91).
COMMENT		
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		/mol_type="genomic DNA"
		/isolates="AM 80.5793 (HH 5793 MPI collection)"
		/db_xref="taxon:4113"
		/chromosomes="II"
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gene		1..1703
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5'UTR		1..733
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CDS		join(734..910,1000..1134,1216..1446)
		/gene="rbcS2b"
		/EC_number="4.1.1.39"
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		/product="ribulose biphosphate carboxylase"
		/protein_id="CAA49415.1"
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PUBMED	829958	REFERENCE	2 (bases 1 to 3323)	DB:	15	Gaps:	2
AUTHORS	Schreier, P.H.	LOCUS	US-10-628-525A-33 (1-56) x STRBCS1 (1-3323)	QY	1	MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgThrAsnProAlaGlnAla	20
TITLE	Direct Submission	DEFINITION	Submitted (01-DEC-1992) P.H. Schreier, Bayer AG, PF-E/FU Gebaeude 6240, 5090 Leverkusen-Bayerwerk, FRG	Db	617	ATGGCTTCCTCTGTTATTTCTCTGCAGCTGTTGCTACACGCCACCAATGTTTACACAGCT	676
JOURNAL	6240, 5090 Leverkusen-Bayerwerk, FRG	ACCESSION	Related sequence: Fritze, C.C., Proc. Natl. Acad. Sci. 88:4458-4462 (91).	QY	21	---SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArg	38
COMMENT	(91).	VERSION	Location/Qualifiers	Db	677	GGCAGCATGATTGCACCTTTCATGCTCAATCTGCTACTTTCCTTCCTTCCTTCAGG	736
FEATURES		KEYWORDS	1. .3323	QY	39	LysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56
source		ORGANISM	/organism="Solanum tuberosum"	Db	737	AAGCAAAACCTTGACATCACTTCATTGCTAGCAATGTTGGAAGAGTTAGGTGC	790
gene			/mol_type="genomic DNA"	RESULT 26			
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			1. .616				
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			/product="ribulose biphosphate carboxylase"				
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intron			/EC number="4.1.1.39"				
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exon			/number=1				
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exon			/number=2				
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intron			/EC number="4.1.1.39"				
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			/genes="rbcS1"				
exon			/number=3				
			2593..2770				
			/genes="rbcS1"				
			/product="ribulose biphosphate carboxylase"				
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			/genes="rbcS1"				
3'UTR							
ORIGIN							
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Score:	226.00	Matches:	50	Db	15	ATGGCTTCCTCTGTTATTTCTCTGCAGCTGTTGCTACACGCCACCAATGTTTACACAGCT	74
Percent Similarity:	93.1%	Conservative:	4	QY	21	SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys	39
Best Local Similarity:	86.2%	Mismatches:	2				
Query Match:	83.4%	Indels:	2				

Db 75 AGCATGGTTGCACCTTTTCACCTGGTCTCAAACTTTCAGCCACTTTCCTCTGTACAAAGAAG 134

QY 40 GlnAsnLeuAspIleThrSerIleAlaValAlaThrArgThrAsnProAlaGlnAla 56  
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Db 135 CAAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTTAGCTGC 185

RESULT 27  
AR428736  
LOCUS AR428736 684 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 16 from patent US 6642036.  
ACCESSION AR428736  
VERSION AR428736.1 GI:40188466  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 684)  
AUTHORS Flint,D., Meyer,K. and Viitanen,P.  
TITLE Sinapoylglucose:malate sinapoyltransferase form malate conjugates  
JOURNAL from benzoic acid glucosides  
Patent: US 6642036-A 16 04-NOV-2003;  
E. I. Du Pont de Nemours and Company; Wilmington;  
WOX;

FEATURES  
source Location/Qualifiers  
1. .684  
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Pred. No.: 6.68e-18 Length: 684  
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Percent Similarity: 93.0% Conservative: 6  
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Query Match: 82.5% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x AR428736 (1-684)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
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Db 1 ATGGCTTCCTCTGTCTTCATTTCTTCAGCAGCTGTGGCCACACGCGCAATGTTACACAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAa---PheProValSerArgLys 39  
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Db 61 AGCATGGTTGCACCTTTTCACCTGGTCTCAAACTTTCAGCCACTTTCCTCTGTACAAAGAAG 120

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Db 121 CAAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTTAGCTGC 171

RESULT 28  
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LOCUS AR455412 684 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 7 from patent US 6683231.  
ACCESSION AR455412  
VERSION AR455412.1 GI:42689960  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 684)  
AUTHORS Meyer,K., Viitanen,P.V. and Van Dyk,D.B.  
TITLE High level production of p-hydroxybenzoic acid in green plants  
JOURNAL Patent: US 6683231-A 7 27-JAN-2004;  
E. I. du Pont de Nemours and Company; Wilmington, DE

FEATURES  
source Location/Qualifiers  
1. .684  
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/mol\_type="genomic DNA"

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Alignment Scores:  
Pred. No.: 6.68e-18 Length: 684  
Score: 223.50 Matches: 47  
Percent Similarity: 93.0% Conservative: 6  
Best Local Similarity: 82.5% Mismatches: 3  
Query Match: 82.5% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x AR455412 (1-684)

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QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
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Db 121 CAAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTTAGCTGC 171

RESULT 29  
AX329368  
LOCUS AX329368 684 bp DNA linear PAT 08-JAN-2002  
DEFINITION Sequence 7 from Patent WO0194607.  
ACCESSION AX329368  
VERSION AX329368.1 GI:18102367  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Meyer,K., van Dyk,D.B. and Viitanen,P.V.  
TITLE High level production of p-hydroxybenzoic acid in green plants  
JOURNAL Patent: WO 0194607-A 7 13-DEC-2001;  
E.I. Dupont De Nemours (US)

FEATURES  
source Location/Qualifiers  
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ORIGIN  
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Percent Similarity: 93.0% Conservative: 6  
Best Local Similarity: 82.5% Mismatches: 3  
Query Match: 82.5% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x AX329368 (1-684)

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QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAa---PheProValSerArgLys 39  
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Db 61 AGCATGGTTGCACCTTTTCACCTGGTCTCAAACTTTCAGCCACTTTCCTCTGTACAAAGAAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
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Db 121 CAAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTTAGCTGC 171

RESULT 30  
AX382258  
LOCUS AX382258 684 bp DNA linear PAT 18-MAR-2002  
DEFINITION Sequence 16 from Patent WO0204653.  
ACCESSION AX382258  
VERSION AX382258.1 GI:19577037  
KEYWORDS



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SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Flint,D., Meyer,K. and Viitanen,P.V.
TITLE        Sinapolyglucose:malate sinapolytransferase form malate conjugates
JOURNAL      Patent: WO 0204653-A 16 17-JAN-2002;
FEATURES     E.I. DUPONT DE NEMOURS AND COMPANY (US)
              Location/Qualifiers
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ORIGIN

Alignment Scores:
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Score:          223.50      Matches:      47
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Best Local Similarity: 82.5%      Mismatches: 3
Query Match:      82.5%      Indels:      1
DB:              6          Gaps:          1

US-10-628-525A-33 (1-56) x AX382258 (1-684)

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Qy      21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db      61 AGCATGGTTGCACCTTTCACTGGTCTCAATCTTCAGCCACTTTCCCTGTTACAAGAG 120

Qy      40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db      121 CAAACCTTGACATCACTTCATTTGCTAGCAATGGTGAAGAGTTAGCTGC 171

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GenCore version 5.1.7  
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Title: US-10-628-525A-33

Perfect score: 271

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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6: geneseqn2002as:\*  
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12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	240.5	88.7	177	2	AAT40794 Chloropla

5	240.5	88.7	177	2	AAT37096
6	240.5	88.7	177	2	AAT41744
7	240.5	88.7	177	2	AAT91545
8	240.5	88.7	204	6	Aai70688 Tobacco R
9	240.5	88.7	297	10	AdK59826 Plant DNA
10	240.5	88.7	377	10	AdK56121 Plant DNA
11	240.5	88.7	489	10	AdK56120 Plant DNA
12	240.5	88.7	492	10	AdC76164 DNA homol
13	240.5	88.7	499	6	AdK35635 Nicotiana
14	240.5	88.7	504	10	AdK59824 Plant DNA
15	240.5	88.7	581	10	AdC75089 N bentham
16	240.5	88.7	608	10	AdC76944 DNA homol
17	240.5	88.7	614	10	AdC76956 DNA homol
18	240.5	88.7	615	10	AdC76949 DNA homol
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21	240.5	88.7	718	10	AdK58382 Plant DNA
22	240.5	88.7	736	10	AdK54321 Plant DNA
23	240.5	88.7	736	10	AdK57660 Plant DNA
24	240.5	88.7	841	11	AdM44879 Insect re
25	240.5	88.7	847	11	AdM45447 Insect re
26	240.5	88.7	859	11	AdM45065 Insect re
27	240.5	88.7	924	10	AdC75566 DNA homol
28	240.5	88.7	958	10	AdC76165 DNA homol
29	240.5	88.7	1442	2	AAQ92327
30	236.5	87.3	619	11	AdM45158 Insect re
31	236.5	87.3	668	10	AdK59825 Plant DNA
32	236.5	87.3	668	11	AdM45687 Insect re
33	235.5	86.9	177	2	AAQ13721
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37	226.5	83.6	169	8	ABA257803
38	223.5	82.5	684	6	ABA91838
39	223.5	82.5	684	6	ABK47712
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45	221	81.5	741	11	AdM45450 Insect re
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54	215	79.3	738	10	AdK54333 Plant DNA
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56	215	79.3	754	10	AdK57645 Plant DNA
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58	215	79.3	834	11	AdM44819 Insect re
59	209.5	77.3	385	12	ADP92165
60	207.5	76.6	315	11	AdM45114 Insect re
61	207.5	76.6	444	3	AAQ37666
62	207.5	76.6	447	11	AdM45105 Insect re
63	207.5	76.6	450	11	AdM45121 Insect re
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69	207.5	76.6	724	6	ABK30640 Plant dna
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75	207.5	76.6	771	6	ABN99150 Arabidops
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79	204.5	75.5	191	1	AA95096	AA95096 Transit p
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81	204.5	75.5	191	4	AA165715	Aa165715 Nucleotid
82	204.5	75.5	1084	6	AA31813	Aad31813 Gossypium
83	204	75.3	177	1	AA95095	AA95095 Transit p
84	204	75.3	177	3	Az98881	Aaz98881 Small sub
85	204	75.3	177	4	AA165714	Aa165714 Nucleotid
86	200.5	74.0	675	13	ADV04475	Adv04475 Nucleotid
87	199.5	73.6	363	6	ABQ85598	Abq85598 Arabidops
88	199.5	73.6	364	11	ADM45548	Adm45548 Insect re
89	199.5	73.6	546	3	AAC48433	Aac48433 Arabidops
90	199.5	73.6	700	11	ADM45118	Adm45118 Insect re
91	199.5	73.6	700	11	ADM44971	Adm44971 Insect re
92	199.5	73.6	711	6	ABK30617	Abk30617 Plant dwa
93	199.5	73.6	711	6	AB149430	Ab149430 Sequence
94	199.5	73.6	737	11	ADM45549	Adm45549 Insect re
95	199.5	73.6	739	6	ABK30768	Abk30768 Plant dwa
96	199.5	73.6	1036	13	ADT17269	Adt17269 Plant cDN
97	199.5	73.6	2581	13	ADT15847	Adt15847 Plant cDN
98	197	72.7	240	3	AAA31345	Aaa31345 Plant mic
99	197	72.7	256	3	AAA31405	Aaa31405 Plant mic
100	197	72.7	339	3	AAA31255	Aaa31255 Plant mic
101	197	72.7	341	3	AAA31253	Aaa31253 Plant mic
102	197	72.7	344	3	AAA31397	Aaa31397 Plant mic
103	197	72.7	351	3	AAA31294	Aaa31294 Plant mic
104	197	72.7	363	3	AAA31381	Aaa31381 Plant mic
105	197	72.7	367	3	AAA31392	Aaa31392 Plant mic
106	197	72.7	383	3	AAA31276	Aaa31276 Plant mic
107	197	72.7	401	3	AAA31391	Aaa31391 Plant mic
108	197	72.7	403	3	AAA31288	Aaa31288 Plant mic
109	197	72.7	407	3	AAA31390	Aaa31390 Plant mic
110	197	72.7	410	3	AAA31259	Aaa31259 Plant mic
111	197	72.7	412	3	AAA31387	Aaa31387 Plant mic
112	197	72.7	413	3	AAA31410	Aaa31410 Plant mic
113	197	72.7	423	3	AAA31314	Aaa31314 Plant mic
114	197	72.7	426	3	AAA31403	Aaa31403 Plant mic
115	197	72.7	430	3	AAA31336	Aaa31336 Plant mic
116	197	72.7	433	3	AAA31284	Aaa31284 Plant mic
117	197	72.7	457	3	AAA31269	Aaa31269 Plant mic
118	197	72.7	479	3	AAA32042	Aaa32042 Plant mic
119	197	72.7	479	3	AAA31291	Aaa31291 Plant mic
120	197	72.7	484	3	AAA31305	Aaa31305 Plant mic
121	197	72.7	502	3	AAA31309	Aaa31309 Plant mic
122	197	72.7	570	3	AAA32041	Aaa32041 Plant mic
123	197	72.7	606	3	AAA32043	Aaa32043 Plant mic
124	197	72.7	2586	14	ADW16694	Adw16694 Eucalyptu
125	195.5	72.1	752	13	ADV04474	Adv04474 Nucleotid
126	195.5	72.1	767	6	ABN99163	Abn99163 Arabidops
127	195.5	72.1	780	6	ABN99112	Abn99112 Arabidops
128	194	71.6	934	8	ABQ83212	Abq83212 Coffee rb
129	194	71.6	2034	8	ABQ83211	Abq83211 Coffee rb
130	193.5	71.4	929	13	ADT16033	Adt16033 Plant cDN
131	193.5	71.4	1000	13	ADT16035	Adt16035 Plant cDN
132	193	71.2	350	3	AAA31396	Aaa31396 Plant mic
133	192.5	71.0	363	6	ABQ85593	Abq85593 Arabidops
134	192.5	71.0	392	8	ABX62856	Abx62856 Arabidops
135	191.5	70.7	386	3	AAC37828	Aac37828 Arabidops
136	191.5	70.7	546	3	AAC48432	Aac48432 Arabidops
137	191	70.5	240	3	AAA31368	Aaa31368 Plant mic
138	190	70.1	481	3	AAA31306	Aaa31306 Plant mic
139	190	70.1	764	10	ADK56736	Adk56736 Plant DNA
140	188	69.4	215	3	AAA31341	Aaa31341 Plant mic
141	188	69.4	424	10	ADK57649	Adk57649 Plant DNA
142	188	69.4	424	10	ADK54327	Adk54327 Plant DNA
143	188	69.4	424	11	ADM45552	Adm45552 Insect re
144	188	69.4	450	3	AAA31250	Aaa31250 Plant mic
145	188	69.4	1299	10	ADK54308	Adk54308 Plant DNA
146	186	68.6	618	10	ADC76975	Adc76975 DNA homol
147	186	68.6	618	10	ADC75104	Adc75104 Poppy phy
148	186	68.6	618	10	ADC75565	Adc75565 DNA homol
149	186	68.6	677	11	ADM45205	Adm45205 Insect re
150	185	68.3	629	10	ADK52842	Adk52842 Plant DNA

ALIGNMENTS

RESULT 1		
AAT66535		
ID	AAT66535 standard; DNA; 171 BP.	
XX		
AC	AAT66535;	
XX		
DT	27-AUG-2003 (revised)	
DT	22-JUL-1997 (first entry)	
XX		
DE	Plastid targetting signal.	
XX		
KW	Transgenic plant; selectable marker; carotenoid; pigment;	
KW	plastid targetting signal; RUBISCO; phytoene synthase; plasmid pET0203;	
SS	ss.	
OS	Unidentified.	
XX		
PN	WO9714807-AL.	
XX		
PD	24-APR-1997.	
XX		
PF	29-MAR-1996; 96WO-US004313.	
XX		
PR	16-OCT-1995; 95US-00543608.	
XX		
PA	(SEMI-) SEMINIS VEGETABLES.	
PI	Trulson AJ, Braun CJ;	
XX		
DR	WPI; 1997-245122/22.	
DR	P-PSDB; AAW16493.	
XX		
PT	Visual identification of transgenic plant material - from production of	
PT	carotenoid pigment encoded by cassette containing Erwinia phytoene	
PT	synthase gene, useful for selecting material for regeneration.	
XX		
PS	Example; Page 36; 62pp; English.	
CC	A plastid targetting signal (AAT66535) is obt'd. from the small subunit of	
CC	the ribulose-1,4-bisphosphate carboxylase oxygenase (RUBISCO). It can be	
CC	used to target the Erwinia herbicola phytoene synthase crtB gene (see	
CC	also AAT6534) to plant plastids, where expression of the gene results in	
CC	carotenoid biosynthesis. The construct is a component of pET0203 (ATCC	
CC	97282), a binary vector used in a method for the visual identification of	
CC	transgenic plant material. The vector includes an expression cassette	
CC	comprising the tomato E8 promoter (see also AAT66533), the plastid	
CC	targetting signal fused to the crtB gene, and a 3' non-translated region	
CC	(AAT66536). Transgenic plant cells and tissues are identified by the	
CC	appearance of orange colour. (Updated on 27-AUG-2003 to correct OS	
CC	field.)	
XX		
SQ	Sequence 171 BP; 38 A; 52 C; 37 G; 44 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	2.03e-24	Length: 171
Score:	240.50	Matches: 52
Percent Similarity:	96.5%	Conservative: 3
Best Local Similarity:	91.2%	Mismatches: 1
Query Match:	88.7%	Indels: 1
DB:	2	Gaps: 1
US-10-628-525A-33 (1-56) x AAT66535 (1-171)		
Oy	1 MetalaserSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20	
Db	1 ATGGCTTCTCAGTTCCTTCCTTCGACAGTTCGCCGCCGACGCAATGTGCTCAAGCT 60	
Oy	21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39	
	:::	

Db 61 AACATGTTGGCGCTTTCACTGGCTTAAGTCAGCTGCCTCATTCCTCTGTTTCAAGGAAG 120

Qy 40 GlnAenLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56  
|||||

Db 121 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 2

ABX93949

ID ABX93949 standard; DNA; 174 BP.

XX AC

XX ABX93949;

DT 04-JUN-2003 (first entry)

XX DE DNA encoding small sub-unit of pea rubisco prSS.

XX KW Plastid transit peptide; Cuphea acyl-ACP thioesterase;

XX KW protein translocation; plastid; transgenic; plant;

XX KW modified fatty acid composition; oilseed crop; transformation;

XX KW medium chain specific condensing enzyme; modified oil content;

XX KW small sub-unit of pea rubisco; prSS; ds; Pea.

XX OS Pisum sativum.

XX PH Key Location/Qualifiers

FT CDS 1..174

FT FT /\*tag= a

FT FT /product= "Plastid transit peptide"

FT FT /partial

FT FT /note= "No stop codon given"

XX US2002178467-A1.

XX 28-NOV-2002.

XX 11-MAY-2001; 2001US-00854286.

XX 12-MAY-2000; 2000US-0203618P.

XX (DEHE/) DEHESH K.

XX Dehesh K;

XX WPI; 2003-352617/33.

XX P-PSDB; ABU08651.

XX New recombinant DNA construct for modifying the fatty acid composition of a plant cell, comprises a promoter that functions in plant cells, linked to a heterologous DNA encoding a plastid transit peptide of Cuphea acyl-ACP thioesterase.

XX Disclosure; Page 19; 32pp; English.

XX The invention describes a recombinant DNA construct (I) comprising a promoter that functions in plant cells, operably linked to a heterologous DNA molecule encoding a plastid transit peptide (PTP) of a Cuphea acyl-ACP thioesterase (AT), operably linked to a heterologous DNA encoding a protein, operably linked to a DNA molecule providing 3' termination functions. (I) is useful in an improved method for translocating a protein to a crop plant cell plastid, by introducing (I) into a crop plant cell, and regenerating the crop plant cell into a transgenic crop plant. (I) is useful for producing a modified fatty acid composition of an oilseed crop, by transforming a plant cell of an oil seed crop with (I) and a DNA construct that provides expression of a medium chain specific condensing enzyme, regenerating the plant cell into a transgenic oil seed crop plant, planting seeds of the transgenic oil seed crop plant, harvesting seeds from the transgenic oil seed crop plant and processing the seeds for purification of a modified oil content. This sequence encodes the small sub-unit of pea rubisco, prSS, a transit peptide of the invention

XX Sequence 174 BP; 40 A; 52 C; 37 G; 45 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2.08e-24 Length: 174  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 8 Gaps: 1

US-10-628-525A-33 (1-56) x ABX93949 (1-174)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
|||||

Db 1 ATGGCTTCCTCAGTCTTTCTCTGACAGAGTTGCCACCCGACGCAATGTTGCTCAAGCT 60

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||

Db 61 AACATGTTGCACCTTTCATCTGGCTTAAGTCAGCTGCCTCATTCCTCTGTTTCAAGGAAG 120

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56  
|||||

Db 121 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

## RESULT 3

AATZ71129

ID AATZ7129 standard; DNA; 177 BP.

XX AC AATZ7129;

DT 17-DEC-1996 (first entry)

XX DE Modified RUBISCO signal peptide coding sequence.

XX KW Ribulose bis-phosphate carboxylase-oxygenase; RUBISCO; signal peptide;

XX KW plastid transit peptide; non-higher plant; phytoene synthase; carotenoid;

XX KW ss.

XX OS Nicotiana tabacum.

XX PH Key Location/Qualifiers

FT mutation 69

FT FT /\*tag= a

FT FT /note= "T>G change"

FT mutation 72

FT FT /\*tag= b

FT FT /note= "A>G change"

XX WO9613149-A1.

XX 09-MAY-1996.

XX 27-OCT-1995; 95WO-US013937.

XX 28-OCT-1994; 94US-00331004.

XX (STAD ) AMOCO CORP.

XX Hauptmann R, Eschenfeldt WH, English J, Brinkhaus FL;

XX WPI; 1996-239176/24.

XX Accumulating coloured native carotenoid(s) in transgenic plants -

XX comprises transforming plants with DNA encoding non-higher plant phytoene

XX synthase and promoter driving storage organ expression of the enzyme.

PS Example 1; Page 79; 103pp; English.

XX This sequence represents a modified version of the ribulose bis-phosphate

XX carboxylase-oxygenase (RUBISCO) signal peptide coding sequence. This

XX sequence contains two changes compared to the wild type coding sequence.

XX Two cytidine residues were added to the 5' end to create a NcoI

XX restriction site. The second change introduces an Nari site that cleaves

XX between bases 73 and 74. This change constituted a G for T replacement at

XX position 69 and a G for A replacement at position 72. Both of these

CC changes left the encoded amino acid sequence unchanged. The final two  
 CC residues at the 3' end were deleted to maintain the fragment length of  
 CC 177 bp and to provide the natural SphI restriction site sticky end. This  
 CC sequence was used in the preparation of a chimeric DNA molecule encoding  
 CC a protein having an N-terminal plastid transit peptide portion whose C-  
 CC terminus is bonded to the N-terminus of a non-higher plant phytoene  
 CC synthase enzyme. This construct allows the accumulation of carotenoids  
 XX  
 SQ Sequence 177 BP; 40 A; 53 C; 39 G; 45 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,13e-24 Length: 177  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x AAT27129 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 |||||  
 Db 1 ATGGCTTCCTCAGTTCTTCTCTGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
 |||||  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::|||  
 Db 61 AACATGGTGGCGCTTTTCACTGCGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 120  
 |||||  
 QY 40 GlnAnLeuAspIleThrSerIleAlaSerAnGlyGlyArgValGlnCys 56  
 |||||  
 Db 121 CAAACCTTGATCATTCTCCATTGCCACNACGGCGGAAGATGCAATGC 171  
 |||||

## RESULT 4

AAT40794  
 ID AAT40794 standard; DNA; 177 BP.

AC AAT40794;  
 DT 25-MAR-2003 (revised)  
 DT 10-DEC-1996 (first entry)  
 XX Chloroplast transit peptide coding sequence.  
 DE  
 XX GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene;  
 KW phytoene dehydrogenase-4H; carotenoid; C40; zeaxanthin; diglucoside;  
 KW pigment; food colourant; chloroplast transit peptide; increase yield;  
 KW tobacco ribulose bis-phosphate carboxylase-oxygenase; ss.  
 XX  
 OS Nicotiana tabacum.

Key Location/Qualifiers  
 FH misc\_difference 69  
 FT /\*tag= a  
 FT /note= "replacement of native T with G"  
 FT misc\_difference 72  
 FT /\*tag= b  
 FT /note= "replacement of native A with G"

US5530188-A.

25-JUN-1996.

21-JUL-1993; 93US-00095726.

02-MAR-1990; 90US-00487613.

18-MAY-1990; 90US-00525551.

03-AUG-1990; 90US-00562674.

28-FEB-1991; 91US-00662921.

30-OCT-1991; 91US-00785566.

(STAD ) AMOCO CORP.

Yen HB, Brinkhaus FL, Proffitt J, Mukharji I, Yarger J;

## PI

Ausich RL;

DR WPI: 1996-308823/31.

DR P-PSDB; AAW01124.

XX

PT Increasing prodn. of total carotenoid(s) in a higher plant - by  
 PT transforming with vector encoding chloroplast transit peptide operably  
 PT linked to the Erwinia herbicola lycopene cyclase structural gene.

PS Example 2; Fig 17; 99pp; English.

XX The present sequence encodes a chloroplast transit peptide (AAW01124) of  
 CC the tobacco ribulose bis-phosphate carboxylase-oxygenase gene which can  
 CC be operatively linked in frame to the 5' end of the lycopene cyclase  
 CC structural gene (AAT40795). This leads to increased production of total  
 CC carotenoids in the chloroplast of transformed plants as compared to  
 CC native, non-transformed plants of the same type. Other enzymes involved  
 CC in the carotenoid biosynthesis pathway include geranylgeranyl  
 CC pyrophosphate (AAW01119), phytoene synthase (W01121) and phytoene  
 CC dehydrogenase-4H (AAW01122). Beta-carotene is an effective and apparently  
 CC harmless food colourant and is also in the pathway for biological  
 CC synthesis of further C40 carotenoids such as zeaxanthin and zeaxanthin  
 CC diglucoside. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 177 BP; 40 A; 53 C; 39 G; 45 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2,13e-24 Length: 177  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x AAT40794 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 |||||  
 Db 1 ATGGCTTCCTCAGTTCTTCTCTGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
 |||||  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::|||  
 Db 61 AACATGGTGGCGCTTTTCACTGCGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 120  
 |||||  
 QY 40 GlnAnLeuAspIleThrSerIleAlaSerAnGlyGlyArgValGlnCys 56  
 |||||  
 Db 121 CAAACCTTGATCATTCTCCATTGCCACNACGGCGGAAGATGCAATGC 171  
 |||||

## RESULT 5

AAT37096

ID AAT37096 standard; DNA; 177 BP.

AC AAT37096;

DT 25-MAR-2003 (revised)

DT 18-OCT-1996 (first entry)

DE Ribulose bis-phosphate carboxylase-oxygenase signal peptide.

XX E. herbicola; geranylgeranyl pyrophosphate synthase; pARC376;

KW GGPP synthase; biosynthesis; carotenoid; lycopene;

KW farnesyl pyrophosphate; phytoene; FPP; isopentenyl pyrophosphate; IPP;

KW tail to tail dimerisation; phytoene synthase; phytoene dehydrogenase-4H;

KW food colourant; herbicide; norflurazon; ss.

XX Nicotiana tabacum.

OS US5530189-A.

PN 25-JUN-1996.

XX 22-JUL-1993; 93US-00096043.

XX

PR 02-MAR-1990; 90US-00487613.  
 PR 18-MAY-1990; 90US-00525551.  
 PR 03-AUG-1990; 90US-00562674.  
 PR 28-FEB-1991; 91US-00662921.  
 PR 30-OCT-1991; 91US-00785568.  
 XX (STAD ) AMOCO CORP.  
 PA  
 XX Yen HB, Brinkhaus FL, Proffitt J, Mukharji I, Yarger J;  
 PI Ausich RL;  
 XX WPI; 1996-308824/31.  
 DR P-PSDB; AAW00175.  
 XX  
 PT DNA encoding Erwinia herbicola phytoene dehydrogenase-4H - used for  
 PT prodn. of lycopene, and to produce transgenic plants resistant to  
 PT norflurazon.  
 XX  
 PS Example 3; Fig 17; 87pp; English.  
 XX  
 CC This sequence is based on the nucleotide sequence encoding the Nicotiana  
 CC tabacum ribulose bis-phosphate carboxylase-oxygenase signal peptide. Two  
 CC changes were made to the wild type sequence in the production of this  
 CC sequence. Firstly, two cytidine residues were added at the 5' end to  
 CC create a NcoI site. Secondly, an NsiI site that cleaves between bases 73  
 CC and 74 was introduced. This change was a G for a T replacement at  
 CC position 69 and a G for A replacement at position 72, both of which  
 CC changes left the amino acid sequence unchanged. This sequence was  
 CC generated using the double stranded fragments given in AAT37097-100. This  
 CC signal peptide sequence was used in the expression of geranylgeranyl  
 CC pyrophosphate (GGPP) synthase in higher plants. GGPP synthase is an  
 CC enzyme which is involved in the biosynthesis of carotenoids, esp.  
 CC lycopene, from the ubiquitous precursor, farnesyl pyrophosphate. In E.  
 CC herbicola, phytoene has been found to be formed biosynthetically in a two  
 CC step process. The initial step is the condensation of farnesyl  
 CC pyrophosphate (FPP) and isopentenyl pyrophosphate (IPP) to form GGPP. This  
 CC reaction is catalysed by GGPP synthase. This first step is immediately  
 CC followed by a tail to tail dimerisation of GGPP, catalysed by the enzyme  
 CC phytoene synthase, to form phytoene. Lycopene is produced from phytoene  
 CC by the catalytic action of phytoene desaturase-4H. The genes encoding  
 CC components of the lycopene biosynthesis pathway may be used to transform  
 CC a host cell for the commercial production of lycopene which is used as a  
 CC food colourant. Plants transformed with the phytoene desaturase-4H  
 CC coding sequence are protected from the herbicide norflurazon. (Updated on  
 CC 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 177 BP; 40 A; 53 C; 39 G; 45 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2.13e-24 Length: 177  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 2 Gaps: 1  
 US-10-628-525A-33 (1-56) x AAT37096 (1-177)  
 QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 DB 1 ATGGCTCTCCTCAGTCTTTCTCTGACGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 DB 61 AACATGGTGGCGCTTTTCAGTGGCTTAAAGTCAGCTGCCTCATTCCTGTTTCAGGAG 120  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56  
 DB 121 CAATACCTTGACATCATCTTCATTTGCCAGCAGCAACGGGGAGAGTGCATATGC 171  
 RESULT 6  
 AAT41744  
 ID AAT41744 standard; DNA; 177 BP.

XX AAT41744;  
 AC 25-MAR-2003 (revised)  
 DT 10-DEC-1996 (first entry)  
 XX  
 DE Tobacco transit peptide coding sequence.  
 XX  
 KW Wild type; N-terminally truncated; geranylgeranyl pyrophosphate; GGPP;  
 KW GGPP synthase; phytoene synthase; carotenoid; phytoene; PARC306A;  
 KW PARC489D; transit peptide; tobacco; chloroplast; skin disorder; ss.  
 XX  
 OS Nicotiana tabacum.  
 PN  
 XX US5545816-A.  
 XX 13-AUG-1996.  
 PD  
 XX 19-JUL-1993; 93US-00093577.  
 XX  
 PR 02-MAR-1990; 90US-00487613.  
 PR 18-MAY-1990; 90US-00525551.  
 PR 03-AUG-1990; 90US-00562674.  
 PR 28-FEB-1991; 91US-00662921.  
 PR 30-OCT-1991; 91US-00785569.  
 XX  
 XX (STAD ) AMOCO CORP.  
 PA  
 XX Yen HB, Brinkhaus FL, Proffitt J, Mukharji I, Yarger J;  
 PI Ausich RL;  
 XX WPI; 1996-383742/38.  
 DR P-PSDB; AAW00344.  
 XX  
 PT Transformed plants containing DNA encoding Erwinia herbicola enzymes -  
 PT esp. geranyl pyrophosphate synthase and phytoene synthase, allows  
 PT large scale production of phytoene.  
 XX  
 PS Example 3; Col 61-62; 61pp; English.  
 XX  
 CC This sequence encodes the tobacco transit peptide which allows transport  
 CC of proteins into the chloroplasts of the plant. This sequence may be  
 CC attached to the phytoene synthase or geranylgeranyl pyrophosphate (GGPP)  
 CC synthase coding sequences, for transport into tobacco chloroplasts. This  
 CC allows the tobacco plants to produce high levels of phytoene for use in  
 CC the treatment of skin disorders. Phytoene synthase and GGPP synthase (see  
 CC also AAT41741-43) are enzymes which catalyse the formation of  
 CC carotenoids, particularly phytoene. An N-terminally truncated form of  
 CC GGPP synthase which has the first thirteen amino acids replaced by four  
 CC heterologous amino acids derived from the plasmid PARC306A was found to  
 CC be about twice as active as the wild type enzyme. A C-terminal truncated  
 CC protein was found to have even higher activity and was cloned into  
 CC plasmid PARC489D. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 177 BP; 40 A; 53 C; 39 G; 45 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2.13e-24 Length: 177  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 2 Gaps: 1  
 US-10-628-525A-33 (1-56) x AAT41744 (1-177)  
 QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 DB 1 ATGGCTCTCCTCAGTCTTTCTCTGACGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 DB 61 AACATGGTGGCGCTTTTCAGTGGCTTAAAGTCAGCTGCCTCATTCCTGTTTCAGGAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyValGlnCys 56  
 DB 121 CAAACCTTGACATCACTTCATTGCGAGCAGCAGCGGAGAGTGCAATGC 171

RESULT 7  
 ID AAT91545  
 XX AAT91545 standard; DNA; 177 BP.  
 AC AAT91545;  
 XX 25-MAR-2003 (revised)  
 DT 15-JAN-1998 (first entry)  
 XX Phytoene dehydrogenase-4H transit peptide encoding DNA.  
 XX Geranylgeranyl pyrophosphate synthase; Erwinia herbicola; GGPP;  
 KW lycopene cyclase; recombinant enzyme; transgenic organism; beta-carotene;  
 KW yeast; plant; vitamin A; cancer; ss.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FH 1..177  
 FT /\*tag= a  
 FT /product= "Transit peptide"  
 FT /note= "No stop codon given"

US5656472-A.  
 PN 07-JUN-1995; 95US-00473512.  
 XX 12-AUG-1997.  
 XX 02-MAR-1990; 90US-00487613.  
 PR 18-MAY-1990; 90US-00525551.  
 PR 03-AUG-1990; 90US-00562674.  
 PR 28-FEB-1991; 91US-00662921.  
 PR 21-JUL-1993; 93US-00095726.  
 XX (STAD ) AMOCO CORP.  
 PA Mukharji I, Proffitt J, Ausich RL, Yarger J, Yen HB;  
 PI Brinkhaus FL;  
 XX WPI; 1997-414592/38.  
 DR P-PSDB; AAW32473.  
 XX DNA encoding Erwinia herbicola lycopene cyclase - for producing  
 PT recombinant enzyme, and transgenic organisms with increased beta-carotene  
 PT levels.  
 XX Example 3; Fig 17; 102pp; English.  
 CC A novel DNA molecule has been isolated which encodes an Erwinia herbicola  
 CC lycopene cyclase enzyme that converts lycopene to beta- carotene. The DNA  
 CC molecule comprises at least 1125 bp and is present in the plasmids  
 CC pARC147, pARC1509, pARC1510 and pARC1520. The present sequence encodes a  
 CC transit peptide which can be attached to the 5'-end of phytoene  
 CC dehydrogenase-4H, for transport into plant chloroplasts. The new DNA  
 CC molecule can be used to produce the recombinant enzyme and transgenic  
 CC organisms, e.g. yeasts or plants, with increased beta- carotene levels.  
 CC Beta-carotene is used as a colourant in margarine and butter and as an  
 CC intermediate for vitamin A, and may prevent cancer. (Updated on 25-MAR-  
 CC 2003 to correct PF field.)  
 XX Sequence 177 BP; 40 A; 53 C; 39 G; 45 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2.13e-24 Length: 177  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1

Query Match: 88.7% Indels: 1  
 DB: 2 Gaps: 1  
 US-10-628-525A-33 (1-56) x AAT91545 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 DB 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 DB 61 AACATGGTGGCGCTTTCACCTGGCTTAACTGAGTCCCTCATTCCTGTTTCAGGAAG 120  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyValGlnCys 56  
 DB 121 CAAACCTTGACATCACTTCATTGCGAGCAGCAGCGGAGAGTGCAATGC 171

RESULT 8  
 AAI70688  
 ID AAI70688 standard; DNA; 204 BP.  
 XX AAI70688;  
 AC AAI70688;  
 XX 04-FEB-2002 (first entry)  
 DT 04-FEB-2002 (first entry)  
 XX Tobacco Rubisco transit peptide small subunit DNA.  
 DE Tobacco; Rubisco; ribulosebiphosphate carboxylase; transit peptide;  
 KW acetyl-CoA carboxylase; transgenic plant; oilseed; vegetable oil;  
 KW Brassica; soybean; ds.  
 XX Nicotiana tabacum.  
 OS  
 XX Key Location/Qualifiers  
 FH transit\_peptide 1..171  
 FT /\*tag= a  
 FT mat\_peptide 172..204  
 FT /\*tag= b  
 FT /note= "5' end of mature protein coding sequence"

WO200181604-A1.  
 XX 01-NOV-2001.  
 XX 20-APR-2001; 2001WO-US012928.  
 PF 20-APR-2000; 2000US-0198794P.  
 PR (CRGI ) CARGILL INC.  
 XX Shorrosh BS, Debonte LR;  
 PI WPI; 2002-041417/05.  
 DR P-PSDB; AAM50331.  
 XX Using Nucleic acids encoding alfalfa cytosolic Acetyl-Coenzyme A  
 PT Carboxylase (ACCase; EC 6.4.1.2) to increase the oil content of Soybean  
 PT and Brassica seeds.  
 XX Disclosure; Fig 1; 62pp; English.  
 PS The present sequence is that of DNA encoding the tobacco small subunit  
 CC Rubisco transit peptide and the 5' portion of the mature small subunit  
 CC Rubisco protein (see AAM50331). Nucleic acid constructs of the invention  
 CC include a nucleic acid encoding a cytosolic acetyl-CoA carboxylase (EC-  
 CC 6.4.1.2) and a promoter, and may also include a nucleic acid encoding the  
 CC tobacco small subunit Rubisco transit peptide. Such constructs can be  
 CC introduced into soybean and Brassica plants (especially Brassica napus  
 CC (oilseed rape), Brassica rapa (turnip), Brassica juncea, Brassica  
 CC carinata, Brassica nigra (black mustard) and Brassica oleracea  
 CC (cauliflower, sprout, cabbage, broccoli)) to increase the oil content of  
 CC their seeds from about 5% to about 25% greater on a dry weight basis  
 CC (claimed)



XX  
SQ Sequence 204 BP; 50 A; 60 C; 43 G; 51 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,58e-24 Length: 204  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: Gaps: 1

US-10-628-525A-33 (1-56) x AAI70688 (1-204)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGTTGACATCTTCACTGGCTTTAAGTCAGCTGCCCTCAATTCCTGTTCAAGGAAG 120  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAACCTTGACATCACTTCCATTGCCAGCAGCGCGGAGAGTGCAATGC 171

RESULT 9  
ADK59826  
ID ADK59826 standard; DNA; 297 BP.  
AC ADK59826;  
XX  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Plant DNA sequence which confers altered metabolic characteristic #7209.  
XX  
KW altered metabolic characteristic; plant; acid metabolism;  
KW alcohol metabolism; fatty acid metabolism;  
KW branched fatty acid metabolism; alkaloid metabolism;  
KW amino acid metabolism; ester metabolism; glyceride metabolism;  
KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;  
KW terpene metabolism; isoprenoid metabolism; alkene metabolism;  
KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.  
XX  
OS Unidentified.  
XX  
XX WO2003020936-A1.  
XX  
XX 13-MAR-2003.  
XX  
XX 30-AUG-2002; 2002WO-US027884.  
XX  
XX 31-AUG-2001; 2001US-0316471P.  
XX  
XX (DOWC ) DOW CHEM CO.  
XX (DOWC ) DOW AGROSCIENCES LLC.  
XX  
XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;  
XX Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;  
XX WPI; 2003-313091/30.  
XX  
XX Novel genes that confer altered metabolic characteristics in Nicotiana  
XX benthamiana plants, useful for altering the levels of metabolites e.g.  
XX acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.  
XX  
XX Claim 1; SEQ ID NO 7209; 2576pp; English.  
XX  
XX The invention comprises DNA sequences which confer an altered metabolic  
XX characteristic when they are expressed in a plant. The DNA sequences of  
XX the invention are useful for producing plants with an altered metabolic  
XX characteristic, such as: altered acid metabolism, alcohol metabolism,  
XX fatty acid metabolism, branched fatty acid metabolism, alkaloid or other

CC base metabolism, altered amino acid metabolism, altered ester metabolism,  
CC altered glyceride metabolism, altered phenolic metabolism, altered  
CC carbohydrate metabolism, altered sterol, oxygenated terpene, or  
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon  
CC metabolism, ketone or quinone metabolism. The DNA sequences of the  
CC invention may be used to provide disease resistance in a plant and gene  
CC shuffling or sexual PCR procedures. The present nucleic acid represents a  
CC DNA sequence of the invention.  
XX  
SQ Sequence 297 BP; 83 A; 70 C; 70 G; 74 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 4,29e-24 Length: 297  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: Gaps: 1

US-10-628-525A-33 (1-56) x ADK59826 (1-297)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAnProAlaGlnAla 20  
Db 97 ATGGCTTCCTCAGTTCTTCTCTGCGAGAGTTGCCACCGCAGCAATGTTGCTCAAGCT 156  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 157 AACATGTTGACATCTTCCATTGCCAGCAGCGCGGAGAGTGCAATGC 216  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 217 CAAACCTTGACATCACTTCCATTGCCAGCAGCGCGGAGAGTGCAATGC 267

RESULT 10  
ADK56121  
ID ADK56121 standard; DNA; 377 BP.  
XX  
XX AC ADK56121;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX Plant DNA sequence which confers altered metabolic characteristic #3504.  
XX  
KW altered metabolic characteristic; plant; acid metabolism;  
KW alcohol metabolism; fatty acid metabolism;  
KW branched fatty acid metabolism; alkaloid metabolism;  
KW amino acid metabolism; ester metabolism; glyceride metabolism;  
KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;  
KW terpene metabolism; isoprenoid metabolism; alkene metabolism;  
KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.  
XX  
OS Unidentified.  
XX  
XX WO2003020936-A1.  
XX  
XX 13-MAR-2003.  
XX  
XX 30-AUG-2002; 2002WO-US027884.  
XX  
XX 31-AUG-2001; 2001US-0316471P.  
XX  
XX (DOWC ) DOW CHEM CO.  
XX (DOWC ) DOW AGROSCIENCES LLC.  
XX  
XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;  
XX Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;  
XX WPI; 2003-313091/30.  
XX  
XX Novel genes that confer altered metabolic characteristics in Nicotiana  
XX benthamiana plants, useful for altering the levels of metabolites e.g.  
XX acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.  
XX  
XX Claim 1; SEQ ID NO 7209; 2576pp; English.  
XX  
XX The invention comprises DNA sequences which confer an altered metabolic  
XX characteristic when they are expressed in a plant. The DNA sequences of  
XX the invention are useful for producing plants with an altered metabolic  
XX characteristic, such as: altered acid metabolism, alcohol metabolism,  
XX fatty acid metabolism, branched fatty acid metabolism, alkaloid or other



XX Shukla V, Butler H, Larrinua I, Reddy AS;  
 XX WPI; 2003-290185/28.  
 XX Novel isolated nucleic acid derived from *Nicotiana benthamiana*, *Oryzae*  
 XX sativa, *Saccharomyces cerevisiae*, *Trichoderma harzianum* and *Papaver*  
 XX *rheoa*, useful for conferring disease resistance in plants.  
 XX Claim 1; SEQ ID NO 1433; 617pp; English.  
 XX The invention relates to a novel isolated nucleic acid derived from  
 XX *Nicotiana benthamiana*, *Oryza sativa* (rice), *Saccharomyces cerevisiae*  
 XX (yeast), *Trichoderma harzianum* (*Hypocrea lixii*) and *Papaver rhoeas*  
 XX (poppy) and a sequence that hybridizes to them under conditions of low  
 XX stringency, where expression of the nucleic acid in a plant results in a  
 XX disease resistance phenotype. The polynucleotides of the invention  
 XX demonstrate anti-plant activity and may be useful in conferring disease  
 XX resistance in a plant against phytopathogen such as *Aspergillus flavus*,  
 XX *Gibberella fujikuroi* and *Gibberella zeae*. Furthermore, the  
 XX polynucleotides may be useful to retrieve unknown sequences and in gene  
 XX shuffling or sexual PCR procedures. The current sequence is that of the  
 XX DNA of the invention which is homologous to that of the phytopathogen  
 XX resistance-related contig cDNAs.  
 XX Sequence 492 BP; 140 A; 115 C; 111 G; 126 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8-5e-24 Length: 492  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADC76164 (1-492)

Qy 1 MetAlaSerSerMetLeuSerSerAlaValAlaThraThrArgThrAsnProAlaGlnAla 20  
 |||||:::|||||:::|||||:::|||||:::|||||  
 Db 66 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 125  
 Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 |||||:::|||||:::|||||:::|||||:::|||||  
 Db 126 AACATGGTTGCACCTTTCACCTGCTTAAAGTCTGCTGCCTCATTCCTGTTTCAAGGAAG 185  
 Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||||:::|||||:::|||||:::|||||:::|||||  
 Db 186 CAAACCTTGACATCACTTCATTCGACGACGACGCGGAGAGTGCATGTC 236

RESULT 13

ADK59824  
 ID AAD35635 standard; cDNA; 499 BP.

XX AAD35635;  
 XX AAD35635;

DT 26-JUL-2002 (first entry)

XX *Nicotiana benthamiana* rubisco partial cDNA sequence.

XX Nucleic acid vector; tobacco rattle virus; virus induced gene silencing;  
 XX TRV; VIGS; ribulose-1,5-bisphosphate carboxylase oxygenase; rubisco;  
 XX transgenic plant; enzyme; ss.

XX *Nicotiana benthamiana*.

XX US6369296-B1.

XX 09-APR-2002.

XX 01-FEB-2000; 2000US-00495797.

XX 01-FEB-2000; 2000US-00495797.

XX

(PLAN-) PLANT BIOSCIENCE LTD.

XX Ratcliff FG, Martin-Hernandez AM, Baulcombe DC;  
 XX WPI; 2002-337969/37.

XX Novel nucleic acid vector, useful for producing transgenic plants,  
 XX comprises a plant active promoter linked to a recombinant tobacco rattle  
 XX virus cDNA.

XX Example 2; Col 37-38; 32pp; English.

XX The invention relates to a nucleic acid vector. The vector comprises a  
 XX plant active promoter operably linked to a recombinant tobacco rattle  
 XX virus (TRV) cDNA which includes cis acting elements of TRV RNA permitting  
 XX in the presence of replicase, replication of the cDNA, a viral subgenomic  
 XX promoter operably linked to a sequence encoding a TRV coat protein, and a  
 XX heterologous sequence, and border sequences for transfer into a plant  
 XX genome. The vector is useful for producing genetically engineered plant  
 XX cells or transgenic plants. The nucleic acids are used to initiate  
 XX virus induced gene silencing (VIGS). The present sequence is *Nicotiana*  
 XX *benthamiana* ribulose-1,5-bisphosphate carboxylase oxygenase (rubisco)  
 XX partial cDNA related to the invention

XX Sequence 499 BP; 132 A; 120 C; 123 G; 124 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8-67e-24 Length: 499  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x AAD35635 (1-499)

Qy 1 MetAlaSerSerMetLeuSerSerAlaValAlaThraThrArgThrAsnProAlaGlnAla 20  
 |||||:::|||||:::|||||:::|||||:::|||||  
 Db 8 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 67  
 Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 |||||:::|||||:::|||||:::|||||:::|||||  
 Db 68 AACATGGTTGCACCTTTCACCTGCTTAAAGTCTGCTGCCTCATTCCTGTTTCAAGGAAG 127  
 Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||||:::|||||:::|||||:::|||||:::|||||  
 Db 128 CAAACCTTGACATCACTTCATTCGACGACGACGCGGAGAGTGCATGTC 178

RESULT 14

ADK59824

ID ADK59824 standard; DNA; 504 BP.

XX ADK59824;  
 XX ADK59824;

DT 06-MAY-2004 (first entry)

XX Plant DNA sequence which confers altered metabolic characteristic #7207.

XX altered metabolic characteristic; plant; acid metabolism;  
 XX alcohol metabolism; fatty acid metabolism;

XX branched fatty acid metabolism; alkaloid metabolism;  
 XX amino acid metabolism; ester metabolism; glyceride metabolism;

XX phenolic metabolism; carboxylate metabolism; sterol metabolism;  
 XX terpene metabolism; isoprenoid metabolism; alkene metabolism;

XX alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
 XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX Unidentified.

XX WO2003020936-A1.

XX 13-MAR-2003.

XX

PF 30-AUG-2002; 2002WO-US027884.  
 XX  
 PR 31-AUG-2001; 2001US-0316471P.  
 XX  
 PA (DOWC ) DOW CHEM CO.  
 PA (DOWC ) DOW AGROSCIENCES LLC.  
 XX  
 PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;  
 PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;  
 XX  
 DR WPI; 2003-313091/30.  
 XX  
 PT Novel genes that confer altered metabolic characteristics in Nicotiana  
 PT benthamiana plants, useful for altering the levels of metabolites e.g.  
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and steroids.  
 XX  
 PS Claim 1; SEQ ID NO 7207; 2576pp; English.  
 XX  
 CC The invention comprises DNA sequences which confer an altered metabolic  
 CC characteristic when they are expressed in a plant. The DNA sequences of  
 CC the invention are useful for producing plants with an altered metabolic  
 CC characteristic, such as: altered acid metabolism, alcohol metabolism,  
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other  
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,  
 CC altered glyceride metabolism, altered phenolic metabolism, altered  
 CC carbohydrate metabolism, altered sterol, oxygenated terpene, or  
 CC isoprenoid metabolism, alkene or alkene metabolism, hydrocarbon  
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the  
 CC invention may be used to provide disease resistance in a plant and gene  
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a  
 CC DNA sequence of the invention.  
 XX  
 SQ Sequence 504 BP; 139 A; 117 C; 118 G; 130 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.78e-24 Length: 504  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADK59824 (1-504)  
 QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProHlaGlnAla 20  
 Db 78 ATGGCTTCCTCAGTCTTCTTCCTCAGCAGCAGTTCACCCGCGCAATGTTGCTCAAGCT 137  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 Db 138 AACATGGTTGCACCTTTTCACAGGCTTAAGTCTGCTGCTCATTCCTCTGTTTCAGAAAG 197  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 198 CAAAACCTTGCATCATCTTCCATTCGACGACGCGGGAAGAGTGCAATGC 248  
 RESULT 15  
 ADC75089  
 ID ADC75089 standard; cDNA; 581 BP.  
 AC  
 XX ADC75089;  
 XX  
 DT 01-JAN-2004 (first entry)  
 DE N benthamiana phytopathogen resistance-related contig cDNA - SEQ ID 13.  
 XX  
 KW rice; yeast; poppy; plant; disease resistance; anti-fungal;  
 KW phytopathogen; gene shuffling; ss.  
 OS  
 XX Nicotiana benthamiana.  
 XX  
 FN WO2003020905-A2.  
 XX  
 XX

PD 13-MAR-2003.  
 XX  
 PF 30-AUG-2002; 2002WO-US027883.  
 XX  
 PR 31-AUG-2001; 2001US-0316392P.  
 XX  
 PA (DOWC ) DOW CHEM CO.  
 XX  
 PI Shukla V, Butler H, Larrinua I, Reddy AS;  
 XX  
 DR WPI; 2003-290185/28.  
 XX  
 PT Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae  
 PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver  
 PT rhoeas, useful for conferring disease resistance in plants.  
 XX  
 PS Claim 1; SEQ ID NO 13; 617pp; English.  
 XX  
 CC The invention relates to a novel isolated nucleic acid derived from  
 CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae  
 CC (yeast), Trichoderma harzianum (Hypocrea lixii) and Papaver rhoeas  
 CC (poppy) and a sequence that hybridises to them under conditions of low  
 CC stringency, where expression of the nucleic acid in a plant results in a  
 CC disease resistance phenotype. The polynucleotides of the invention  
 CC demonstrate anti-fungal activity and may be useful in conferring disease  
 CC resistance in a plant against phytopathogen such as Aspergillus flavus,  
 CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the  
 CC polynucleotides may be useful to retrieve unknown sequences and in gene  
 CC shuffling or sexual PCR procedures. The current sequence is that of the  
 CC phytopathogen resistance-related contig cDNA of the invention.  
 XX  
 SQ Sequence 581 BP; 162 A; 132 C; 143 G; 144 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.06e-23 Length: 581  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADC75089 (1-581)  
 QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProHlaGlnAla 20  
 Db 63 ATGGCTTCCTCAGTCTTCTTCCTCAGCAGCAGTTCACCCGCGCAATGTTGCTCAAGCT 122  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 Db 123 AACATGGTTGCACCTTTTCACAGGCTTAAGTCTGCTGCTCATTCCTCTGTTTCAGAAAG 182  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 183 CAAAACCTTGCATCATCTTCCATTCGACGACGCGGGAAGAGTGCAATGC 233  
 RESULT 16  
 ADC76944  
 ID ADC76944 standard; DNA; 608 BP.  
 AC  
 XX ADC76944;  
 XX  
 DT 01-JAN-2004 (first entry)  
 DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1213.  
 XX  
 KW rice; yeast; poppy; plant; disease resistance; anti-fungal;  
 KW phytopathogen; gene shuffling; ds.  
 XX  
 OS Unidentified.  
 XX  
 FN WO2003020905-A2.  
 XX  
 XX 13-MAR-2003.  
 PD



```
XX 30-AUG-2002; 2002WO-US027883.
XX PF
XX 31-AUG-2001; 2001US-0316392P.
XX PR
XX PA (DOWC ) DOW CHEM CO.
XX PI Shukla V, Butler H, Larrinua I, Reddy AS;
XX WPI; 2003-290185/28.
XX DR
XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver
PT rhoeas, useful for conferring disease resistance in plants.
XX PS Claim 1; SEQ ID NO 1218; 617pp; English.
XX CC
XX The invention relates to a novel isolated nucleic acid derived from
CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae
CC (yeast), Trichoderma harzianum (Hypocrea lixii) and Papaver rhoeas
CC (poppy) and a sequence that hybridises to them under conditions of low
CC stringency, where expression of the nucleic acid in a plant results in a
CC disease resistance phenotype. The polynucleotides of the invention
CC demonstrate anti-fungal activity and may be useful in conferring disease
CC resistance in a plant against phytopathogen such as Aspergillus flavus,
CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the
CC polynucleotides may be useful to retrieve unknown sequences and in gene
CC shuffling or sexual PCR procedures. The current sequence is that of the
CC DNA of the invention which is homologous to that of the phytopathogen
CC resistance-related contig cDNAs.
XX SQ Sequence 615 BP; 168 A; 144 C; 146 G; 156 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 1.15e-23 Length: 615
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADC76949 (1-615)
QY 1 MetAlaSerSerMetLeuSerSerAlaValAlaThraArgThraAsnProAlaGlnAla 20
DB 47 ATGGCTTCTCAGTCTTTCTCAGCAGCAGTTGCCACCCGCGCAATGTTGCTCAAGCT 106
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 107 AACATGGTTGCACCTTTTCACAGGTCCTTAAGTCTGCTGCCTCATTCCTCTGTTCAAGAAAG 166
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 167 CAAACCTTTGACATCATCTTCCATTGCGCAGCAACGGCGGAAGAGTGCAATGC 217

RESULT 19
ADC76953
ID ADC76953 standard; DNA; 632 BP.
XX AC
XX ADC76953;
XX DT 01-JAN-2004 (first entry)
XX DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1222.
XX KW rice; yeast; poppy; plant; disease resistance; anti-fungal;
XX KW phytopathogen; gene shuffling; ds.
XX OS Unidentified.
XX PN WO2003020905-A2.
XX XX
XX 13-MAR-2003.
```

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XX 30-AUG-2002; 2002WO-US027883.
XX PF
XX 31-AUG-2001; 2001US-0316392P.
XX PR
XX PA (DOWC ) DOW CHEM CO.
XX PI Shukla V, Butler H, Larrinua I, Reddy AS;
XX WPI; 2003-290185/28.
XX DR
XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver
PT rhoeas, useful for conferring disease resistance in plants.
XX PS Claim 1; SEQ ID NO 1222; 617pp; English.
XX CC
XX The invention relates to a novel isolated nucleic acid derived from
CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae
CC (yeast), Trichoderma harzianum (Hypocrea lixii) and Papaver rhoeas
CC (poppy) and a sequence that hybridises to them under conditions of low
CC stringency, where expression of the nucleic acid in a plant results in a
CC disease resistance phenotype. The polynucleotides of the invention
CC demonstrate anti-fungal activity and may be useful in conferring disease
CC resistance in a plant against phytopathogen such as Aspergillus flavus,
CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the
CC polynucleotides may be useful to retrieve unknown sequences and in gene
CC shuffling or sexual PCR procedures. The current sequence is that of the
CC DNA of the invention which is homologous to that of the phytopathogen
CC resistance-related contig cDNAs.
XX SQ Sequence 632 BP; 177 A; 146 C; 149 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.19e-23 Length: 632
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADC76953 (1-632)
QY 1 MetAlaSerSerMetLeuSerSerAlaValAlaThraArgThraAsnProAlaGlnAla 20
DB 52 ATGGCTTCTCAGTCTTTCTCAGCAGCAGTTGCCACCCGCGCAATGTTGCTCAAGCT 111
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 112 AACATGGTTGCACCTTTTCACAGGTCCTTAAGTCTGCTGCCTCTCCCTGTTCAAGGAAG 171
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 172 CAAACCTTTGACATCATCTTCCATTGCGCAGCAACGGCGGAAGAGTGCAATGC 222

RESULT 20
ADC76948
ID ADC76948 standard; DNA; 684 BP.
XX AC
XX ADC76948;
XX DT 01-JAN-2004 (first entry)
XX DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1217.
XX KW rice; yeast; poppy; plant; disease resistance; anti-fungal;
XX KW phytopathogen; gene shuffling; ds.
XX OS Unidentified.
XX PN WO2003020905-A2.
XX XX
XX 13-MAR-2003.
```

XX 30-AUG-2002; 2002WO-US027883.  
 XX 31-AUG-2001; 2001US-0316392P.  
 XX (DOWC ) DOW CHEM CO.  
 XX Shukla V, Butler H, Larrinua I, Reddy AS;  
 XX WPI; 2003-290185/28.  
 XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae  
 PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver  
 PT rhoeas, useful for conferring disease resistance in plants.  
 XX Claim 1; SEQ ID NO 1217; 617pp; English.  
 XX The invention relates to a novel isolated nucleic acid derived from  
 CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae  
 CC (yeast), Trichoderma harzianum (Hypocrea lixi) and Papaver rhoeas  
 CC (poppy) and a sequence that hybridises to them under conditions of low  
 CC stringency, where expression of the nucleic acid in a plant results in a  
 CC disease resistance phenotype. The polynucleotides of the invention  
 CC demonstrate anti-fungal activity and may be useful in conferring disease  
 CC resistance in a plant against phytopathogen such as Aspergillus flavus,  
 CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the  
 CC polynucleotides may be useful to retrieve unknown sequences and in gene  
 CC shuffling or sexual PCR procedures. The current sequence is that of the  
 CC DNA of the invention which is homologous to that of the phytopathogen  
 CC resistance-related contig cDNAs.  
 XX SQ Sequence 684 BP; 181 A; 155 C; 160 G; 188 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.33e-23 Length: 684  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 10 Gaps: 1  
 US-10-628-525A-33 (1-56) x ADC76948 (1-684)  
 QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
 Db 47 ATGGCTTCCTCAGTCTTTCTCCAGCAGCAGTGGCCACCGCAGCAATGTTGCTCAAGCT 106  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 Db 107 AACATGTTGCACCTTTTCACAGGTCTTAAGTCTGCTGCCTCCTTCCTGTTTCAAGAAAG 166  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 167 CAAACCTTGCATCATCTTCATTCAGCAGCAACGGCGGAGAGTGCAATGC 217  
 RESULT 21  
 ID ADK58382  
 XX ADK58382 standard; DNA; 718 BP.  
 XX AC ADK58382;  
 XX 06-MAY-2004 (first entry)  
 XX Plant DNA sequence which confers altered metabolic characteristic #5765.  
 DE altered metabolic characteristic; plant; acid metabolism;  
 KW alcohol metabolism; fatty acid metabolism;  
 KW branched fatty acid metabolism; alkaloid metabolism;  
 KW amino acid metabolism; ester metabolism; glyceride metabolism;  
 KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;  
 KW terpene metabolism; isoprenoid metabolism; alkene metabolism;  
 KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
 KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

XX Unidentified.  
 XX OS WO2003020936-A1.  
 XX PN 13-MAR-2003.  
 XX PD 30-AUG-2002; 2002WO-US027884.  
 XX PF 31-AUG-2001; 2001US-0316471P.  
 XX PR (DOWC ) DOW CHEM CO.  
 XX PA (DOWC ) DOW AGROSCIENCES LLC.  
 XX PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;  
 XX PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;  
 XX WPI; 2003-313091/30.  
 XX Novel genes that confer altered metabolic characteristics in Nicotiana  
 PT benthamiana plants, useful for altering the levels of metabolites e.g.  
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.  
 XX Claim 1; SEQ ID NO 5765; 2576pp; English.  
 XX The invention comprises DNA sequences which confer an altered metabolic  
 CC characteristic when they are expressed in a plant. The DNA sequences of  
 CC the invention are useful for producing plants with an altered metabolic  
 CC characteristic, such as: altered acid metabolism, alcohol metabolism,  
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other  
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,  
 CC carbohydrate metabolism, altered phenolic metabolism, altered  
 CC isoprenoid metabolism, altered sterol, oxygenated terpene, or  
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the  
 CC invention may be used to provide disease resistance in a plant and gene  
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a  
 CC DNA sequence of the invention.  
 XX SQ Sequence 718 BP; 190 A; 162 C; 162 G; 204 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.42e-23 Length: 718  
 Score: 240.50 Matches: 52  
 Percent Similarity: 96.5% Conservative: 3  
 Best Local Similarity: 91.2% Mismatches: 1  
 Query Match: 88.7% Indels: 1  
 DB: 10 Gaps: 1  
 US-10-628-525A-33 (1-56) x ADK58382 (1-718)  
 QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
 Db 45 ATGGCTTCCTCAGTCTTTCTCCAGCAGCAGTGGCCACCGCAGCAATGTTGCTCAAGCT 104  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 Db 105 AACATGTTGCACCTTTTCACAGGTCTTAAGTCTGCTGCCTCCTTCCTGTTTCAAGAAAG 164  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 165 CAAACCTTGCATCATCTTCATTCAGCAGCAACGGCGGAGAGTGCAATGC 215  
 RESULT 22  
 ID ADK54321  
 XX ADK54321 standard; DNA; 736 BP.  
 XX AC ADK54321;  
 XX 06-MAY-2004 (first entry)  
 XX Plant DNA sequence which confers altered metabolic characteristic #1704.  
 XX





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Db 123 AACATGTTGCACCTTTCACCTGCTTAACTCAGTCCTCGTTCCTGTTTCAAGGAG 182
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 183 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 233

RESULT 24
ADM44879
ID ADM44879 standard; DNA; 841 BP.
XX
AC ADM44879;
XX
DT 03-JUN-2004 (first entry)
XX
DE Insect resistance associated DNA sequence SeqID286.
XX
KW Insect resistant phenotype; plant protectant; gene therapy;
KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
OS Unidentified.
XX
PN WO2003020025-A2.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-US027882.
XX
PR 31-AUG-2001; 2001US-0316319P.
XX
PA (DOWC ) DOW CHEM CO.
XX
PI Shukla V, Meade T, Larrinua I;
XX
DR WPI; 2003-290133/28.
XX
PT New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
XX
PS Claim 1; SEQ ID NO 286; 396pp; English.
XX
CC This invention relates to a novel isolated nucleic acid comprising, or
CC hybridising under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
CC invention may be useful as a plant protectant or for gene therapy. The
CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.
XX
SQ Sequence 841 BP; 218 A; 174 C; 187 G; 262 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.76e-23 Length: 841
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 11 Gaps: 1

US-10-628-525A-33 (1-56) x ADM44879 (1-841)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 57 ATGGCTTCTCAGTCTTTCTTCCTCAGCAGAGTGCACCCGCAATGTTGCTCAAGCT 116
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 117 AACATGTTGCACCTTTCACCTGCTTAACTCAGTCCTCGTTCCTGTTTCAAGGAG 176
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Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 177 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 227

RESULT 25
ADM45447
ID ADM45447 standard; DNA; 847 BP.
XX
AC ADM45447;
XX
DT 03-JUN-2004 (first entry)
XX
DE Insect resistance associated DNA sequence SeqID854.
XX
KW Insect resistant phenotype; plant protectant; gene therapy;
KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
XX
OS Unidentified.
XX
PN WO2003020025-A2.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-US027882.
XX
PR 31-AUG-2001; 2001US-0316319P.
XX
PA (DOWC ) DOW CHEM CO.
XX
PI Shukla V, Meade T, Larrinua I;
XX
DR WPI; 2003-290133/28.
XX
PT New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.
XX
PS Claim 1; SEQ ID NO 854; 396pp; English.
XX
CC This invention relates to a novel isolated nucleic acid comprising, or
CC hybridising under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
CC invention may be useful as a plant protectant or for gene therapy. The
CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza
CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.
XX
SQ Sequence 847 BP; 221 A; 174 C; 189 G; 263 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.77e-23 Length: 847
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 11 Gaps: 1

US-10-628-525A-33 (1-56) x ADM45447 (1-847)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 63 ATGGCTTCTCAGTCTTTCTTCCTCAGCAGAGTGCACCCGCAATGTTGCTCAAGCT 122
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 123 AACATGTTGCACCTTTCACCTGCTTAACTCAGTCCTCGTTCCTGTTTCAAGGAG 182
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
```

Db 183 CAAAACCTTGACATCATCTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 233

## RESULT 26

ADM45065

ID ADM45065 standard; DNA; 859 BP.

XX AC ADM45065;

XX DT 03-JUN-2004 (first entry)

XX DE Insect resistance associated DNA sequence SeqID472.

XX KW insect resistant phenotype; plant protectant; gene therapy;

XX KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;

XX KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.

XX OS Unidentified.

XX PN WO2003020025-A2.

XX PD 13-MAR-2003.

XX PF 30-AUG-2002; 2002WO-US027882.

XX PR 31-AUG-2001; 2001US-0316319P.

XX PA (DOWC ) DOW CHEM CO.

XX PI Shukla V, Meade T, Larrinua I;

XX DR WPI; 2003-290133/28.

XX PT New isolated nucleic acid having expression that results in an insect

XX PT resistant phenotype, useful for conferring insect resistance and for

XX PT producing insect-resistant plants.

XX PS Claim 1; SEQ ID NO 472; 396pp; English.

XX CC This invention relates to a novel isolated nucleic acid comprising, or

XX CC hybridising under low stringent conditions to, any of the 1214 nucleic

XX CC acid sequences given in the specification, where the expression of the

XX CC nucleic acid in a plant results in an insect resistant phenotype. The

XX CC invention may be useful as a plant protectant or for gene therapy. The

XX CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza

XX CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are

XX CC useful for conferring insect resistance and for producing insect-

XX CC resistant plants. The present sequence is that of a DNA sequence of the

XX CC invention which may confer insect resistance to plants.

XX SQ Sequence 859 BP; 219 A; 177 C; 194 G; 269 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 1-81e-23 Length: 859

Score: 240.50 Matches: 52

Percent Similarity: 96.5% Conservative: 3

Best Local Similarity: 91.2% Mismatches: 1

Query Match: 88.7% Indels: 1

DB: 11 Gaps: 1

US-10-628-525A-33 (1-56) x ADM45065 (1-859)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

DB 79 ATGGCTTCTCAGTCTTCTTCAGCAGCAGTTCACCCGCGGAAGAGTGCTCAAGCT 138

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39

DB 139 AACATGGTTCACACCTTTCACAGGCTTAAAGTCTGCTGCTCATTCCTGTTTCAAGAAAG 198

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

DB 199 CAAAACCTTGACATCATCTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 249

## RESULT 27

ADC75566

ID ADC75566 standard; DNA; 924 BP.

XX AC ADC75566;

XX DT 01-JAN-2004 (first entry)

XX DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 490.

XX KW rice; yeast; poppy; plant; disease resistance; anti-fungal;

XX KW phytopathogen; gene shuffling; ds.

XX OS Unidentified.

XX PN WO2003020905-A2.

XX PD 13-MAR-2003.

XX PF 30-AUG-2002; 2002WO-US027883.

XX PR 31-AUG-2001; 2001US-0316392P.

XX PA (DOWC ) DOW CHEM CO.

XX PI Shukla V, Butler H, Larrinua I, Reddy AS;

XX DR WPI; 2003-290185/28.

XX PT Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae

XX PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver

XX PT rhoeas, useful for conferring disease resistance in plants.

XX PS Claim 1; SEQ ID NO 490; 617pp; English.

XX CC The invention relates to a novel isolated nucleic acid derived from

XX CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae

XX CC (yeast), Trichoderma harzianum (Hypocrea lixi) and Papaver rhoeas

XX CC (poppy) and a sequence that hybridises to them under conditions of low

XX CC stringency, where expression of the nucleic acid in a plant results in a

XX CC disease resistance phenotype. The polynucleotides of the invention

XX CC demonstrate anti-fungal activity and may be useful in conferring disease

XX CC resistance in a plant against phytopathogen such as Aspergillus flavus,

XX CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the

XX CC polynucleotides may be useful to retrieve unknown sequences and in gene

XX CC shuffling or sexual PCR procedures. The current sequence is that of the

XX CC DNA of the invention which is homologous to that of the phytopathogen

XX CC resistance-related contig cDNAs.

XX SQ Sequence 924 BP; 257 A; 189 C; 186 G; 292 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 2e-23 Length: 924

Score: 240.50 Matches: 52

Percent Similarity: 96.5% Conservative: 3

Best Local Similarity: 91.2% Mismatches: 1

Query Match: 88.7% Indels: 1

DB: 10 Gaps: 1

US-10-628-525A-33 (1-56) x ADC75566 (1-924)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

DB 56 ATGGCTTCTCAGTCTTCTTCAGCAGCAGTTCACCCGCGGAAGAGTGCTCAAGCT 115

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39

DB 116 AACATGGTTCACACCTTTCACAGGCTTAAAGTCTGCTGCTCATTCCTGTTTCAAGAAAG 175

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

DB 176 CAAAACCTTGACATCATCTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 226

```
RESULT 28
ADC76165
ID ADC76165 standard; DNA; 958 BP.
XX AC
XX ADC76165;
XX
XX 01-JAN-2004 (first entry)
XX
XX DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1434.
XX rice; yeast; poppy; plant; disease resistance; anti-fungal;
XX phytopathogen; gene shuffling; ds.
XX
XX Unidentified.
XX
XX WO2003020905-A2.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WO-US027883.
XX
XX 31-AUG-2001; 2001US-0316392P.
XX (DOW ) DOW CHEM CO.
XX
XX Shukla V, Butler H, Larrinua I, Reddy AS;
XX WPI; 2003-290185/28.
XX
XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
XX sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver
XX rhoeas, useful for conferring disease resistance in plants.
XX
XX Claim 1; SEQ ID NO 1434; 617pp; English.
XX
XX The invention relates to a novel isolated nucleic acid derived from
XX Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae
XX (yeast), Trichoderma harzianum (Hypocrea lixi) and Papaver rhoeas
XX (poppy) and a sequence that hybridises to them under conditions of low
XX stringency, where expression of the nucleic acid in a plant results in a
XX disease resistance phenotype. The polynucleotides of the invention
XX demonstrate anti-fungal activity and may be useful in conferring disease
XX resistance in a plant against phytopathogen such as Aspergillus flavus,
XX Gibberella fujikuroi and Gibberella zeae. Furthermore, the
XX polynucleotides may be useful to retrieve unknown sequences and in gene
XX shuffling or sexual PCR procedures. The current sequence is that of the
XX DNA of the invention which is homologous to that of the phytopathogen
XX resistance-related contig cDNAs.
XX
XX Sequence 958 BP; 265 A; 195 C; 199 G; 299 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2 1e-23 Length: 958
XX Score: 240.50 Matches: 52
XX Percent Similarity: 96.5% Conservative: 3
XX Best Local Similarity: 91.2% Mismatches: 1
XX Query Match: 88.7% Indels: 1
XX DB: 10 Gaps: 1
XX
XX US-10-628-525A-33 (1-56) x ADC76165 (1-958)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 90 ATGGCTTCCTCAGTCTTTCTCAGCAGCAGTGTGCCACCGCAGCAATGTGCTCAAGCT 149
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 150 AACATGGTGGACCTTTCACTGCTGTAAAGTCAGCTGCTCGTTCCTGTTCAAGGAAG 209
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 210 CAAACCTTGACATCACTTCCATTGCGACGACGCGGAGAGATGTCATGTC 260
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```
RESULT 29
AAQ92327
ID AAQ92327 standard; DNA; 1442 BP.
XX AC
XX AAQ92327;
XX
XX 25-MAR-2003 (revised)
XX 11-NOV-1995 (first entry)
XX
XX Chloroplast transit peptide, tyrosinase activator protein and tyrosinase
XX gene fusion.
XX
XX Tyrosinase; tyrosinase activator protein; fusion enzyme;
XX Streptomyces antibioticus; ORF438; Chloroplast transit peptide; tobacco;
XX ribulosebiphosphate-carboxylase; transgenic plant; vector; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 9..1442
XX FT /tag= a
XX FT /product= "Chloroplast transit peptide, tyrosinase"
XX FT misc_difference 396..398
XX FT /tag= b
XX FT /codon= seq:CAC, aa:Asp
XX FT misc_difference 1083..1085
XX FT /tag= c
XX FT /codon= seq:CAG, aa:Glu
XX FT misc_difference 1386..1388
XX FT /tag= d
XX FT /codon= seq:CAC, aa:Asp
XX
XX WO9513386-A2.
XX
XX 18-MAY-1995.
XX
XX 08-NOV-1994; 94WO-US012857.
XX
XX 12-NOV-1993; 93US-00152483.
XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.
XX
XX Della-Cioppa G, Kumagai MH;
XX WPI; 1995-194104/25.
XX P-PSDB; AAR74174.
XX
XX DNA encoding fusion enzyme including tyrosinase and tyrosinase activator
XX protein - useful for in vivo or in vitro prodn. of melanin(s).
XX
XX Example 6; Page 36-37; 54pp; English.
XX
XX The sequence encodes a fusion protein of a tyrosinase, tyrosinase
XX activator protein and a chloroplast transit peptide (CTP) from tobacco
XX ribulosebiphosphate-carboxylase. The CTP gene is fused to the N-terminal
XX SpH1 site of ORF438 (containing a tyrosinase activator protein gene). The
XX resulting fusion is exchanged in plasmid Bluescript containing the ORF438
XX -tyrosinase gene fusion. The gene fusion allows import of the protein
XX into higher plant chloroplasts, followed by transit peptide cleavage to
XX give an active enzyme. Expression gives a melanin-positive phenotype.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 1442 BP; 220 A; 538 C; 465 G; 219 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 3.65e-23 Length: 1442
XX Score: 240.50 Matches: 52
XX Percent Similarity: 96.5% Conservative: 3
XX Best Local Similarity: 91.2% Mismatches: 1
XX Query Match: 88.7% Indels: 1
XX DB: 2 Gaps: 1
XX
XX US-10-628-525A-33 (1-56) x AAQ92327 (1-1442)
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QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 Db 9 ATGGCTTCCTCAGTCTTTCCTCTGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 58  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 Db 69 AACATGGTTGCACCTTTCAGTGCCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 128  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 129 CAAACCTTGCATCATCTTCCATTGCCAAGCGCGGAAGAGTGCAATGC 179

RESULT 30

ADM45158  
 ID ADM45158 standard; DNA; 619 BP.  
 XX  
 AC ADM45158;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Insect resistance associated DNA sequence SeqID565.  
 XX  
 KW insect resistant phenotype; plant protectant; gene therapy;  
 KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;  
 KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003020025-A2.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 30-AUG-2002; 2002WO-US027882.  
 XX  
 PR 31-AUG-2001; 2001US-0316319P.  
 XX  
 PA (DOWC ) DOW CHEM CO.  
 XX  
 PI Shukla V, Meade T, Larrinua I;  
 XX  
 DR WPI; 2003-290133/28.

PT New isolated nucleic acid having expression that results in an insect  
 PT resistant phenotype, useful for conferring insect resistance and for  
 PT producing insect-resistant plants.

PS Claim 1; SEQ ID NO 565; 396pp; English.

CC This invention relates to a novel isolated nucleic acid comprising, or  
 CC hybridizing under low stringent conditions to, any of the 1214 nucleic  
 CC acid sequences given in the specification, where the expression of the  
 CC nucleic acid in a plant results in an insect resistant phenotype. The  
 CC invention may be useful as a plant protectant or for gene therapy. The  
 CC genes are derived from Arabidopsis thaliana, Nicotiana benthamiana, Oryza  
 CC sativa and Papaver rhoeas. The isolated nucleic acid and vector are  
 CC useful for conferring insect resistance and for producing insect-  
 CC resistant plants. The present sequence is that of a DNA sequence of the  
 CC invention which may confer insect resistance to plants.

SQ Sequence 619 BP; 163 A; 146 C; 146 G; 164 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,16e-23	Length:	619
Score:	236.50	Matches:	51
Percent Similarity:	96.5%	Conservative:	4
Best Local Similarity:	89.5%	Mismatches:	1
Query Match:	87.3%	Indels:	1
DB:	11	Gaps:	1

US-10-628-525A-33 (1-56) x ADM45158 (1-619)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

Db 39 GTGGCTTCCTCAGTCTTTCCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 98  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 Db 99 AACATGGTTGCACCTTTCAGGTCCTTAAGTCGCTGCCTCATTCCTGTTTCAAGGAAG 158  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 159 CAAACCTTGCATCATCTTCCATTGCCAAGCGCGGAAGAGTGCAATGC 209

Search completed: April 1, 2006, 04:26:21  
 Job time : 136.845 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 903.068 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

Title: US-10-628-525A-33

Perfect score: 271

Sequence: 1 MASSMLSSRAVATRTNPAQA.....SRKQNLDTITSASNGGRVQC 56

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abs/ABSSWEB spool-SUFFIX=p2n.rst -MINMATCH=0\_1 -LOOPECL=0 -LOOPEXT=0  
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0\_1 -LOOPECL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs06h  
-USER=US10628525 @CGN 1.1 11098 @runat 31032006 095118 16742 -NCPUs=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hc1:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gest1:\*  
10: gb\_gest2:\*  
11: gb\_gest3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	246.5	91.0	347	7	CV017043 tbt_00452
2	244.5	90.2	244	7	CV019289 tbt_00055
3	244.5	90.2	256	7	CV016318 tbt_00421
4	244.5	90.2	265	5	BU673933 pSKD64 To
5	244.5	90.2	282	1	AB001554 AB001554
6	244.5	90.2	288	7	CV016732 tbt_00200
7	244.5	90.2	324	7	CV019439 tbt_00202

8	244.5	90.2	326	7	CV017891
9	244.5	90.2	331	7	CV016591 tbt_01115
10	244.5	90.2	333	7	CV019882 tbt_00624
11	244.5	90.2	341	7	CV019568 tbt_00605
12	244.5	90.2	348	7	CV021773 tbt_00613
13	244.5	90.2	362	7	CV016438 tbt_00410
14	244.5	90.2	364	7	CV016988 tbt_00432
15	244.5	90.2	369	7	CV017159 tbt_01105
16	244.5	90.2	371	7	CV019231 tbt_00971
17	244.5	90.2	386	7	CV021480 tbt_01114
18	244.5	90.2	387	7	CV016216 tbt_01106
19	244.5	90.2	404	7	CV016980 tbt_01123
20	244.5	90.2	412	7	CV017309 tbt_00275
21	244.5	90.2	422	7	CV021557 tbt_00766
22	244.5	90.2	428	7	CV017696 tbt_00470
23	244.5	90.2	431	7	CV018759 tbt_00176
24	244.5	90.2	431	7	CV021294 tbt_00766
25	244.5	90.2	440	7	CV020505 tbt_00336
26	244.5	90.2	443	7	CV020326 tbt_00284
27	244.5	90.2	443	7	CV021799 tbt_00770
28	244.5	90.2	454	7	CV016694 tbt_00739
29	244.5	90.2	459	7	CV020329 tbt_00612
30	244.5	90.2	460	7	CV019815 tbt_00482
31	244.5	90.2	462	7	CV020983 tbt_00487
32	244.5	90.2	464	7	CV016611 tbt_01167
33	244.5	90.2	470	7	CV019915 tbt_00620
34	244.5	90.2	481	7	CV021008 tbt_00426
35	244.5	90.2	484	7	CV017787 tbt_00693
36	244.5	90.2	485	7	CV019762 tbt_00808
37	244.5	90.2	489	7	CV018137 tbt_01104
38	244.5	90.2	492	7	CV018376 tbt_00855
39	244.5	90.2	493	7	CV019394 tbt_00972
40	244.5	90.2	495	7	CV017271 tbt_00216
41	244.5	90.2	496	7	CV018748 tbt_00216
42	244.5	90.2	498	7	CV016349 tbt_00031
43	244.5	90.2	502	7	CV018962 tbt_00683
44	244.5	90.2	510	7	CV017397 tbt_00274
45	244.5	90.2	511	7	CV019644 tbt_00147
46	244.5	90.2	520	7	CV019831 tbt_01009
47	244.5	90.2	520	7	CV020302 tbt_00861
48	244.5	90.2	528	7	CV019398 tbt_00998
49	244.5	90.2	533	7	CV018405 tbt_00977
50	244.5	90.2	552	7	CV016524 tbt_00593
51	244.5	90.2	554	7	CV016821 tbt_00576
52	244.5	90.2	561	7	CV018308 tbt_01109
53	244.5	90.2	561	7	CV019628 tbt_00267
54	244.5	90.2	567	7	CV018478 tbt_00356
55	244.5	90.2	567	7	CV019281 tbt_00301
56	244.5	90.2	569	7	CV021484 tbt_00296
57	244.5	90.2	572	7	CV016734 tbt_00974
58	244.5	90.2	577	7	CV019916 tbt_00208
59	244.5	90.2	585	7	CV017207 tbt_00253
60	244.5	90.2	586	7	CV021286 tbt_01129
61	244.5	90.2	587	7	CV019355 tbt_00461
62	244.5	90.2	589	7	CV016194 tbt_00709
63	244.5	90.2	589	7	CV021210 tbt_00965
64	244.5	90.2	591	7	CV016565 tbt_00579
65	244.5	90.2	606	7	CV017003 tbt_00930
66	244.5	90.2	610	7	CV021592 tbt_00194
67	244.5	90.2	616	7	CV017574 tbt_00139
68	244.5	90.2	617	7	CV017362 tbt_00196
69	244.5	90.2	617	7	CV020154 tbt_00138
70	244.5	90.2	618	7	CV020759 tbt_00134
71	244.5	90.2	623	7	CV019792 tbt_00484
72	244.5	90.2	625	7	CV021007 tbt_00353
73	244.5	90.2	633	7	CV016314 tbt_00229
74	244.5	90.2	642	7	CV020007 tbt_00228
75	244.5	90.2	647	7	CV018894 tbt_00239
76	244.5	90.2	653	7	CV017348 tbt_01037
77	243.5	89.9	410	7	CV017911 tbt_00056
78	241.5	89.1	316	7	CV019087 tbt_00982
79	241.5	89.1	474	7	CV020949 tbt_00741
80	241.5	89.1	571	7	CV018812 tbt_00223

[illegible]

**ORGANISM** Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.

**REFERENCE**  
**AUTHORS** Li, W.Z., Shao, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Dong, H.T. and Li, D.B.

**TITLE** Large-scale identification of ESTs from Nicotiana tabacum by normalized cDNA library sequencing

**JOURNAL**  
**COMMENT** Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

**FEATURES**  
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Location/Qualifiers  
/organism="Nicotiana tabacum"  
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/notes="Vector: pBS-SK+"

**ORIGIN**

Alignment Scores:  
Pred. No.: 6e-23 Length: 244  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV019289 (1-244)

**QY** 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
|||||...|||  
**Db** 8 ATGGCTTCCTGTAATCTTCCTCTGAGCAGTAGCCACTGCGACCAATGTAGTCAAGCT 67  
|||||...|||

**QY** 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||...|||  
**Db** 68 AACATGGTTGCACCTTTCATCTGCTTAAGTCAGCTGCCTCATTCCTGTATCAGGAAG 127  
|||||...|||

**QY** 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||...|||  
**Db** 128 CAAACCTTTGACATCATCTTCATTTAGTGAAGAGTGCAATGC 178  
|||||...|||

**RESULT 3**  
CV016318  
**LOCUS** 256 bp mRNA linear EST 19-AUG-2004  
**DEFINITION** tbt\_004219 Normalized Nicotiana tabacum cDNA library Nicotiana tabacum cDNA clone tbt\_004219 5', mRNA sequence.

**ACCESSION** CV016318  
**VERSION** CV016318.1 GI:51454670  
**KEYWORDS** EST.  
**SOURCE** Nicotiana tabacum (common tobacco)  
**ORGANISM** Nicotiana tabacum

**REFERENCE**  
**AUTHORS** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 256)  
Li, W.Z., Shao, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Dong, H.T. and Li, D.B.  
**TITLE** Large-scale identification of ESTs from Nicotiana tabacum by normalized cDNA library sequencing

**JOURNAL**  
**COMMENT** Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

**FEATURES**  
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/organism="Nicotiana tabacum"  
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/notes="Vector: pBS-SK+"

**ORIGIN**

Alignment Scores:  
Pred. No.: 6.38e-23 Length: 256  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV016318 (1-256)

**QY** 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20  
|||||...|||  
**Db** 59 ATGGCTTCCTGTAATCTTCCTCTGAGCAGTAGCCACTGCGACCAATGTAGTCAAGCT 118  
|||||...|||

**QY** 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||...|||  
**Db** 119 AACATGGTTGCACCTTTCATCTGCTTAAGTCAGCTGCCTCATTCCTGTATCAGGAAG 178  
|||||...|||

**QY** 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||...|||  
**Db** 179 CAAACCTTTGACATCATCTTCATTTAGTGAAGAGTGCAATGC 229  
|||||...|||

**RESULT 4**  
BU673933  
**LOCUS** 265 bp mRNA linear EST 20-MAY-2003  
**DEFINITION** pSK064 Tobacco PCRscript cDNA library Nicotiana tabacum cDNA 5', 3' similar to RbcS, mRNA sequence.

**ACCESSION** BU673933  
**VERSION** BU673933.1 GI:23515061  
**KEYWORDS** EST.  
**SOURCE** Nicotiana tabacum (common tobacco)  
**ORGANISM** Nicotiana tabacum

**REFERENCE**  
**AUTHORS** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 265)  
Tang, L., Bhat, S., Phillips, A., Guo, X., Krueger, A. and Petracek, M.  
**TITLE** Photosynthetic control of nuclear mRNA gene expression in tobacco  
**JOURNAL** Unpublished (2002)  
**COMMENT** Contact: Marie Petracek  
Department of Biochemistry and Molecular Biology  
Oklahoma State University  
360 Noble Research Center, Stillwater, OK 74078, USA  
Tel: (405) 744-6199  
Fax: (405) 744-7799  
Email: marie.petracek@biochem.okstate.edu  
95% identity at nucleotides 1067-1292 to Nicotiana plumbaginifolia rbc-8B gene for ribulose biphosphate carboxylase  
Seq primer: M13 forward and reverse  
High quality sequence stop: 265.  
Location/Qualifiers





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DB: 7 Gaps: 1
US-10-628-525A-33 (1-56) x CV016732 (1-288)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20
Db 2 ATGGCTTCCTCTGACTTCTCTGAGCAGTTGCCACTGCCACCAATGTTGCAAGCT 61

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 62 AACATGGTTGCACCTTTCACTGGTCTTAAGTCAGCTGCCCTCATTCCTCGTTTCAAGGAAG 121

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 122 CAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 172

RESULT 7
LOCUS CV019439 324 bp mRNA linear EST 19-AUG-2004
DEFINITION tbt_002022 Normalized Nicotiana tabacum cDNA library Nicotiana
ACCESSION CV019439
VERSION tbt_002022 5', mRNA sequence.
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 324)
AUTHORS Li, W. Z., Shao, Y., Li, Y. P., Lu, X. P., Montero, D. C., Alvarez, S. P.,
Deng, Y., Jin, Q. C., Wang, S., Dai, C. E., Zeng, Z. L., Wang, Y. Q.,
Dong, H. T. and Li, D. B.
Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
Unpublished (2004)
CONTACT: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.

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/organism="Nicotiana tabacum"
/mol_type="mRNA"
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Alignment Scores: 8.59e-23 Length: 324
Pred. No.: 244.50 Matches: 53
Score: 96.5% Conservative: 2
Percent Similarity: 93.0% Mismatches: 1
Best Local Similarity: 90.2% Indels: 1
Query Match: 7 Gaps: 1
DB: 1

US-10-628-525A-33 (1-56) x CV019439 (1-324)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20
Db 53 ATGGCTTCCTCTGACTTCTCTGAGCAGTTGCCACTGCCACCAATGTTGCTCAAGCT 112

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 53 ATGGCTTCCTCTGACTTCTCTGAGCAGTTGCCACTGCCACCAATGTTGCTCAAGCT 112

DB: 7 Gaps: 1
US-10-628-525A-33 (1-56) x CV016732 (1-288)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20
Db 2 ATGGCTTCCTCTGACTTCTCTGAGCAGTTGCCACTGCCACCAATGTTGCAAGCT 61

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 62 AACATGGTTGCACCTTTCACTGGTCTTAAGTCAGCTGCCCTCATTCCTCGTTTCAAGGAAG 121

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 122 CAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 172

RESULT 7
LOCUS CV019439 324 bp mRNA linear EST 19-AUG-2004
DEFINITION tbt_002022 Normalized Nicotiana tabacum cDNA library Nicotiana
ACCESSION CV019439
VERSION tbt_002022 5', mRNA sequence.
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 324)
AUTHORS Li, W. Z., Shao, Y., Li, Y. P., Lu, X. P., Montero, D. C., Alvarez, S. P.,
Deng, Y., Jin, Q. C., Wang, S., Dai, C. E., Zeng, Z. L., Wang, Y. Q.,
Dong, H. T. and Li, D. B.
Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
Unpublished (2004)
CONTACT: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.

FEATURES
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1..324
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/db_xref="taxon:4097"
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/tissue_type="Mixed"
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/note="Vector: pBS-SK+."

ORIGIN
Alignment Scores: 8.59e-23 Length: 324
Pred. No.: 244.50 Matches: 53
Score: 96.5% Conservative: 2
Percent Similarity: 93.0% Mismatches: 1
Best Local Similarity: 90.2% Indels: 1
Query Match: 7 Gaps: 1
DB: 1

US-10-628-525A-33 (1-56) x CV017891 (1-326)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20
Db 44 ATGGCTTCCTCTGACTTCTCTGAGCAGTTGCCACTGCCACCAATGTTGCTCAAGCT 103

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 104 AACATGGTTGCACCTTTCACTGGTCTTAAGTCAGCTGCCCTCATTCCTCGTTTCAAGGAAG 163

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 164 CAAACCTTGACATCACTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 214

RESULT 9
LOCUS CV016591 331 bp mRNA linear EST 19-AUG-2004
DEFINITION tbt_011159 Normalized Nicotiana tabacum cDNA library Nicotiana

```

tabacum cDNA clone tbt\_011159 5', mRNA sequence.  
CV016591 GI:51454943  
EST.  
Nicotiana tabacum (common tobacco)  
Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 331)  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P., Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Dong, H.T. and Li, D.B.  
Large-scale identification of ESTs from Nicotiana tabacum by normalized cDNA library sequencing  
Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Seq primer: M13.  
Only the high quality region of sequence was submitted.

FEATURES  
Location/Qualifiers  
source 1..331  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_011159"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+."

ORIGIN  
Alignment Scores:  
Pred. No.: 8,83e-23 Length: 331  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV016591 (1-331)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 40 ATGGCTTCCTCTGTTCTCTGAGCAGTTGCCACTCGCCTAAATGTTGCTCAAGCT 99  
QY 21 SerMetValAlaProPheThrGlyLeuLySerAlaAla---PheProValSerArgLys 39  
Db 100 AACATGGTTGCACCTTTCACTGGCTTAAGTCAGCTGCCTCACTTCCTGTTTCAAGGAAG 159  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 160 CAAACCTTGACATCACTTCCTTGGTAGCAATGGTGAAGAGTGCAATGC 210

RESULT 10  
CV019882  
LOCUS  
DEFINITION  
tbt\_006241 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_006241 5', mRNA sequence.  
CV019882  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Nicotiana tabacum (common tobacco)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 333)

AUTHORS  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P., Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Dong, H.T. and Li, D.B.  
Large-scale identification of ESTs from Nicotiana tabacum by normalized cDNA library sequencing  
Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.

FEATURES  
Location/Qualifiers  
source 1..333  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_006241"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+."

ORIGIN  
Alignment Scores:  
Pred. No.: 8,89e-23 Length: 333  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV019882 (1-333)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 47 ATGGCTTCCTCTGTTCTCTGAGCAGTTGCCACTCGCCTAAATGTTGCTCAAGCT 106  
QY 21 SerMetValAlaProPheThrGlyLeuLySerAlaAla---PheProValSerArgLys 39  
Db 107 AACATGGTTGCACCTTTCACTGGCTTAAGTCAGCTGCCTCACTTCCTGTTTCAAGGAAG 166  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 167 CAAACCTTGACATCACTTCCTTGGTAGCAATGGTGAAGAGTGCAATGC 217

RESULT 11  
CV019568  
LOCUS  
DEFINITION  
tbt\_006054 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_006054 5', mRNA sequence.  
CV019568  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Nicotiana tabacum (common tobacco)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 341)  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P., Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q., Dong, H.T. and Li, D.B.  
Large-scale identification of ESTs from Nicotiana tabacum by normalized cDNA library sequencing  
Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene

Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

#### FEATURES

source  
1..341  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clones="tbt\_006135"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

#### ORIGIN

##### Alignment Scores:

Pred. No.: 9.16e-23 Length: 341  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV019568 (1-341)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
|||||:::|||||  
Db 40 ATGGCTTCCTCTGTTCTTCTCTGCAGCAGTTGCCACTCGCACCATTGTTGCTCAAGCT 99  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::|||||  
Db 100 AACATGGTTGCACCTTTCACTGTGTTAAGTCAGCTGCTCAATTCCTGTTTCAAGGAAG 159  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||  
Db 160 CAAACCTTGACATCACTTCATTTGCTAGCAATGGTGAAGATGCAATGC 210

#### RESULT 12

CV021773  
LOCUS  
DEFINITION  
tbt\_006135 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum CDNA clone tbt\_006135 5', mRNA sequence.

CV021773

CV021773.1 GI:51463281

EST.

SOURCE

ORGANISM

Nicotiana tabacum (common tobacco)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.

#### REFERENCE

AUTHORS  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.

TITLE  
Large-scale identification of ESTs from Nicotiana tabacum by

normalized cDNA library sequencing

Unpublished (2004)

#### JOURNAL

COMMENT  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin

Song, Haitao Dong, Debao Li

The Tobacco Science Research Institute of Yunnan Province; Yunnan

Provincial Tobacco Group Dali Branch; Bioinformatics and Gene

Network Research Group, Zhejiang University

The Tobacco Science Research Institute of Yunnan Province, Yuxi

653100, China

Email: webmaster@estarray.org, URL: http://www.estarray.org

Only the high quality region of sequence was submitted.

#### FEATURES

source  
1..348  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"

#### ORIGIN

##### Alignment Scores:

Pred. No.: 9.4e-23 Length: 348  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021773 (1-348)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

|||||:::|||||

Db 21 ATGGCTTCCTCTGTTCTTCTCTGCAGCAGTTGCCACTCGCACCATTGTTGCTCAAGCT 80

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39

:::|||||

Db 81 AACATGGTTGCACCTTTCACTGTGTTAAGTCAGCTGCTCAATTCCTGTTTCAAGGAAG 140

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

|||||

Db 141 CAAACCTTGACATCACTTCATTTGCTAGCAATGGTGAAGATGCAATGC 191

#### RESULT 13

CV016438

LOCUS

DEFINITION

tbt\_004103 Normalized Nicotiana tabacum cDNA library Nicotiana

tabacum CDNA clone tbt\_004103 5', mRNA sequence.

CV016438

CV016438.1 GI:51454790

EST.

SOURCE

ORGANISM

Nicotiana tabacum (common tobacco)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE

AUTHORS

Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,

Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,

Dong, H.T. and Li, D.B.

TITLE

Large-scale identification of ESTs from Nicotiana tabacum by

normalized cDNA library sequencing

Unpublished (2004)

JOURNAL

COMMENT

Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin

Song, Haitao Dong, Debao Li

The Tobacco Science Research Institute of Yunnan Province; Yunnan

Provincial Tobacco Group Dali Branch; Bioinformatics and Gene

Network Research Group, Zhejiang University

The Tobacco Science Research Institute of Yunnan Province, Yuxi

653100, China

Email: webmaster@estarray.org, URL: http://www.estarray.org

Only the high quality region of sequence was submitted.

Seq primer: M13.

FEATURES

source

1..362

/organism="Nicotiana tabacum"

/mol\_type="mRNA"

/db\_xref="taxon:4097"

/clone="tbt\_004103"

/tissue\_type="Mixed"

/note="Normalized Nicotiana tabacum cDNA library"

/note="Vector: pBS-SK+"

##### Alignment Scores:

Pred. No.: 9.88e-23 Length: 362  
Score: 244.50 Matches: 53

Percent Similarity: 96.5%  
 Best Local Similarity: 93.0%  
 Query Match: 7  
 DB: 1

Conservative: 2  
 Mismatches: 1  
 Indels: 1  
 Gaps: 1

US-10-628-525A-33 (1-56) x CV016438 (1-362)

QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20  
 |||  
 Db 39 ATGGCTTCTCTGTTCTTCTCTGAGAGTTGCCACTCGCACCATTGTTGCTCAAGCT 98  
 ::|  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::|  
 Db 99 AACATGGTTGCACCTTTCACCTGCTTAAGTCAGCTGCCTCATCTCCCTGTTTCAAGGAAG 158  
 |||  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||  
 Db 159 CAAACCTTGCATCATCTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 209  
 |||

RESULT 14  
 CV016988  
 LOCUS  
 DEFINITION  
 tbt\_004320 Normalized Nicotiana tabacum cDNA library Nicotiana  
 tabacum cDNA clone tbt\_004320 5', mRNA sequence.

ACCESSION  
 CV016988

VERSION  
 CV016988.1 GI:51455340

KEYWORDS  
 EST.

SOURCE  
 Nicotiana tabacum (common tobacco)

ORGANISM  
 Nicotiana tabacum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE  
 AUTHORS  
 Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
 Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
 Dong, H.T. and Li, D.B.

TITLE  
 Large-scale identification of ESTs from Nicotiana tabacum by

normalized cDNA library sequencing

JOURNAL  
 Unpublished (2004)

COMMENT  
 Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
 Song, Haitao Dong, Debao Li  
 The Tobacco Science Research Institute of Yunnan Province; Yunnan  
 Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
 Network Research Group, Zhejiang University  
 The Tobacco Science Research Institute of Yunnan Province, Yuxi  
 653100, China  
 Email: webmaster@estarray.org, URL: http://www.estarray.org  
 Only the high quality region of sequence was submitted.  
 Seq primer: M13.

FEATURES  
 Location/Qualifiers

1..364  
 /organism="Nicotiana tabacum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4097"  
 /clone="tbt\_004320"  
 /tissue\_type="Mixed"  
 /clone\_lib="Normalized Nicotiana tabacum cDNA library"  
 /note="Vector: pBS-SK+."

ORIGIN

Alignment Scores:

Pred. No.: 9,95E-23 Length: 364  
 Score: 244.50 Matches: 53  
 Percent Similarity: 96.5% Conservative: 2  
 Best Local Similarity: 93.0% Mismatches: 1  
 Query Match: 90.2% Indels: 1  
 DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV016988 (1-364)

QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20  
 |||  
 Db 41 ATGGCTTCTCTGTTCTTCTCTGAGAGTTGCCACTCGCACCATTGTTGCTCAAGCT 100  
 |||

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::|  
 Db 101 AACATGGTTGCACCTTTCACCTGCTTAAGTCAGCTGCCTCATCTCCCTGTTTCAAGGAAG 160  
 |||  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||  
 Db 161 CAAACCTTGCATCATCTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 211  
 |||

RESULT 15

CV017159

LOCUS

DEFINITION  
 tbt\_011057 Normalized Nicotiana tabacum cDNA library Nicotiana  
 tabacum cDNA clone tbt\_011057 5', mRNA sequence.

ACCESSION  
 CV017159

VERSION  
 CV017159.1 GI:51455511

KEYWORDS  
 EST.

SOURCE  
 Nicotiana tabacum (common tobacco)

ORGANISM  
 Nicotiana tabacum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE  
 AUTHORS  
 Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
 Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
 Dong, H.T. and Li, D.B.

TITLE  
 Large-scale identification of ESTs from Nicotiana tabacum by  
 normalized cDNA library sequencing

JOURNAL  
 Unpublished (2004)

COMMENT  
 Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
 Song, Haitao Dong, Debao Li  
 The Tobacco Science Research Institute of Yunnan Province; Yunnan  
 Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
 Network Research Group, Zhejiang University  
 The Tobacco Science Research Institute of Yunnan Province, Yuxi  
 653100, China  
 Email: webmaster@estarray.org, URL: http://www.estarray.org  
 Only the high quality region of sequence was submitted.  
 Seq primer: M13.

FEATURES  
 Location/Qualifiers

1..369  
 /organism="Nicotiana tabacum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4097"  
 /clone="tbt\_011057"  
 /tissue\_type="Mixed"  
 /clone\_lib="Normalized Nicotiana tabacum cDNA library"  
 /note="Vector: pBS-SK+."

ORIGIN

Alignment Scores:

Pred. No.: 1.01E-22 Length: 369  
 Score: 244.50 Matches: 53  
 Percent Similarity: 96.5% Conservative: 2  
 Best Local Similarity: 93.0% Mismatches: 1  
 Query Match: 90.2% Indels: 1  
 DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV017159 (1-369)

QY 1 MetAlaSerSerMetLeuSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20  
 |||  
 Db 34 ATGGCTTCTCTGTTCTTCTCTGAGAGTTGCCACTCGCACCATTGTTGCTCAAGCT 93  
 ::|  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::|  
 Db 94 AACATGGTTGCACCTTTCACCTGCTTAAGTCAGCTGCCTCATCTCCCTGTTTCAAGGAAG 153  
 |||  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||  
 Db 154 CAAACCTTGCATCATCTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 204  
 |||

RESULT 16

CV019231 371 bp mRNA linear EST 19-AUG-2004  
LOCUS tbt\_009718 Normalized Nicotiana tabacum cDNA library Nicotiana  
DEFINITION tbt\_009718 Normalized Nicotiana tabacum cDNA library Nicotiana  
ACCESSION CV019231  
VERSION tbt\_009718.1 GI:51457583  
KEYWORDS EST.  
SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 371)  
REFERENCE AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL Unpublished (2004)  
COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source Location/Qualifiers  
1..371  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_009718"  
/tissue type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/notes="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.02e-22 Length: 371  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV019231 (1-371)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 41 ATGGCTTCCTCTGTTCTTCTCTGAGCAGTTGCCACTCGCACCATTGTTCTCAAGCT 100  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 101 AACATGGTTGCACCTTTCATCGCTTAAGTCAGCTGCCTCATCTGTTTCAGGAAG 160  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 161 CAAACCTTGACATCACTTCCATTCCTAGCAATGGTGAAGAGTGCAATGC 211

RESULT 17  
CV021480  
LOCUS tbt\_011140 Normalized Nicotiana tabacum cDNA library Nicotiana  
DEFINITION tbt\_011140 Normalized Nicotiana tabacum cDNA library Nicotiana  
ACCESSION CV021480  
VERSION tbt\_011140.1 GI:51462998  
KEYWORDS EST.  
SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 371)  
REFERENCE AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL Unpublished (2004)  
COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source Location/Qualifiers  
1..386  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_011140"  
/tissue type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/notes="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.07e-22 Length: 386  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021480 (1-386)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 42 ATGGCTTCCTCTGTTCTTCTCTGAGCAGTTGCCACTCGCACCATTGTTCTCAAGCT 101  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 102 AACATGGTTGCACCTTTCATCGCTTAAGTCAGCTGCCTCATCTGTTTCAGGAAG 161  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 162 CAAACCTTGACATCACTTCCATTCCTAGCAATGGTGAAGAGTGCAATGC 212

RESULT 18  
CV016216  
LOCUS tbt\_011065 Normalized Nicotiana tabacum cDNA library Nicotiana  
DEFINITION tbt\_011065 Normalized Nicotiana tabacum cDNA library Nicotiana  
ACCESSION CV016216  
VERSION tbt\_011065.1 GI:51454568  
KEYWORDS EST.  
SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 387)  
REFERENCE AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL Unpublished (2004)  
COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 386)  
REFERENCE AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source Location/Qualifiers  
1..386  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_011140"  
/tissue type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/notes="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.07e-22 Length: 386  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021480 (1-386)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 42 ATGGCTTCCTCTGTTCTTCTCTGAGCAGTTGCCACTCGCACCATTGTTCTCAAGCT 101  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 102 AACATGGTTGCACCTTTCATCGCTTAAGTCAGCTGCCTCATCTGTTTCAGGAAG 161  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 162 CAAACCTTGACATCACTTCCATTCCTAGCAATGGTGAAGAGTGCAATGC 212

RESULT 18  
CV016216  
LOCUS tbt\_011065 Normalized Nicotiana tabacum cDNA library Nicotiana  
DEFINITION tbt\_011065 Normalized Nicotiana tabacum cDNA library Nicotiana  
ACCESSION CV016216  
VERSION tbt\_011065.1 GI:51454568  
KEYWORDS EST.  
SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
1 (bases 1 to 387)  
REFERENCE AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.  
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653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL Unpublished (2004)  
COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

Song,Haitao Dong,Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source  
1. .387  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_011065"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.08e-22 Length: 387  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV016216 (1-387)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20  
|||||  
Db 47 ATGGCTCTCTGTTCTTTCTCTGAGCAGTTGCCACTCGCACCATTGTTCTCAAGCT 106  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::  
Db 107 AACATGGTTGCACCTTTCACTGGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 166  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||  
Db 167 CAAACCTTTGACATCATCTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 217

RESULT 19  
CV016980  
LOCUS  
DEFINITION  
tabacum cDNA clone tbt\_011231 5', mRNA sequence.  
ACCESSION  
CV016980  
VERSION  
CV016980.1 GI:51455332  
KEYWORDS  
EST.  
SOURCE  
Nicotiana tabacum (common tobacco)

ORGANISM  
Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
REFERENCE  
AUTHORS  
Li,W.Z., Shao,Y., Li,Y.P., Lu,X.P., Montero,D.C., Alvarez,S.P.,  
Deng,Y., Jin,Q.C., Wang,S., Dai,C.E., Zeng,Z.L., Wang,Y.Q.,  
Dong,H.T. and Li,D.B.

TITLE  
Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL  
COMMENT  
Unpublished (2004)  
Contact: Wenzheng Li,Yan Shao,Yongping Li,Xiuping Lu,Limin  
Song,Haitao Dong,Debao Li

The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
Location/Qualifiers

source  
1. .404  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_011231"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

ORIGIN  
Alignment Scores:  
Pred. No.: 1.14e-22 Length: 404  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV016980 (1-404)  
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20  
|||||  
Db 57 ATGGCTTCTCTGTTCTTTCTCTGAGCAGTTGCCACTCGCACCATTGTTCTCAAGCT 116  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
:::  
Db 117 AACATGGTTGCACCTTTCACTGGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 176  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
|||||  
Db 177 CAAACCTTTGACATCATCTTCCATTGCTAGCAATGGTGAAGAGTGCAATGC 227

RESULT 20  
CV017309  
LOCUS  
DEFINITION  
tabacum cDNA clone tbt\_002756 5', mRNA sequence.  
ACCESSION  
CV017309  
VERSION  
CV017309.1 GI:51455661  
KEYWORDS  
EST.  
SOURCE  
Nicotiana tabacum (common tobacco)

ORGANISM  
Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.  
REFERENCE  
AUTHORS  
Li,W.Z., Shao,Y., Li,Y.P., Lu,X.P., Montero,D.C., Alvarez,S.P.,  
Deng,Y., Jin,Q.C., Wang,S., Dai,C.E., Zeng,Z.L., Wang,Y.Q.,  
Dong,H.T. and Li,D.B.

TITLE  
Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing  
JOURNAL  
COMMENT  
Unpublished (2004)  
Contact: Wenzheng Li,Yan Shao,Yongping Li,Xiuping Lu,Limin  
Song,Haitao Dong,Debao Li

The Tobacco Science Research Institute of Yunnan Province; Yunnan  
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi  
653100, China  
Email: webmaster@estarray.org, URL: http://www.estarray.org  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source  
1. .412  
Location/Qualifiers  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_002756"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

ORIGIN

## Alignment Scores:

Pred. No.: 1.16e-22 Length: 412  
 Score: 244.50 Matches: 53  
 Percent Similarity: 96.5% Conservative: 2  
 Best Local Similarity: 93.0% Mismatches: 1  
 Query Match: 90.2% Indels: 1  
 DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV017309 (1-412)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 |||||  
 Db 70 ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTCGCCACTGCGACCAATGTTGCTCAAGCT 129  
 |||||  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::::|  
 Db 130 AACATGGTTGCACCTTTTCACTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 189  
 |||||  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||||  
 Db 190 CAAACCTTGACATCACTTCATTCCTAGCATGCTGGAAGAGTGCAATGC 240  
 |||||

## RESULT 21

CV021557 422 bp mRNA linear EST 19-AUG-2004  
 LOCUS tbt\_007663 Normalized Nicotiana tabacum cDNA library Nicotiana  
 DEFINITION tbt\_007663 Normalized Nicotiana tabacum cDNA library Nicotiana  
 VERSION CV021557  
 KEYWORDS tbt\_007663 5', mRNA sequence.

ACCESSION CV021557.1 GI:51463065

SOURCE Nicotiana tabacum (common tobacco)

ORGANISM Nicotiana tabacum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamids; Solanales; Solanaceae; Nicotiana.  
 1 (bases 1 to 422)

AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
 Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
 Dong, H.T. and Li, D.B.

TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
 normalized cDNA library sequencing

JOURNAL Unpublished (2004)

COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
 Song, Haitao Dong, Debao Li  
 The Tobacco Science Research Institute of Yunnan Province; Yunnan  
 Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
 Network Research Group, Zhejiang University  
 The Tobacco Science Research Institute of Yunnan Province, Yuxi  
 653100, China

Email: webmaster@estarray.org, URL: http://www.estarray.org  
 Only the high quality region of sequence was submitted.

Seq primer: M13.

## FEATURES

source Location/Qualifiers  
 1..422  
 /organism="Nicotiana tabacum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4097"  
 /clone="tbt\_007663"  
 /tissue\_type="Mixed"  
 /clone\_lib="Normalized Nicotiana tabacum cDNA library"  
 /note="Vector: pBS-SK+"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.2e-22 Length: 422  
 Score: 244.50 Matches: 53  
 Percent Similarity: 96.5% Conservative: 2  
 Best Local Similarity: 93.0% Mismatches: 1  
 Query Match: 90.2% Indels: 1  
 DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021557 (1-422)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 |||||  
 Db 44 ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTCGCCACTGCGACCAATGTTGCTCAAGCT 103  
 |||||  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::::|  
 Db 104 AACATGGTTGCACCTTTTCACTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 163  
 |||||  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||||  
 Db 164 CAAACCTTGACATCACTTCATTCCTAGCATGCTGGAAGAGTGCAATGC 214  
 |||||

## RESULT 22

CV017696

LOCUS tbt\_004704

DEFINITION Normalized Nicotiana tabacum cDNA library Nicotiana  
 tabacum cDNA clone tbt\_004704 5', mRNA sequence.

ACCESSION CV017696

VERSION CV017696.1 GI:51456048

KEYWORDS EST.

SOURCE Nicotiana tabacum (common tobacco)

ORGANISM Nicotiana tabacum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamids; Solanales; Solanaceae; Nicotiana.  
 1 (bases 1 to 428)

AUTHORS Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
 Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
 Dong, H.T. and Li, D.B.

TITLE Large-scale identification of ESTs from Nicotiana tabacum by  
 normalized cDNA library sequencing  
 Unpublished (2004)

JOURNAL

COMMENT Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin  
 Song, Haitao Dong, Debao Li  
 The Tobacco Science Research Institute of Yunnan Province; Yunnan  
 Provincial Tobacco Group Dali Branch; Bioinformatics and Gene  
 Network Research Group, Zhejiang University  
 The Tobacco Science Research Institute of Yunnan Province, Yuxi  
 653100, China

Email: webmaster@estarray.org, URL: http://www.estarray.org  
 Only the high quality region of sequence was submitted.

Seq primer: M13.

## FEATURES

source Location/Qualifiers  
 1..428  
 /organism="Nicotiana tabacum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4097"  
 /clone="tbt\_004704"  
 /tissue\_type="Mixed"  
 /clone\_lib="Normalized Nicotiana tabacum cDNA library"  
 /note="Vector: pBS-SK+"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.22e-22 Length: 428  
 Score: 244.50 Matches: 53  
 Percent Similarity: 96.5% Conservative: 2  
 Best Local Similarity: 93.0% Mismatches: 1  
 Query Match: 90.2% Indels: 1  
 DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV017696 (1-428)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 |||||  
 Db 60 ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTCGCCACTGCGACCAATGTTGCTCAAGCT 119  
 |||||  
 QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
 ::::|  
 Db 120 AACATGGTTGCACCTTTTCACTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 179  
 |||||  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 |||||

```

Db      180 CAAAACCTTGACATCATCTTCATTGCTAGCAATGGTGAAGAGTGCATGC 230
RESULT 23
CV018759
LOCUS   431 bp mRNA linear EST 19-AUG-2004
DEFINITION tbt_001767 Normalized Nicotiana tabacum cDNA library Nicotiana
ACCESSION CV018759
VERSION   tbt_001767 5', mRNA sequence.
KEYWORDS  CV018759.1 GI:51457111
SOURCE   EST.
ORGANISM Nicotiana tabacum (common tobacco)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 431)
AUTHORS  Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,
Dong, H.T. and Li, D.B.
TITLE    Large-scale identification of ESTs from Nicotiana tabacum by
normalised cDNA library sequencing
JOURNAL  Unpublished (2004)
COMMENT  Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: MJ3.

FEATURES             Location/Qualifiers
     source           1..431
     mol_type="mRNA"
     db_xref="taxon:4097"
     clone="tbt_001767"
     tissue_type="Mixed"
     clone_lib="Normalized Nicotiana tabacum cDNA library"
     note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.:      1..23e-22      Length:      431
Score:          244.50      Matches:      53
Percent Similarity: 96.5%      Conservative: 2
Best Local Similarity: 93.0%      Mismatches:  1
Query Match:    90.2%      Indels:      1
DB:             7      Gaps:          1

US-10-628-525A-33 (1-56) x CV018759 (1-431)

QY      1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db      45 ATGGCTTCCTCTGTACTTTCTCTGAGCAGTTGCCACTCGCAACCAATGTTGCTCAAGCT 104
QY      21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db      105 AACATGGTTGGACCTTTCACTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 164
QY      40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db      165 CAAAACCTTGACATCATCTTCATTGCTAGCAATGGTGAAGAGTGCATGC 215

RESULT 24
CV021294
LOCUS   431 bp mRNA linear EST 19-AUG-2004
DEFINITION tbt_007662 Normalized Nicotiana tabacum cDNA library Nicotiana
ACCESSION CV021294
VERSION   tbt_007662 5', mRNA sequence.
KEYWORDS  CV021294.1 GI:51462802
SOURCE   EST.
ORGANISM Nicotiana tabacum (common tobacco)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 431)
AUTHORS  Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,
Dong, H.T. and Li, D.B.
TITLE    Large-scale identification of ESTs from Nicotiana tabacum by
normalised cDNA library sequencing
JOURNAL  Unpublished (2004)
COMMENT  Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: MJ3.

FEATURES             Location/Qualifiers
     source           1..431
     mol_type="mRNA"
     db_xref="taxon:4097"
     clone="tbt_001767"
     tissue_type="Mixed"
     clone_lib="Normalized Nicotiana tabacum cDNA library"
     note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.:      1..23e-22      Length:      431
Score:          244.50      Matches:      53
Percent Similarity: 96.5%      Conservative: 2
Best Local Similarity: 93.0%      Mismatches:  1
Query Match:    90.2%      Indels:      1
DB:             7      Gaps:          1

US-10-628-525A-33 (1-56) x CV018759 (1-431)

QY      1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db      45 ATGGCTTCCTCTGTACTTTCTCTGAGCAGTTGCCACTCGCAACCAATGTTGCTCAAGCT 104
QY      21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db      105 AACATGGTTGGACCTTTCACTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 164
QY      40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db      165 CAAAACCTTGACATCATCTTCATTGCTAGCAATGGTGAAGAGTGCATGC 215

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SOURCE      Nicotiana tabacum (common tobacco)
ORGANISM    Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 431)
AUTHORS  Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,
Dong, H.T. and Li, D.B.
TITLE    Large-scale identification of ESTs from Nicotiana tabacum by
normalised cDNA library sequencing
JOURNAL  Unpublished (2004)
COMMENT  Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: MJ3.

FEATURES             Location/Qualifiers
     source           1..431
     mol_type="mRNA"
     db_xref="taxon:4097"
     clone="tbt_007662"
     tissue_type="Mixed"
     clone_lib="Normalized Nicotiana tabacum cDNA library"
     note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.:      1..23e-22      Length:      431
Score:          244.50      Matches:      53
Percent Similarity: 96.5%      Conservative: 2
Best Local Similarity: 93.0%      Mismatches:  1
Query Match:    90.2%      Indels:      1
DB:             7      Gaps:          1

US-10-628-525A-33 (1-56) x CV021294 (1-431)

QY      1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db      60 ATGGCTTCCTCTGTACTTTCTCTGAGCAGTTGCCACTCGCAACCAATGTTGCTCAAGCT 119
QY      21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db      120 AACATGGTTGGACCTTTCACTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 179
QY      40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db      180 CAAAACCTTGACATCATCTTCATTGCTAGCAATGGTGAAGAGTGCATGC 230

RESULT 25
CV020505
LOCUS   440 bp mRNA linear EST 19-AUG-2004
DEFINITION tbt_003364 Normalized Nicotiana tabacum cDNA library Nicotiana
ACCESSION CV020505
VERSION   tbt_003364 5', mRNA sequence.
KEYWORDS  CV020505.1 GI:51462013
SOURCE   EST.
ORGANISM Nicotiana tabacum (common tobacco)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 440)
AUTHORS  Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,
Dong, H.T. and Li, D.B.
TITLE    Large-scale identification of ESTs from Nicotiana tabacum by

```



JOURNAL COMMENT  
normalized cDNA library sequencing  
Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: <http://www.estarray.org>  
Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source  
Location/Qualifiers  
1..440  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_003364"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

## ORIGIN

Alignment Scores:  
Pred. No.: 1,27e-22 Length: 440  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV020505 (1-440)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20  
Db ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTGCCACTCGCACCATTGTTGCTCAAGCT 106  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db AACATGGTTGCACCTTTCATCTGCTTAAGTCAGCTGCCTCATCTCCCTGTTTCAAGGAAG 166  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db CAAACCTTGACATCATCTCCATTGCTAGCAATGGTGAAGAGTGCATATGC 217

RESULT 26  
CV020326  
LOCUS  
DEFINITION  
tbt\_002849 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_002849 5', mRNA sequence.  
CV020326  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Nicotiana tabacum (common tobacco)

CV020326 443 bp mRNA linear EST 19-AUG-2004  
tbt\_002849 Normalized Nicotiana tabacum cDNA library Nicotiana  
tabacum cDNA clone tbt\_002849 5', mRNA sequence.

CV020326.1 GI:51461834  
EST.  
Nicotiana tabacum (common tobacco)  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE  
AUTHORS  
Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,  
Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,  
Dong, H.T. and Li, D.B.

TITLE  
Large-scale identification of ESTs from Nicotiana tabacum by  
normalized cDNA library sequencing

JOURNAL COMMENT  
Unpublished (2004)  
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin Song, Haitao Dong, Debao Li  
The Tobacco Science Research Institute of Yunnan Province; Yunnan Provincial Tobacco Group Dali Branch; Bioinformatics and Gene Network Research Group, Zhejiang University  
The Tobacco Science Research Institute of Yunnan Province, Yuxi 653100, China  
Email: webmaster@estarray.org, URL: <http://www.estarray.org>

Only the high quality region of sequence was submitted.  
Seq primer: M13.

FEATURES  
source  
Location/Qualifiers  
1..443  
/organism="Nicotiana tabacum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4097"  
/clone="tbt\_002849"  
/tissue\_type="Mixed"  
/clone\_lib="Normalized Nicotiana tabacum cDNA library"  
/note="Vector: pBS-SK+"

## ORIGIN

Alignment Scores:  
Pred. No.: 1,28e-22 Length: 443  
Score: 244.50 Matches: 53  
Percent Similarity: 96.5% Conservative: 2  
Best Local Similarity: 93.0% Mismatches: 1  
Query Match: 90.2% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV020326 (1-443)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAsnProAlaGlnAla 20  
Db ATGGCTTCCTCTGTTCTTTCTCTGAGCAGTTGCCACTCGCACCATTGTTGCTCAAGCT 107  
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db AACATGGTTGCACCTTTCATCTGCTTAAGTCAGCTGCCTCATCTCCCTGTTTCAAGGAAG 167  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db CAAACCTTGACATCATCTCCATTGCTAGCAATGGTGAAGAGTGCATATGC 218

## RESULT 27

CV021799

LOCUS

DEFINITION

tbt\_007702 Normalized Nicotiana tabacum cDNA library Nicotiana

tabacum cDNA clone tbt\_007702 5', mRNA sequence.

CV021799

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Nicotiana tabacum (common tobacco)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE

AUTHORS

Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,

Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,

Dong, H.T. and Li, D.B.

Large-scale identification of ESTs from Nicotiana tabacum by

normalized cDNA library sequencing

Unpublished (2004)

Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin

Song, Haitao Dong, Debao Li

The Tobacco Science Research Institute of Yunnan Province; Yunnan

Provincial Tobacco Group Dali Branch; Bioinformatics and Gene

Network Research Group, Zhejiang University

The Tobacco Science Research Institute of Yunnan Province, Yuxi

653100, China

Email: webmaster@estarray.org, URL: <http://www.estarray.org>

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/Note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.: 1-28e-22 Length: 443
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021799 (1-443)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 67 ATGGCTTCCTGTTCTTCTCTGAGCAGTTCGACCAATGTTGCTCAAGCT 126

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 127 AACATGGTTGCACCTTTCACCTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 186

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 187 CAAACCTTGACATCATTCCATTGCTAGCAATGTTGGAAGAGTGCATGC 237

RESULT 28
CV016694
LOCUS
DEFINITION
tbt_007392 Normalized Nicotiana tabacum cDNA library Nicotiana
CV016694
CV016694.1 GI:51455046
EST.
Nicotiana tabacum (common tobacco)
ORGANISM
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 454)
AUTHORS
Li,W.Z., Shao,Y., Li,Y.P., Lu,X.P., Montero,D.C., Alvarez,S.P.,
Deng,Y., Jin,Q.C., Wang,S., Dai,C.E., Zeng,Z.L., Wang,Y.Q.,
Dong,H.T. and Li,D.B.
TITLE
Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
JOURNAL
Unpublished (2004)
COMMENT
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.

FEATURES
Source
Location/Qualifiers
1..454
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/db_xref="taxon:4097"
/clone="tbt_007392"
/tissue_type="Mixed"
/clone_lib="Normalized Nicotiana tabacum cDNA library"
/note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.: 1-32e-22 Length: 454
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021799 (1-443)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 67 ATGGCTTCCTGTTCTTCTCTGAGCAGTTCGACCAATGTTGCTCAAGCT 126

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 127 AACATGGTTGCACCTTTCACCTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 186

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 187 CAAACCTTGACATCATTCCATTGCTAGCAATGTTGGAAGAGTGCATGC 237

RESULT 28
CV016694
LOCUS
DEFINITION
tbt_007392 Normalized Nicotiana tabacum cDNA library Nicotiana
CV016694
CV016694.1 GI:51455046
EST.
Nicotiana tabacum (common tobacco)
ORGANISM
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 454)
AUTHORS
Li,W.Z., Shao,Y., Li,Y.P., Lu,X.P., Montero,D.C., Alvarez,S.P.,
Deng,Y., Jin,Q.C., Wang,S., Dai,C.E., Zeng,Z.L., Wang,Y.Q.,
Dong,H.T. and Li,D.B.
TITLE
Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
JOURNAL
Unpublished (2004)
COMMENT
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.

FEATURES
Source
Location/Qualifiers
1..454
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/db_xref="taxon:4097"
/clone="tbt_007392"
/tissue_type="Mixed"
/clone_lib="Normalized Nicotiana tabacum cDNA library"
/note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.: 1-32e-22 Length: 454
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV021799 (1-443)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 44 ATGGCTTCCTGTTCTTCTCTGAGCAGTTCGACCAATGTTGCTCAAGCT 103

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 104 AACATGGTTGCACCTTTCACCTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 163

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 163 CAAACCTTGACATCATTCCATTGCTAGCAATGTTGGAAGAGTGCATGC 213

RESULT 29
CV020329
LOCUS
DEFINITION
tbt_006124 Normalized Nicotiana tabacum cDNA library Nicotiana
CV020329
CV020329.1 GI:51461837
EST.
Nicotiana tabacum (common tobacco)
ORGANISM
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 459)
AUTHORS
Li,W.Z., Shao,Y., Li,Y.P., Lu,X.P., Montero,D.C., Alvarez,S.P.,
Deng,Y., Jin,Q.C., Wang,S., Dai,C.E., Zeng,Z.L., Wang,Y.Q.,
Dong,H.T. and Li,D.B.
TITLE
Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
JOURNAL
Unpublished (2004)
COMMENT
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.

FEATURES
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Location/Qualifiers
1..459
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/mol_type="mRNA"
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/tissue_type="Mixed"
/clone_lib="Normalized Nicotiana tabacum cDNA library"
/note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.: 1-33e-22 Length: 459
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV020329 (1-459)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 44 ATGGCTTCCTGTTCTTCTCTGAGCAGTTCGACCAATGTTGCTCAAGCT 103

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 104 AACATGGTTGCACCTTTCACCTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 163

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 163 CAAACCTTGACATCATTCCATTGCTAGCAATGTTGGAAGAGTGCATGC 213

RESULT 29
CV020329
LOCUS
DEFINITION
tbt_006124 Normalized Nicotiana tabacum cDNA library Nicotiana
CV020329
CV020329.1 GI:51461837
EST.
Nicotiana tabacum (common tobacco)
ORGANISM
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 459)
AUTHORS
Li,W.Z., Shao,Y., Li,Y.P., Lu,X.P., Montero,D.C., Alvarez,S.P.,
Deng,Y., Jin,Q.C., Wang,S., Dai,C.E., Zeng,Z.L., Wang,Y.Q.,
Dong,H.T. and Li,D.B.
TITLE
Large-scale identification of ESTs from Nicotiana tabacum by
normalized cDNA library sequencing
JOURNAL
Unpublished (2004)
COMMENT
Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
Song, Haitao Dong, Debao Li
The Tobacco Science Research Institute of Yunnan Province; Yunnan
Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
Network Research Group, Zhejiang University
The Tobacco Science Research Institute of Yunnan Province, Yuxi
653100, China
Email: webmaster@estarray.org, URL: http://www.estarray.org
Only the high quality region of sequence was submitted.
Seq primer: M13.

FEATURES
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Location/Qualifiers
1..459
/organism="Nicotiana tabacum"
/mol_type="mRNA"
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/clone="tbt_006124"
/tissue_type="Mixed"
/clone_lib="Normalized Nicotiana tabacum cDNA library"
/note="Vector: pBS-SK+"

ORIGIN
Alignment Scores:
Pred. No.: 1-33e-22 Length: 459
Score: 244.50 Matches: 53
Percent Similarity: 96.5% Conservative: 2
Best Local Similarity: 93.0% Mismatches: 1
Query Match: 90.2% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x CV020329 (1-459)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 44 ATGGCTTCCTGTTCTTCTCTGAGCAGTTCGACCAATGTTGCTCAAGCT 103

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 104 AACATGGTTGCACCTTTCACCTGGTCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGGAAG 163

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 163 CAAACCTTGACATCATTCCATTGCTAGCAATGTTGGAAGAGTGCATGC 213

RESULT 29
CV020329
LOCUS
DEFINITION
tbt_006124 Normalized Nicotiana tabacum cDNA library Nicotiana
CV020329
CV020329.1 GI:51461837
EST.
Nicotiana tabacum (common tobacco)
ORGANISM
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 459)
AUTHORS
Li,W.Z., Shao,Y., Li,Y.P., Lu,X.P., Montero,D.C., Alvarez,S.P.,

```

```

QY      40  GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db      164  CAAACCTTGACATTACCTGCTAGCAATGGTGGAGAGGTTCAATGC 214

RESULT 30
CV019815
LOCUS   CV019815               460 bp      mRNA      linear      EST 19-AUG-2004
DEFINITION tbt_004829 Normalized Nicotiana tabacum cDNA library Nicotiana
tabacum cDNA clone tbt_004829 5', mRNA sequence.
ACCESSION CV019815
VERSION   CV019815.1 GI:51461323
KEYWORDS  EST.
SOURCE    Nicotiana tabacum (common tobacco)
ORGANISM  Nicotiana tabacum
          Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 460)
AUTHORS   Li, W.Z., Shao, Y., Li, Y.P., Lu, X.P., Montero, D.C., Alvarez, S.P.,
          Deng, Y., Jin, Q.C., Wang, S., Dai, C.E., Zeng, Z.L., Wang, Y.Q.,
          Dong, H.T. and Li, D.B.
TITLE     Large-scale identification of ESTs from Nicotiana tabacum by
          normalized cDNA library sequencing
JOURNAL   Unpublished (2004)
COMMENT   Contact: Wenzheng Li, Yan Shao, Yongping Li, Xiuping Lu, Limin
          Song, Haitao Dong, Debao Li
          The Tobacco Science Research Institute of Yunnan Province; Yunnan
          Provincial Tobacco Group Dali Branch; Bioinformatics and Gene
          Network Research Group, Zhejiang University
          The Tobacco Science Research Institute of Yunnan Province, Yuxi
          653100, China
          Email: webmaster@estarray.org, URL: http://www.estarray.org
          Only the high quality region of sequence was submitted.
          Seq primer: M13.
FEATURES             Location/Qualifiers
     source           1..460
                     /organism="Nicotiana tabacum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4097"
                     /clone="tbt_004829"
                     /tissue_type="Mixed"
                     /clone_lib="Normalized Nicotiana tabacum cDNA library"
                     /note="Vector: pBS-SK+"

ORIGIN

Alignment Scores:
Pred. No.:          1.34e-22      Length:          460
Score:              244.50        Matches:         53
Percent Similarity: 96.5%         Conservative:    2
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US-10-628-525A-33 (1-56) x CV019815 (1-460)

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Db      107  AACATGGTTGCACCTTTCACCTGCTCTTAAGTCAGTCGCTCATTCCTGTTTCAAGGAAG 166

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Db      167  CAAACCTTGACATCATCTTCCATTGCTAGCAATGGTGGAGAGTTCATATGC 217

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Search completed: April 1, 2006, 19:23:02  
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 31, 2006, 22:47:42 ; Search time 74.8932 Seconds  
(without alignments)  
1329.139 Million cell updates/sec

Title: US-10-628-525A-33

Perfect score: 271

Sequence: 1 MASSMLSSRAVATRTNPAQA.....SRQNLDITSIASNGRVC 56

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	240.5	88.7	177	2	US-08-096-043-12
3	240.5	88.7	177	2	US-08-093-577-8
4	240.5	88.7	177	2	US-08-331-004A-6
5	240.5	88.7	177	2	US-08-096-623A-12
6	240.5	88.7	177	6	PCT-US95-13937A-6
7	240.5	88.7	204	3	US-09-839-477-3
8	240.5	88.7	499	3	US-09-495-797-41
9	240.5	88.7	1442	2	US-08-152-483B-8
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					Sequence 12, Appl
					Sequence 8, Appl
					Sequence 6, Appl
					Sequence 12, Appl
					Sequence 6, Appl
					Sequence 12, Appl
					Sequence 12, Appl
					Sequence 3, Appl
					Sequence 41, Appl
					Sequence 8, Appl

10	223.5	82.5	684	3	US-09-896-866B-16	Sequence 16, Appl
11	223.5	82.5	684	3	US-09-855-341-7	Sequence 7, Appl
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13	204	75.3	177	3	US-09-021-203-3	Sequence 3, Appl
14	181.5	67.0	174	3	US-09-441-340-14	Sequence 14, Appl
15	181.5	67.0	178	3	US-09-186-002-7	Sequence 7, Appl
16	181.5	67.0	264	3	US-09-441-340-9	Sequence 9, Appl
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18	181.5	67.0	279	2	US-08-391-339-9	Sequence 9, Appl
19	181.5	67.0	279	2	US-08-484-274A-9	Sequence 9, Appl
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## ALIGNMENTS

## RESULT 2

US-08-096-043-12  
; Sequence 12, Application US/08096043  
; Patent No. 5530189  
; GENERAL INFORMATION:

US-08-095-726-12  
; Sequence 12, Application US/08095726  
; Patent No. 5530188  
; GENERAL INFORMATION:  
; APPLICANT: Ausich, Rodney L  
; APPLICANT: Brinkhaus, Friedhelm L  
; APPLICANT: Mukharji, Indrani  
; APPLICANT: Proffitt, John H  
; APPLICANT: Yarger, James G  
; APPLICANT: Yen, Huel-Che B  
; TITLE OF INVENTION: Beta-Carotene Biosynthesis in  
; TITLE OF INVENTION: Genetically Engineered Hosts  
; NUMBER OF SEQUENCES: 79  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
; STREET: 200 E Randolph St  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60680-0703  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/095,726  
; FILING DATE: 21-JUL-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/785,566  
; FILING DATE: 30-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Galloway, No. 5530188val B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3128564780  
; TELEFAX: 3128564972  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-095-726-12  
Alignment Scores:  
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Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
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US-10-628-525A-33 (1-56) x US-08-095-726-12 (1-177)  
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QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
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RESULT 2  
US-08-096-043-12  
; Sequence 12, Application US/08096043  
; Patent No. 5530189  
; GENERAL INFORMATION:

APPLICANT: Ausich, Rodney L  
APPLICANT: Brinkhaus, Friedhelm L  
APPLICANT: Mukharji, Indrani  
APPLICANT: Proffitt, John H  
APPLICANT: Yarger, James G  
APPLICANT: Yen, Hwei-Che B  
TITLE OF INVENTION: Lycopene Biosynthesis in Genetically Engineered Hosts  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
STREET: 200 E Randolph St  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60680-0703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/096,043  
FILING DATE: 22-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/785,568  
FILING DATE: 30-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, No. 5530189val B  
TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-096-043-12

Alignment Scores:  
Pred. No.: 4,23e-27 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x US-08-096-043-12 (1-177)

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Db 1 ATGGCTTCCTCAGTTCTTTCTCTGAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
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## RESULT 3

US-08-093-577-8  
Sequence 8, Application US/08093577  
Patent No. 5545816  
GENERAL INFORMATION:  
APPLICANT: Ausich, Rodney L  
APPLICANT: Brinkhaus, Friedhelm L  
APPLICANT: Mukharji, Indrani  
APPLICANT: Proffitt, John H

APPLICANT: Yarger, James G  
APPLICANT: Yen, Hwei-Che B  
TITLE OF INVENTION: Phytoene Biosynthesis in Genetically Engineered Hosts  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
STREET: 200 E Randolph St  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60680-0703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,577  
FILING DATE: 19-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/785,569  
FILING DATE: 30-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, No. 5545816val B  
TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-093-577-8

Alignment Scores:  
Pred. No.: 4,23e-27 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 2 Gaps: 1

US-10-628-525A-33 (1-56) x US-08-093-577-8 (1-177)

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QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
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## RESULT 4

US-08-331-004A-6  
Sequence 6, Application US/08331004A  
Patent No. 5618988  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Randal  
APPLICANT: Eschenfeldt, William H  
APPLICANT: English, Jami  
APPLICANT: Brinkhaus, Friedhelm L  
TITLE OF INVENTION: Enhanced Carotenoid Accumulation in Storage Organs of Genetically Engineered Plants  
NUMBER OF SEQUENCES: 9

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Amoco Corporation, Law Dept
/ STREET: 55 Shuman Boulevard, Suite 600
/ CITY: Naperville
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60563-8437
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/331,004A
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Galloway, No. 5618988val B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 7087172447
/ TELEFAX: 7087172430
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 177 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-331-004A-6
/
/ Alignment Scores:
/ Pred. No.: 4,23e-27 Length: 177
/ Score: 240.50 Matches: 52
/ Percent Similarity: 96.5% Conservative: 3
/ Best Local Similarity: 91.2% Mismatches: 1
/ Query Match: 88.7% Indels: 1
/ DB: 2 Gaps: 1
/
/ US-10-628-525A-33 (1-56) x US-08-331-004A-6 (1-177)
/
/ QY 1 MetaLaserSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
/ Db 1 ATGGCTTCCTCAGTTCTTTCTCTGAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60
/
/ QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
/ Db 61 AACATGGTGGCGCCCTTCTACCTGGCCCTTAAGTCAGCTGCCTCATCTCCCTGTTTCAAGGAAG 120
/
/ QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
/ Db 121 CAAACCTTGACATCACTTCCTTCCATTCGCACGACGCGGGAAGAGTGCATATGC 171
/
/ RESULT 5
/ US-08-096-623A-12
/ Sequence 12, Application US/08096623A
/ Patent No. 5684238
/ GENERAL INFORMATION:
/ APPLICANT: Ausich, Rodney L.
/ APPLICANT: Brinkhaus, Friedhelm L.
/ APPLICANT: Mukharji, Indrani
/ APPLICANT: Proffitt, John H.
/ APPLICANT: Yarger, James G.
/ APPLICANT: Yen, Huel-Che B.
/ TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
/ TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
/ NUMBER OF SEQUENCES: 104
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Welsh & Katz, Ltd.
/ STREET: 120 S. Riverside Plaza, 22nd Floor
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60606
/
```

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/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/096,623A
/ FILING DATE: 22-JUL-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/805,061
/ FILING DATE: 09-DEC-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/662,921
/ FILING DATE: 28-FEB-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/562,674
/ FILING DATE: 03-AUG-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/525,551
/ FILING DATE: 18-MAY-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/487,613
/ FILING DATE: 02-MAR-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gamson, Edward P.
/ REGISTRATION NUMBER: 29,381
/ REFERENCE/DOCKET NUMBER: AMO-006.1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 655-1500
/ TELEFAX: (312) 655-1501
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 177 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ POSITION IN GENOME:
/ MAP POSITION: 1 to 177
/ UNITS: bp
/ US-08-096-623A-12
/
/ Alignment Scores:
/ Pred. No.: 4,23e-27 Length: 177
/ Score: 240.50 Matches: 52
/ Percent Similarity: 96.5% Conservative: 3
/ Best Local Similarity: 91.2% Mismatches: 1
/ Query Match: 88.7% Indels: 1
/ DB: 2 Gaps: 1
/
/ US-10-628-525A-33 (1-56) x US-08-096-623A-12 (1-177)
/
/ QY 1 MetaLaserSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
/ Db 1 ATGGCTTCCTCAGTTCTTTCTCTGAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60
/
/ QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
/ Db 61 AACATGGTGGCGCCCTTCTACCTGGCCCTTAAGTCAGCTGCCTCATCTCCCTGTTTCAAGGAAG 120
/
/ QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
/ Db 121 CAAACCTTGACATCACTTCCTTCCATTCGCACGACGCGGGAAGAGTGCATATGC 171
/
/ RESULT 6
/ PCT-US95-13937A-6
/ Sequence 6, Application PC/TUS9513937A
/ GENERAL INFORMATION:
/ APPLICANT: Hauptmann, Randal
/ APPLICANT: Eschenfeldt, William H
/ APPLICANT: English, Jami
/ APPLICANT: Brinkhaus, Friedhelm L
/
```







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; TITLE OF INVENTION: HIGH LEVEL PRODUCTION OF P-HYDROXYBENZZOIC ACID
; FILE REFERENCE: BCI015 US NA
; CURRENT APPLICATION NUMBER: US/09/855,341
; CURRENT FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: MICROSOFT OFFICE 97
; SEQ ID NO 7
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic CPL
US-09-855-341-7

Alignment Scores:
Pred. No.: 1.04e-23 Length: 684
Score: 223.50 Matches: 47
Percent Similarity: 93.0% Conservative: 6
Best Local Similarity: 82.5% Mismatches: 3
Query Match: 82.5% Indels: 1
DB: 3 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-855-341-7 (1-684)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20
Db 1 ATGGCTTCTCTGTCATTTCTTCAGCAGCTGTTGCCACACGCAATGTTACACAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 61 AGCATGTTGCACCTTTCACCTGGTCTCAAAATCTTCAGCCACTTTCCTCTGTTCACAAAGAAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCACTTCTCATTGCTAGCAATGTTGGAGAGTGTAGTGC 171

RESULT 12
US-09-021-203-5
; Sequence 5, Application US/09021203
; Patent No. 6040504
; GENERAL INFORMATION:
; APPLICANT: De Framond, Annick
; TITLE OF INVENTION: Cotton Promoter
; FILE REFERENCE: CGC1313/CIP/CONT3
; CURRENT APPLICATION NUMBER: US/09/021,203
; CURRENT FILING DATE: 1998-02-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(191)
US-09-021-203-5

Alignment Scores:
Pred. No.: 1.05e-21 Length: 191
Score: 204.50 Matches: 45
Percent Similarity: 88.1% Conservative: 7
Best Local Similarity: 76.3% Mismatches: 4
Query Match: 75.5% Indels: 3
DB: 3 Gaps: 2

US-10-628-525A-33 (1-56) x US-09-021-203-5 (1-191)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 15 ATGGCTCTCTCCATGATCTCATCGGCAACCATTCGACCGTGAAGTCTCTCCCGCGCA 74

QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
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Db 75 CAGGCCAACATGCTGGGCCCTTTCACCGGCTCAAGTCTGCCTCTCTCCCAAGTCACT 134
QY 38 ArgGlyGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 135 AGGAAGCCCAACCAACGACATCACTTCTTTCGAAGCAATGGTGGAGAGTGCATATGC 191

RESULT 13
US-09-021-203-3
; Sequence 3, Application US/09021203
; Patent No. 6040504
; GENERAL INFORMATION:
; APPLICANT: De Framond, Annick
; TITLE OF INVENTION: Cotton Promoter
; FILE REFERENCE: CGC1313/CIP/CONT3
; CURRENT APPLICATION NUMBER: US/09/021,203
; CURRENT FILING DATE: 1998-02-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(177)
US-09-021-203-3

Alignment Scores:
Pred. No.: 1.12e-21 Length: 177
Score: 204.00 Matches: 45
Percent Similarity: 87.7% Conservative: 5
Best Local Similarity: 78.9% Mismatches: 5
Query Match: 75.3% Indels: 2
DB: 3 Gaps: 2

US-10-628-525A-33 (1-56) x US-09-021-203-3 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20
Db 10 ATGGCTTCTCTCAATGATCTCATCGGTACATTCACCT---GCCTCTCCGCGACAGGCT 66

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSerArgLys 39
Db 67 AACATGCTGCTCTCTTTCACCGGCTCAAGTCTGCCTCTGCTTCCAGTCATCAGGAAG 126

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 127 GCCAACACGACATTAATTTCTTCGCAAGCAATGGCGGAGAGTGCATATGC 177

RESULT 14
US-09-441-340-14
; Sequence 14, Application US/09441340
; Patent No. 6448476
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/09/441,340
; CURRENT FILING DATE: 1999-11-16
; EARLIER APPLICATION NUMBER: 60/108,763
; EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chloroplast or
; OTHER INFORMATION: plastid transit peptide coding sequence and amino
; OTHER INFORMATION: acid sequence translation
; FEATURE:
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Percent Similarity: 78.9% Conservatives: 4  
 Best Local Similarity: 71.9% Mismatches: 9  
 Query Match: 67.0% Indels: 3  
 DB: 3 Gaps: 2

US-10-628-525A-33 (1-56) x US-09-186-002-5 (1-268)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 Db 1 ATGGCTTCCTCTATGCTCTCTCCGCTACTATGTT-----GCCTCTCCGGCTCAGGCC 54  
 QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
 Db 55 ACTATGTCGCTCTTTCACGGACTTAAGTCTCCGCTCCCTTCCCGCCACCCGCAAG 114  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 115 GCTAACCAACGACATTACTTCCATCACAACGCGGAGAGAGTTAACTGC 165

## RESULT 18

US-08-391-339-9  
 ; Sequence 9, Application US/08391339  
 ; Patent No. 5463175  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kishore, Ganesh M.  
 ; APPLICANT: Barry, Gerard F.  
 ; TITLE OF INVENTION: Glyphosate Tolerant Plants  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dennis R. Hoerner, Jr.,  
 ; ADDRESSEE: Monsanto Co. B44F  
 ; STREET: 700 Chesterfield Village Parkway  
 ; CITY: St. Louis  
 ; STATE: Missouri  
 ; COUNTRY: USA  
 ; ZIP: 63198  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/391,339  
 ; FILING DATE:  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/156,968  
 ; FILING DATE:  
 ; APPLICATION NUMBER: US/07/717,370  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hoerner, Dennis R., Jr.  
 ; REGISTRATION NUMBER: 30,914  
 ; REFERENCE/DOCKET NUMBER: 38-21(10533)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (314)537-6099  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 279 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (recombinant)  
 ; US-08-391-339-9

Alignment Scores:  
 Pred. No.: 4.8e-18 Length: 279  
 Score: 181.50 Matches: 41  
 Percent Similarity: 78.9% Conservatives: 4  
 Best Local Similarity: 71.9% Mismatches: 9  
 Query Match: 67.0% Indels: 3  
 DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-391-339-9 (1-279)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 Db 12 ATGGCTTCCTCTATGCTCTCTCCGCTACTATGTT-----GCCTCTCCGGCTCAGGCC 65  
 QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
 Db 66 ACTATGTCGCTCTTTCACGGACTTAAGTCTCCGCTCCCTTCCCGCCACCCGCAAG 125  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 126 GCTAACCAACGACATTACTTCCATCACAACGCGGAGAGAGTTAACTGC 176

## RESULT 19

US-08-484-274A-9  
 ; Sequence 9, Application US/08484274A  
 ; Patent No. 5776760  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kishore, Ganesh M.  
 ; APPLICANT: Barry, Gerard F.  
 ; TITLE OF INVENTION: Glyphosate Tolerant Plants  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: USA  
 ; ZIP: 77210-4433  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/484,274A  
 ; FILING DATE: 07 June 1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Patterson, Melinda L.  
 ; REGISTRATION NUMBER: 33,062  
 ; REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (713)789-2679  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 279 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (recombinant)  
 ; US-08-484-274A-9

Alignment Scores:  
 Pred. No.: 4.8e-18 Length: 279  
 Score: 181.50 Matches: 41  
 Percent Similarity: 78.9% Conservatives: 4  
 Best Local Similarity: 71.9% Mismatches: 9  
 Query Match: 67.0% Indels: 3  
 DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-484-274A-9 (1-279)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
 Db 12 ATGGCTTCCTCTATGCTCTCTCCGCTACTATGTT-----GCCTCTCCGGCTCAGGCC 65  
 QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
 Db 66 ACTATGTCGCTCTTTCACGGACTTAAGTCTCCGCTCCCTTCCCGCCACCCGCAAG 125  
 QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

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126 GCTAACAGCAGCATTACTTCATCACAGCAACGCGGAGAGTTAACTGC 176
DB

RESULT 20
US-09-612-404-9
; Sequence 9, Application US/09612404
; Patent No. RE38825
; GENERAL INFORMATION:
; APPLICANT: Kishore, Ganesh M.
; Barry, Gerard F.
; TITLE OF INVENTION: Glycosate Tolerant Plants
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/612,404
; FILING DATE: 07-Jul-2000
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,274A
; FILING DATE: 07 June 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT130 38-21(135560)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713)789-2679
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 279 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-612-404-9

```

GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Stark, David M.  
TITLE OF INVENTION: Enhanced Starch Biosynthesis  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Grace L. Bonner, Monsanto Co. BB4F  
STREET: 700 Chesterfield Parkway No. 5608149th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/398,627  
FILING DATE: 03-MAR-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/090,523  
FILING DATE: 12-JUL-1993  
APPLICATION NUMBER: US 07/709663  
FILING DATE: 07-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/539763  
FILING DATE: 18-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Bonner, Grace L.  
REGISTRATION NUMBER: 32,963  
REFERENCE/DOCKET NUMBER: 38-21(10559)A  
TELEPHONE: (314) 537-7286  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 88..354  
US-08-398-627-5

Alignment Scores:  
Pred. No.: 6,84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-398-627-5 (1-355)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 88 ATGGCTTCCTCTATGCTCTCTCCGCTACTATGGTT-----GCCTCTCGGCTCAGGCC 141  
QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
Db 142 ACTATGGTCGCTCTTTCACGAGCTTAAGTCTCCGCTGCCTCCAGCCACCCGCAAG 201  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 202 GCTAACACGACATTACTTCCATCACAACGCGGGAAGAGTTAACTGC 252  
RESULT 23  
US-08-406-858-5

Sequence 5, Application US/08406858  
Patent No. 5648249  
GENERAL INFORMATION:  
APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Stark, David M.  
APPLICANT: Zalewski, James C.  
TITLE OF INVENTION: Method of Improving the Quality of  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F  
STREET: 700 Chesterfield Parkway No. 5648249th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/406,858  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05275  
FILING DATE: 18-MAY-1994  
APPLICATION NUMBER: US 08/070,155  
FILING DATE: 28-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bonner, Grace L.  
REGISTRATION NUMBER: 32,963  
REFERENCE/DOCKET NUMBER: 38-21(10654)A  
TELEPHONE: (314) 537-7286  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 88..354  
US-08-406-858-5

Alignment Scores:  
Pred. No.: 6,84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 2 Gaps: 2

US-10-628-525A-33 (1-56) x US-08-406-858-5 (1-355)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 88 ATGGCTTCCTCTATGCTCTCTCCGCTACTATGGTT-----GCCTCTCGGCTCAGGCC 141  
QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
Db 142 ACTATGGTCGCTCTTTCACGAGCTTAAGTCTCCGCTGCCTCCAGCCACCCGCAAG 201  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 202 GCTAACACGACATTACTTCCATCACAACGCGGGAAGAGTTAACTGC 252

RESULT 24  
US-08-476-519-7  
; Sequence 7, Application US/08476519  
; Patent No. 5750876  
; GENERAL INFORMATION:  
; APPLICANT: Barry, Gerard F.  
; APPLICANT: Kishore, Ganesh M.  
; APPLICANT: Krohn, Bradley M.  
; TITLE OF INVENTION: No. 5750876el Isomylase Gene, Compositions  
; TITLE OF INVENTION: Containing It and Methods of Using Isomylases  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Parkway No. 5750876th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,519  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION NUMBER:  
; FILING DATE:  
; APPLICATION DATA:  
; APPLICATION NUMBER: 32,963  
; REGISTRATION NUMBER: 38-21(13577)A  
; REFERENCE/DOCKET NUMBER:  
; TELEPHONE: (314)537-7286  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; PUBLICATION INFORMATION:  
; DOCUMENT NUMBER: WO 91/19806  
; FILING DATE: 07-JUN-1991  
; PUBLICATION DATE: 26-DEC-1991  
; RELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 355  
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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
DB 142 ACTATGGTTCGCTCTCTTCAACGGACTTAAGTCTCGCTGCTTCCAGCCACCCTGCGCAG 201  
QY 40 GlnAenLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56  
DB 202 GCTAACACGACATTACTTCCATCATCAAGCAACGGCGGAAGAGTTAACTGC 252

RESULT 25  
US-08-120-703A-5  
; Sequence 5, Application US/08120703A  
; Patent No. 6538178  
; GENERAL INFORMATION:  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: Increased Starch Content in Plants  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Grace L. Bonner, Monsanto Co. BB4F  
; STREET: 700 Chesterfield Village Parkway No. 6538178th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/120,703A  
; FILING DATE: 13-SEP-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION NUMBER:  
; FILING DATE:  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/709663  
; FILING DATE: 07-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bonner, Grace L.  
; REGISTRATION NUMBER: 32,963  
; REFERENCE/DOCKET NUMBER: 38-21(10639)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 537-7357  
; TELEFAX: (314) 537-6047  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 88..354  
US-08-120-703A-5  
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Pred. No.: 6.84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 2 Gaps: 2  
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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
DB 142 ACTATGGTTCGCTCTCTTCAACGGACTTAAGTCTCGCTGCTTCCAGCCACCCTGCGCAG 201  
QY 40 GlnAenLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56  
DB 202 GCTAACACGACATTACTTCCATCATCAAGCAACGGCGGAAGAGTTAACTGC 252  
RESULT 26  
US-08-399-023-5  
; Sequence 5, Application US/08399023  
; Patent No. 6538179  
; GENERAL INFORMATION:



APPLICANT: Barry, Gerard F.  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Stark, David M.  
TITLE OF INVENTION: Enhanced Starch Biosynthesis  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Grace L. Bonner, Monsanto Co. B84P  
STREET: 700 Chesterfield Parkway No. 6538179th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/399,023  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/090,523  
FILING DATE:  
APPLICATION NUMBER: US 07/709663  
FILING DATE: 07-JUN-1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/539763  
FILING DATE: 18-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Bonner, Grace L.  
REGISTRATION NUMBER: 32,963  
REFERENCE/DOCKET NUMBER: 38-21(10559)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-7286  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 88..354  
US-08-399-023-5

Alignment Scores:  
Pred. No.: 6.84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 2

US-10-628-525A-33 (1-56) x US-08-399-023-5 (1-355)

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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
Db 142 ACTATGGTCGCTCTTCAACGGACTTAAGTCTCGCTCCGCTTCCAGGCCACCCGCAAG 201  
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 202 GCTAACACAGCATTACTTCCATCAACAGCAACGGCGAAGAGTTAACTGC 252

RESULT 27

PCT-US91-04036-5

; Sequence 5, Application PC/TUS9104036

GENERAL INFORMATION:  
APPLICANT: Kishore, Ganesh M.  
TITLE OF INVENTION: Increased Starch Content in Plants  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Monsanto Co.  
STREET: 700 Chesterfield Village Parkway  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/04036  
FILING DATE: 19910607  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: McBride, Thomas P.  
REGISTRATION NUMBER: 32706  
REFERENCE/DOCKET NUMBER: 38-21(10530)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-7357  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 88..354  
PCT-US91-04036-5

Alignment Scores:  
Pred. No.: 6.84e-18 Length: 355  
Score: 181.50 Matches: 41  
Percent Similarity: 78.9% Conservative: 4  
Best Local Similarity: 71.9% Mismatches: 9  
Query Match: 67.0% Indels: 3  
DB: 2

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QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAnProAlaGlnAla 20  
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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39  
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QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 202 GCTAACACAGCATTACTTCCATCAACAGCAACGGCGAAGAGTTAACTGC 252

RESULT 28

PCT-US94-05275-5

; Sequence 5, Application PC/TUS9405275

GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: Method of Improving the Quality of Stored  
NUMBER OF SEQUENCES: 26  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/05275
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/070155
/ FILING DATE: 28-MAY-1993
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 355 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 88..354
PCT-US94-05275-5

Alignment Scores:
Pred. No.: 6.84e-18 Length: 355
Score: 181.50 Matches: 41
Percent Similarity: 78.9% Conservative: 4
Best Local Similarity: 71.9% Mismatches: 9
Query Match: 67.0% Indels: 3
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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39
Db 142 ACTATGGTCGCTCTTCAACGGACTTAAGTCTCCGCTGCCTTCCAGCCACCCGCAAG 201
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
Db 202 GCTAACACGACATTACTTCCATCACAAGCAACGGCGGAAGAGTTAACTGC 252

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/ Sequence 1, Application PC/TUS9509323
/ Patent No. 6380463
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/ APPLICANT: Jenson, Ian
/ TITLE OF INVENTION: DNA Constructs
/ FILE REFERENCE: PPD 50059/UST
/ CURRENT APPLICATION NUMBER: US/09/011,151
/ PRIOR FILING DATE: 1998-01-29
/ PRIOR APPLICATION NUMBER: PCT/GB96/01883
/ PRIOR FILING DATE: 1996-08-02
/ PRIOR APPLICATION NUMBER: GB 9515941.4
/ PRIOR FILING DATE: 1995-08-03
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 509
/ TYPE: DNA
/ ORGANISM: Arabidopsis sp.
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(507)
US-09-011-151-1

Alignment Scores:
Pred. No.: 1.16e-17 Length: 509
Score: 181.50 Matches: 41
Percent Similarity: 78.9% Conservative: 4
Best Local Similarity: 71.9% Mismatches: 9
Query Match: 67.0% Indels: 3
DB: 3 Gaps: 2

US-10-628-525A-33 (1-56) x US-09-011-151-1 (1-509)
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Db 64 ACTATGGTCGCTCTTCAACGGACTTAAGTCTCCGCTGCCTTCCAGCCACCCGCAAG 123
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
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/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
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/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/070155
/ FILING DATE: 28-MAY-1993
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 355 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 88..354
PCT-US94-05275-5

Alignment Scores:
Pred. No.: 6.84e-18 Length: 355
Score: 181.50 Matches: 41
Percent Similarity: 78.9% Conservative: 4
Best Local Similarity: 71.9% Mismatches: 9
Query Match: 67.0% Indels: 3
DB: 6 Gaps: 2

US-10-628-525A-33 (1-56) x PCT-US94-05275-5 (1-355)
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QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39
Db 142 ACTATGGTCGCTCTTCAACGGACTTAAGTCTCCGCTGCCTTCCAGCCACCCGCAAG 201
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
Db 202 GCTAACACGACATTACTTCCATCACAAGCAACGGCGGAAGAGTTAACTGC 252

RESULT 29
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/ Sequence 7, Application PC/TUS9509323
/ Patent No. 6380463
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: Novel Isoamylase Gene, Compositions
/ FILE REFERENCE: Containing It and Methods of Using Isoamylases
/ NUMBER OF SEQUENCES: 11
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/09323
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/281902
/ FILING DATE: 28-JUL-1994
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 355 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ PUBLICATION INFORMATION:
/ DOCUMENT NUMBER: WO 91/19806
/ FILING DATE: 07-JUN-1991
/ PUBLICATION DATE: 26-DEC-1991
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Job time : 79.8932 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: April 2, 2006, 00:58:46 ; Search time 264.573 Seconds  
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Database :

Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	240.5	88.7	297	US-10-487-901-7209
5	240.5	88.7	377	US-10-487-901-3504
6	240.5	88.7	489	US-10-487-901-3503
7	240.5	88.7	504	US-10-487-901-7207
8	240.5	88.7	174	US-09-854-286-15
9	240.5	88.7	204	US-09-839-477-3
10	240.5	88.7	204	US-10-758-064-3
11	240.5	88.7	297	US-10-487-901-7209
12	240.5	88.7	377	US-10-487-901-3504
13	240.5	88.7	489	US-10-487-901-3503
14	240.5	88.7	504	US-10-487-901-7207
15	240.5	88.7	174	US-09-854-286-15
16	240.5	88.7	204	US-09-839-477-3
17	240.5	88.7	204	US-10-758-064-3
18	240.5	88.7	297	US-10-487-901-7209
19	240.5	88.7	377	US-10-487-901-3504
20	240.5	88.7	489	US-10-487-901-3503
21	240.5	88.7	504	US-10-487-901-7207
22	240.5	88.7	174	US-09-854-286-15
23	240.5	88.7	204	US-09-839-477-3
24	240.5	88.7	204	US-10-758-064-3
25	240.5	88.7	297	US-10-487-901-7209
26	240.5	88.7	377	US-10-487-901-3504
27	240.5	88.7	489	US-10-487-901-3503
28	240.5	88.7	504	US-10-487-901-7207
29	240.5	88.7	174	US-09-854-286-15
30	240.5	88.7	204	US-09-839-477-3
31	240.5	88.7	204	US-10-758-064-3
32	240.5	88.7	297	US-10-487-901-7209
33	240.5	88.7	377	US-10-487-901-3504
34	240.5	88.7	489	US-10-487-901-3503
35	240.5	88.7	504	US-10-487-901-7207
36	240.5	88.7	174	US-09-854-286-15
37	240.5	88.7	204	US-09-839-477-3
38	240.5	88.7	204	US-10-758-064-3
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41	240.5	88.7	489	US-10-487-901-3503
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49	240.5	88.7	504	US-10-487-901-7207
50	240.5	88.7	174	US-09-854-286-15
51	240.5	88.7	204	US-09-839-477-3
52	240.5	88.7	204	US-10-758-064-3
53	240.5	88.7	297	US-10-487-901-7209
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55	240.5	88.7	489	US-10-487-901-3503
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62	240.5	88.7	489	US-10-487-901-3503
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65	240.5	88.7	204	US-09-839-477-3
66	240.5	88.7	204	US-10-758-064-3
67	240.5	88.7	297	US-10-487-901-7209
68	240.5	88.7	377	US-10-487-901-3504
69	240.5	88.7	489	US-10-487-901-3503
70	240.5	88.7	504	US-10-487-901-7207
71	240.5	88.7	174	US-09-854-286-15
72	240.5	88.7	204	US-09-839-477-3
73	240.5	88.7	204	US-10-758-064-3
74	240.5	88.7	297	US-10-487-901-7209
75	240.5	88.7	377	US-10-487-901-3504
76	240.5	88.7	489	US-10-487-901-3503
77	240.5	88.7	504	US-10-487-901-7207
78	240.5	88.7	174	US-09-854-286-15
79	240.5	88.7	204	US-09-839-477-3
80	240.5	88.7	204	US-10-758-064-3

Sequence 5765, Ap  
Sequence 1704, Ap  
Sequence 5043, Ap  
Sequence 7208, Ap  
Sequence 3, Appli  
Sequence 7, Appli  
Sequence 16, Appl  
Sequence 16, Appl  
Sequence 7, Appli  
Sequence 33, Appl  
Sequence 1703, Ap  
Sequence 5044, Ap  
Sequence 1713, Ap  
Sequence 5045, Ap  
Sequence 5766, Ap  
Sequence 1716, Ap  
Sequence 5764, Ap  
Sequence 5028, Ap  
Sequence 1176, Ap  
Sequence 55, Appl  
Sequence 54, Appl  
Sequence 202, App  
Sequence 918, App  
Sequence 41, Appl  
Sequence 5042, Ap  
Sequence 85509, A  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 3, Appli  
Sequence 31, Appl  
Sequence 182, App  
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Sequence 1173, Ap  
Sequence 306, App  
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Sequence 214, App  
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Sequence 351, App  
Sequence 220, App  
Sequence 348, App  
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Sequence 364, App  
Sequence 297, App  
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Sequence 1004, Ap  
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Sequence 971, App  
Sequence 329, App

81	190	70.1	481	5	US-10-062-727-267	Sequence 267, App
82	190	70.1	764	9	US-10-487-901-4119	Sequence 4119, App
83	188	69.4	215	5	US-10-062-727-302	Sequence 302, App
84	188	69.4	424	9	US-10-487-901-1710	Sequence 1710, App
85	188	69.4	424	9	US-10-487-901-5032	Sequence 5032, App
86	188	69.4	450	5	US-10-062-727-211	Sequence 211, App
87	188	69.4	1299	9	US-10-487-901-1691	Sequence 1691, App
88	185	68.3	629	9	US-10-487-901-225	Sequence 225, App
89	184.5	68.1	768	8	US-10-739-930-1358	Sequence 1358, App
90	184	67.9	479	5	US-10-062-727-253	Sequence 253, App
91	183.5	67.7	180	9	US-10-487-901-88	Sequence 88, App
92	181.5	67.0	174	5	US-10-213-791-14	Sequence 14, App
93	181.5	67.0	174	7	US-10-602-395-29	Sequence 29, App
94	181.5	67.0	178	6	US-10-198-478-7	Sequence 7, App
95	181.5	67.0	237	5	US-10-214-932-31	Sequence 31, App
96	181.5	67.0	264	5	US-10-138-927-71	Sequence 71, App
97	181.5	67.0	264	5	US-10-138-927-73	Sequence 73, App
98	181.5	67.0	264	5	US-10-213-791-9	Sequence 9, App
99	181.5	67.0	264	6	US-10-430-011-71	Sequence 71, App
100	181.5	67.0	264	6	US-10-430-011-71	Sequence 71, App
101	181.5	67.0	264	7	US-10-602-395-27	Sequence 27, App
102	181.5	67.0	268	6	US-10-198-478-5	Sequence 5, App
103	181.5	67.0	370	3	US-09-770-791-365	Sequence 365, App
104	181.5	67.0	696	5	US-10-213-791-11	Sequence 11, App
c 105	181.5	67.0	785	3	US-09-770-445-862	Sequence 862, App
c 106	181.5	67.0	1630	5	US-10-213-791-23	Sequence 23, App
c 107	181.5	67.0	5560	8	US-10-849-939-5	Sequence 5, App
108	181.5	67.0	10249	6	US-10-198-478-14	Sequence 14, App
109	181.5	67.0	10339	6	US-10-198-478-13	Sequence 13, App
110	181.5	67.0	10846	3	US-09-923-109-5	Sequence 5, App
111	181.5	67.0	10846	7	US-10-164-204-5	Sequence 5, App
112	181.5	67.0	10846	6	US-10-705-430-5	Sequence 5, App
113	181.5	67.0	20119	6	US-10-148-907A-35	Sequence 35, App
114	181	66.8	231	5	US-10-062-727-260	Sequence 260, App
115	181	66.8	244	5	US-10-062-727-304	Sequence 304, App
116	178.5	65.9	272	3	US-09-987-899-661	Sequence 661, App
117	178.5	65.9	295	3	US-09-987-899-842	Sequence 842, App
118	176.5	65.1	388	3	US-09-987-899-814	Sequence 814, App
119	175.5	64.8	236	3	US-09-987-899-653	Sequence 653, App
120	174.5	64.4	213	3	US-09-987-899-643	Sequence 643, App
121	174.5	64.4	217	3	US-09-987-899-652	Sequence 652, App
122	174.5	64.4	220	3	US-09-987-899-606	Sequence 606, App
123	174.5	64.4	220	3	US-09-987-899-621	Sequence 621, App
124	174.5	64.4	221	3	US-09-987-899-658	Sequence 658, App
125	174.5	64.4	223	3	US-09-987-899-613	Sequence 613, App
126	174.5	64.4	228	3	US-09-987-899-604	Sequence 604, App
127	174.5	64.4	228	3	US-09-987-899-622	Sequence 622, App
128	174.5	64.4	229	3	US-09-987-899-599	Sequence 599, App
129	174.5	64.4	230	3	US-09-987-899-605	Sequence 605, App
130	174.5	64.4	233	3	US-09-987-899-584	Sequence 584, App
131	174.5	64.4	235	3	US-09-987-899-603	Sequence 603, App
132	174.5	64.4	237	3	US-09-987-899-642	Sequence 642, App
133	174.5	64.4	238	3	US-09-987-899-579	Sequence 579, App
134	174.5	64.4	239	3	US-09-987-899-526	Sequence 526, App
135	174.5	64.4	239	3	US-09-987-899-560	Sequence 560, App
136	174.5	64.4	240	3	US-09-987-899-497	Sequence 497, App
137	174.5	64.4	240	3	US-09-987-899-607	Sequence 607, App
138	174.5	64.4	241	3	US-09-987-899-522	Sequence 522, App
139	174.5	64.4	241	3	US-09-987-899-539	Sequence 539, App
140	174.5	64.4	241	3	US-09-987-899-551	Sequence 551, App
141	174.5	64.4	242	3	US-09-987-899-485	Sequence 485, App
142	174.5	64.4	242	3	US-09-987-899-500	Sequence 500, App
143	174.5	64.4	243	3	US-09-987-899-486	Sequence 486, App
144	174.5	64.4	243	3	US-09-987-899-499	Sequence 499, App
145	174.5	64.4	244	3	US-09-987-899-467	Sequence 467, App
146	174.5	64.4	244	3	US-09-987-899-530	Sequence 530, App
147	174.5	64.4	245	3	US-09-987-899-525	Sequence 525, App
148	174.5	64.4	245	3	US-09-987-899-573	Sequence 573, App
149	174.5	64.4	245	3	US-09-987-899-574	Sequence 574, App
150	174.5	64.4	245	3	US-09-987-899-647	Sequence 647, App

ALIGNMENTS

RESULT 1		US-09-854-286-15		; Sequence 15, Application US/09854286	
		; Patent No. US20020178467A1		; GENERAL INFORMATION:	
		; APPLICANT: Monsanto Technology LLC		; APPLICANT: Dehesh, Katayoon	
		; TITLE OF INVENTION: Plastid Transit Peptide Sequences for Efficient Plastid Targeting		; FILE REFERENCE: US 60/203,618 38-77(15378)	
		; CURRENT APPLICATION NUMBER: US/09/854,286		; CURRENT FILING DATE: 2001-05-11	
		; PRIOR APPLICATION NUMBER: US 60/203,618		; PRIOR FILING DATE: 2000-05-12	
		; NUMBER OF SEQ ID NOS: 30		; SOFTWARE: PatentIn version 3.0	
		; SEQ ID NO 15		; LENGTH: 174	
		; TYPE: DNA		; ORGANISM: Pisum sativum	
		; FEATURE:		; NAME/KEY: CDS	
		; LOCATION: (1) .. (174)		US-09-854-286-15	
Alignment Scores:		7.99e-28		Length: 174	
Pred. No.:		240.50		Matches: 52	
Percent Similarity:		96.5%		Conservative: 3	
Best Local Similarity:		91.2%		Mismatches: 1	
Query Match:		88.7%		Indels: 1	
DB:		3		Gaps: 1	
US-10-628-525A-33 (1-56) x US-09-854-286-15 (1-174)					
QY	1	MetAlaSerSerMetLeuSerSerAlaValAlaValAlaThrArgThrAsnProAlaGlnAla	20		
Db	1	ATGGCTTCTCAGTCTTCTCTGCGAGCAGTTCGCCCGCAGCAATGTTGCTCAGCT	60		
QY	21	SerMetValAlaProPheThrGlyLeuIysSerAlaAla---PheProValSerArgLys	39		
Db	61	AACATGGTTGCACCTTTTCACCTGGCCTTAAGTCAGCTGCCTCCTGTTTCAAGGAAG	120		
QY	40	GlnAsnLeuAppIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56		
Db	121	CAAAACCTTGACATCACCTTCATTGCCAGCAACGGCGAAGAGTGCAATGC	171		
RESULT 2		US-09-839-477-3		; Sequence 3, Application US/09839477	
		; Publication No. US20030167523A1		; GENERAL INFORMATION:	
		; APPLICANT: Shorrosh, Basil S.		; APPLICANT: DeBonte, Lorin R.	
		; TITLE OF INVENTION: PLANTS CONTAINING A CYTOSOLIC ACETYL		; FILE REFERENCE: 07148-094001	
		; CURRENT APPLICATION NUMBER: US/09/839,477		; CURRENT FILING DATE: 2001-04-20	
		; PRIOR APPLICATION NUMBER: US 60/198,794		; PRIOR FILING DATE: 2000-04-20	
		; NUMBER OF SEQ ID NOS: 12		; SOFTWARE: FastSeq for Windows Version 4.0	
		; SEQ ID NO 3		; LENGTH: 204	
		; TYPE: DNA		; ORGANISM: Nicotiana tabacum	
		; FEATURE:		; NAME/KEY: CDS	
		; LOCATION: (1) ... (204)		US-09-839-477-3	
Alignment Scores:					

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Pred. No.: 9,87e-28 Length: 204
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 3 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-839-477-3 (1-204)

Qy 1 MetAlaSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 1 ATGGCTTCCTCAGTCTTCTCTGACGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60

Qy 21 SerMetValAlaProPheThrGlyLeuYsSerAlaAla---PheProValSerArgLys 39
Db 61 AACATGGTTGCACCTTTTCACTGGGCTTAAGTCAGCTGCCTCATTTCCCTGTTTCAAGGAAG 120

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 3
US-10-758-064-3
; Sequence 3, Application US/10758064
; Publication No. US20040128718A1
; GENERAL INFORMATION:
; APPLICANT: Shorosh, Basil S.
; APPLICANT: DeBonte, Lorin R.
; TITLE OF INVENTION: PLANTS CONTAINING A CYTOSOLIC ACETYL
; FILE REFERENCE: 07148-094001
; CURRENT APPLICATION NUMBER: US/10758,064
; PRIOR FILING DATE: 2004-01-15
; PRIOR FILING DATE: 2001-04-20
; PRIOR FILING DATE: 2001-04-20
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(204)
US-10-758-064-3

Alignment Scores:
Pred. No.: 9,87e-28 Length: 204
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-758-064-3 (1-204)

Qy 1 MetAlaSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 1 ATGGCTTCCTCAGTCTTCTCTGACGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 60

Qy 21 SerMetValAlaProPheThrGlyLeuYsSerAlaAla---PheProValSerArgLys 39
Db 61 AACATGGTTGCACCTTTTCACTGGGCTTAAGTCAGCTGCCTCATTTCCCTGTTTCAAGGAAG 120

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 171

RESULT 4
US-10-487-901-7209
; Sequence 7209, Application US/10487901
```

```
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7209
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-7209

Alignment Scores:
Pred. No.: 1,62e-27 Length: 297
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 9 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-7209 (1-297)

Qy 1 MetAlaSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 97 ATGGCTTCCTCAGTCTTCTCTGACGAGTGGCCACCGCAGCAATGTTGCTCAAGCT 156

Qy 21 SerMetValAlaProPheThrGlyLeuYsSerAlaAla---PheProValSerArgLys 39
Db 157 AACATGGTTGCACCTTTTCACTGGGCTTAAGTCAGCTGCCTCATTTCCCTGTTTCAAGGAAG 216

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 217 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 267

RESULT 5
US-10-487-901-3504
; Sequence 3504, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3504
; LENGTH: 377
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; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5765
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-5765

Alignment Scores:
Pred. No.: 5.21e-27 Length: 718
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-5765 (1-718)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 45 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 104
Qy 21 SerMetValAlaProPheThrGlyLeuLeuSerAlaAla---PheProValSerArgLys 39
Db 105 AACATGTTGCACCTTTCCTGCTTAAAGTCAGTCGCTGCTTCCTGTTTCAAGGAAG 164
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 165 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 215

RESULT 9
US-10-487-901-1704
; Sequence 1704, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1704
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-1704

Alignment Scores:
Pred. No.: 5.38e-27 Length: 736
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-1704 (1-736)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 63 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 122
Qy 21 SerMetValAlaProPheThrGlyLeuLeuSerAlaAla---PheProValSerArgLys 39
Db 123 AACATGTTGCACCTTTCCTGCTTAAAGTCAGTCGCTGCTTCCTGTTTCAAGGAAG 182
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 183 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 233

RESULT 11
US-10-487-901-7208
; Sequence 7208, Application US/10487901
; Publication No. US20050091708A1
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Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-1704 (1-736)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 63 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 122
Qy 21 SerMetValAlaProPheThrGlyLeuLeuSerAlaAla---PheProValSerArgLys 39
Db 123 AACATGTTGCACCTTTCCTGCTTAAAGTCAGTCGCTGCTTCCTGTTTCAAGGAAG 182
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 183 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 233
```

```

RESULT 10
US-10-487-901-5043
; Sequence 5043, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5043
; LENGTH: 736
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-5043

Alignment Scores:
Pred. No.: 5.38e-27 Length: 736
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-5043 (1-736)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 63 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 122
Qy 21 SerMetValAlaProPheThrGlyLeuLeuSerAlaAla---PheProValSerArgLys 39
Db 123 AACATGTTGCACCTTTCCTGCTTAAAGTCAGTCGCTGCTTCCTGTTTCAAGGAAG 182
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 183 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAGAGTGCAATGC 233

RESULT 11
US-10-487-901-7208
; Sequence 7208, Application US/10487901
; Publication No. US20050091708A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Lartinus, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; FILE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7208
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-487-901-7208

Alignment Scores:
Pred. No.: 1,97e-26 Length: 668
Score: 236.50 Matches: 51
Percent Similarity: 94.7% Conservative: 3
Best Local Similarity: 89.5% Mismatches: 2
Query Match: 87.3% Indels: 1
DB: 9 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-7208 (1-668)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 50 ATGGCGGGCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 109
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 110 AACATGGTTGCACCTTTTCACAGGCTCTTAAGTCTGCTCCTCATTCCTCTGTTTCAAGAAG 169
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
Db 170 CAAAACCTTGACATCATTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 220

RESULT 12
US-10-165-420-3
; Sequence 3, Application US/10165420
; Publication No. US20030084482A1
; GENERAL INFORMATION:
; APPLICANT: HALL, GERALD
; APPLICANT: BASCOMB, NEWELL
; APPLICANT: BOSSIE, MARK
; FILE OF INVENTION: PRODUCTION OF PROTEINS IN PLANTS
; FILE REFERENCE: 57117 (71758)
; CURRENT APPLICATION NUMBER: US/10/165,420
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/297,103
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 169
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(167)
; US-10-165-420-3

```

```

Alignment Scores:
Pred. No.: 1,14e-25 Length: 169
Score: 226.50 Matches: 50
Percent Similarity: 96.4% Conservative: 3
Best Local Similarity: 90.9% Mismatches: 1
Query Match: 83.1% Indels: 1
DB: 5 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-165-420-3 (1-169)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 3 ATGGCTTCTCAGTCTTCTTCTCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 62
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 63 AACATGGTTGCACCTTTTCACAGGCTCTTAAGTCTGCTCCTCATTCCTCTGTTTCAAGAAG 122
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgVal 54
Db 123 CAAAACCTTGACATCATTCCATTGCCAGCAACGGCGGAAGAGTG 167

RESULT 13
US-09-855-341-7
; Sequence 7, Application US/09855341
; Patent No. US2002002715A1
; GENERAL INFORMATION:
; APPLICANT: VIITANEN, PAUL V.
; APPLICANT: MEYER, KNUD
; APPLICANT: VAN DYK, DREW
; TITLE OF INVENTION: HIGH LEVEL PRODUCTION OF P-HYDROXYBENZOIC ACID
; TITLE OF INVENTION: IN GREEN PLANTS
; FILE REFERENCE: BC1015 US NA
; CURRENT APPLICATION NUMBER: US/09/855,341
; CURRENT FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: MICROSOFT OFFICE 97
; SEQ ID NO 7
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic CPL
; US-09-855-341-7

Alignment Scores:
Pred. No.: 2,11e-24 Length: 684
Score: 223.50 Matches: 47
Percent Similarity: 93.0% Conservative: 6
Best Local Similarity: 82.5% Mismatches: 3
Query Match: 82.5% Indels: 1
DB: 3 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-855-341-7 (1-684)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 1 ATGGCTTCTCAGTCTTCTTCTCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 61 AGCATGGTTGCACCTTTTCACAGGCTCTCAAAATCTTCAGCCACTTCCTCTGTTTCAAGAAG 120
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAenGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCATTCCATTGCCAGCAATGTTGGAAGAGTTAGTCGC 171

RESULT 14
US-09-896-866B-16
; Sequence 16, Application US/09896866B
; Patent No. US20020151002A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Dennis

```

```
; APPLICANT: Meyer, Knut
; APPLICANT: Viitanen, Paul
; TITLE OF INVENTION: Sinapoylglucose:Malate Sinapoyltransferase Form Malate Conjugates
; FILE OF INVENTION: Benzoic Acid Glucosides
; FILE REFERENCE: BC1034 US NA
; CURRENT APPLICATION NUMBER: US/09/896,866B
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/216,615
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: open reading frame of the chloroplast-targeted CPL fusion protein
US-09-896-866B-16

Alignment Scores:
Pred. No.: 2,11e-24 Length: 684
Score: 223.50 Matches: 47
Percent Similarity: 93.0% Conservative: 6
Best Local Similarity: 82.5% Mismatches: 3
Query Match: 82.5% Indels: 1
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-896-866B-16 (1-684)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20
Db 1 ATGGCTTCCTCTGTCATTTCTTCAGCAGCTGTTGCCACAGCAGCAATGTTACACAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39
Db 61 AGCATGGTTGCACCTTTCACCTGCTCAATCTTCAGCCACTTTCCTCTGTACAAAGAAG 120
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCATCTTCATTGCTAGCAATGGTGGGAAGAGTTAGCTGC 171

RESULT 15
US-10-359-369-41
; Sequence 41, Application US/10359369
; Publication No. US20030215927A1
; GENERAL INFORMATION:
; APPLICANT: E. I. duPont de Nemours and Company, Inc.
; APPLICANT: Viitanen, Paul
; APPLICANT: Meyer, Knut
; APPLICANT: Van Dyk, Drew
; TITLE OF INVENTION: UDP-Glucosyltransferases
; FILE REFERENCE: CL1821 US NA
; CURRENT APPLICATION NUMBER: US/10/359,369
; CURRENT FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 60/355,511
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 41
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
US-10-359-369-41

Alignment Scores:
Pred. No.: 2,11e-24 Length: 684
Score: 223.50 Matches: 47
Percent Similarity: 93.0% Conservative: 6
Best Local Similarity: 82.5% Mismatches: 3
```

```
Query Match: 82.5% Indels: 1
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-359-369-41 (1-684)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20
Db 1 ATGGCTTCCTCTGTCATTTCTTCAGCAGCTGTTGCCACAGCAGCAATGTTACACAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39
Db 61 AGCATGGTTGCACCTTTCACCTGCTCAATCTTCAGCCACTTTCCTCTGTACAAAGAAG 120
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCATCTTCATTGCTAGCAATGGTGGGAAGAGTTAGCTGC 171

RESULT 16
US-10-699-050-16
; Sequence 16, Application US/10699050
; Publication No. US20040142437A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Dennis
; APPLICANT: Meyer, Knut
; APPLICANT: Viitanen, Paul
; TITLE OF INVENTION: Sinapoylglucose:Malate Sinapoyltransferase Form Malate Conjugates
; FILE REFERENCE: BC1034 US NA
; CURRENT APPLICATION NUMBER: US/10/699,050
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US/09/896,866B
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/216,615
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: open reading frame of the chloroplast-targeted CPL fusion protein
US-10-699-050-16

Alignment Scores:
Pred. No.: 2,11e-24 Length: 684
Score: 223.50 Matches: 47
Percent Similarity: 93.0% Conservative: 6
Best Local Similarity: 82.5% Mismatches: 3
Query Match: 82.5% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-699-050-16 (1-684)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrArgProAlaGlnAla 20
Db 1 ATGGCTTCCTCTGTCATTTCTTCAGCAGCTGTTGCCACAGCAGCAATGTTACACAAGCT 60
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAala---PheProValSerArgLys 39
Db 61 AGCATGGTTGCACCTTTCACCTGCTCAATCTTCAGCCACTTTCCTCTGTACAAAGAAG 120
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 121 CAAAACCTTGACATCATCTTCATTGCTAGCAATGGTGGGAAGAGTTAGCTGC 171

RESULT 17
US-10-718-311-7
; Sequence 7, Application US/10718311
; Publication No. US20040143867A1
; GENERAL INFORMATION:
; APPLICANT: VIITANEN, PAUL V.
```



Pred. No.:	1.5e-23	Length:	693
Score:	218.00	Matches:	49
Percent Similarity:	91.4%	Conservative:	4
Best Local Similarity:	84.5%	Mismatches:	3
Query Match:	80.4%	Indels:	2
DB:	9	Gaps:	2

US-10-628-525A-33 (1-56) x US-10-487-901-1713 (1-683)

Qy	1	MetAlaSerSerMetLeuSerSer	---AlaAlaValAlaThrArgThrAsnProAlaGln	19
Db	40	ATGGCTTCCTCTGTGATTTCTTCAGCTGTGCGGTGGCCACGGCGCTAAATGCTGCTCAA	99	
Qy	20	AlaSerMetValAlaProPheThrGlyLeuIysSerAla	---AlaPheProValSerArg	38
Db	100	GCACGACATGTTGCACCCCTTCACCTGGCCCTCAAAATGTCTTCCTTCCTCCCTGTTACCAGA	151	
Qy	39	LysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56	
Db	160	AAACAAACCTTGACATTACATCCATTGCTAGCAATGTTGGAGAGATCCAAATGC	213	

RESULT 22

US-10-487-901-5045

; Sequence 5045, Application US/10487901

; Publication No. US20050091708A1

GENERAL INFORMATION:

; APPLICANT: Oreido, Jeremiah Vincent

; APPLICANT: McCrery, David

; APPLICANT: Pell, Randy

; APPLICANT: Miller, Barbara

; APPLICANT: Weglarz, Thaddeus

; APPLICANT: Gachotte, Daniel

; APPLICANT: Blakeslee, Beth

; APPLICANT: Larrinua, Ignacio

; APPLICANT: Reddy, Avutu

; APPLICANT: Shukla, Vipula

; APPLICANT: Crosley, Rodney

; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic

; FILE REFERENCE: DOW-08552

; CURRENT APPLICATION NUMBER: US/10/487, 901

; CURRENT FILING DATE: 2004-02-26

; NUMBER OF SEQ ID NOS: 7560

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5045

; LENGTH: 737

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-487-901-5045

Alignment Scores:			
Pred. No.:	1.66e-23	Length:	737
Score:	218.00	Matches:	49
Percent Similarity:	91.4%	Conservative:	4
Best Local Similarity:	84.5%	Mismatches:	3
Query Match:	80.4%	Indels:	2
DB:	9	Gaps:	2

US-10-628-525A-33 (1-56) x US-10-487-901-5045 (1-737)

Qy	1	MetAlaSerSerMetLeuSerSer	---AlaAlaValAlaThrArgThrAsnProAlaGln	19
Db	40	ATGGCTTCCTCTGTGATTTCTTCAGCTGTGCGGTGGCCACGGCGCTAAATGCTGCTCAA	99	
Qy	20	AlaSerMetValAlaProPheThrGlyLeuIysSerAla	---AlaPheProValSerArg	38
Db	100	GCACGACATGTTGCACCCCTTCACCTGGCCCTCAAAATGCTTCCTTCCTCCCTGTTACCAGA	151	
Qy	39	LysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56	
Db	160	AAACAAACCTTGACATTACATCCATTGCTAGCAATGTTGGAGAGATCCAAATGC	213	



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Db 62 ATGGCTTCTCAGTTATGCTCCTCAGCAGCTGCTGTTGGACCGCGCCAAATGCTGCTCAA 121
Qy 20 AlaSerMetValAlaProPheThrGlyLeuYseAla---AlaPheProValSerArg 38
Db 122 GCCAACATGGTTGACCCCTTCACTGGGCTCAAGTCCGCTCTCTCTTCCCTGTTACCAAG 181
Qy 39 LysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 182 AAACAAACCTTGACATTACCTCCATTGCTAGCAATGGTGGAGAGATTCAATGC 235

RESULT 26
US-10-487-901-5028
; Sequence 5028, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5028
; LENGTH: 754
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-5028

Alignment Scores:
Pred. No.: 4.98e-23 Length: 754
Score: 215.00 Matches: 48
Percent Similarity: 91.4% Conservative: 5
Best Local Similarity: 82.8% Mismatches: 3
Query Match: 79.3% Indels: 2
DB: 9 Gaps: 2

US-10-628-525A-33 (1-56) x US-10-487-901-5028 (1-754)
Qy 1 MetAlaSerSerMetLeuSerSer---AlaAlaValAlaThrArgThrAsnProAlaGln 19
Db 64 ATGGCTTCTCAGTTATGCTCCTCAGCAGCTGCTGTTGGACCGCGCCAAATGCTGCTCAA 123
Qy 20 AlaSerMetValAlaProPheThrGlyLeuYseAla---AlaPheProValSerArg 38
Db 124 GCCAACATGGTTGACCCCTTCACTGGGCTCAAGTCCGCTCTCTCTTCCCTGTTACCAAG 183
Qy 39 LysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 184 AAACAAACCTTGACATTACCTCCATTGCTAGCAATGGTGGAGAGATTCAATGC 237

RESULT 27
US-09-732-627A-1176
; Sequence 1176, Application US/09732627A
; Publication No. US20040123338A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51770)B
; CURRENT APPLICATION NUMBER: US/09/732,627A
; CURRENT FILING DATE: 2000-12-08
```

```
; NUMBER OF SEQ ID NOS: 4930
; SEQ ID NO 1176
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3493-057-P1-M1-D1
US-09-732-627A-1176

Alignment Scores:
Pred. No.: 1.46e-22 Length: 385
Score: 209.50 Matches: 45
Percent Similarity: 89.8% Conservative: 8
Best Local Similarity: 76.3% Mismatches: 3
Query Match: 77.3% Indels: 3
DB: 3 Gaps: 2

US-10-628-525A-33 (1-56) x US-09-732-627A-1176 (1-385)
Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 159 ATGGCTTCTCCTCCATGATCTCATCGGCAACCATTTGCCACCGTGAACCGCTCTCTCCCGGCA 218
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuYseSer---AlaAlaPheProValSer 37
Db 219 CAGGCCAACATGGTGGCCCCCTTTCACCGGCTCAAAATCTGGCTCTGCTTTCCAGTCACC 278
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 279 AGGAGGCCAACCAACACGACATCACTTCTCTTGCAGCAACGCTGGGAGAGTGCATATGC 335

RESULT 28
US-09-910-664-55
; Sequence 55, Application US/09910664
; Publication No. US20020194646A1
; GENERAL INFORMATION:
; APPLICANT: FOGUE, Greg P.
; APPLICANT: DELLA-CIOPPA, Guy R.
; APPLICANT: WOLFE, Gerson M.
; APPLICANT: ZHENG, Wenjin
; TITLE OF INVENTION: METHODS OF CREATING DWARF PHENOTYPES IN
; FILE REFERENCE: 008010189000S01
; CURRENT APPLICATION NUMBER: US/09/910,664
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 724
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-910-664-55

Alignment Scores:
Pred. No.: 6.86e-22 Length: 724
Score: 207.50 Matches: 47
Percent Similarity: 87.7% Conservative: 3
Best Local Similarity: 82.5% Mismatches: 4
Query Match: 76.6% Indels: 3
DB: 3 Gaps: 2

US-10-628-525A-33 (1-56) x US-09-910-664-55 (1-724)
Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 43 ATGGCTTCTCTATGCTCTCTCCCGCGCTGTGGTT-----ACATCCCGGCTCAGGCC 96
Qy 21 SerMetValAlaProPheThrGlyLeuYseSer---SerAlaAlaPheProValSerArgLys 39
Db 97 ACCATGGTCGCTCCATTCAACCGGCTTGAAGTCATCGCTGCATTCGCGGTCAACCGCAG 156
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
```

Db 157 ACCAACAGGACATCATCTTCATCGCAAGCAACGGGGGAAGAGTTAGCTGC 207

## RESULT 29

US-10-333-184-54

; Sequence 54, Application US/10333184

; Publication No. US20040088762A1

; GENERAL INFORMATION:

; APPLICANT: Reddy, Avutu

; APPLICANT: Larrinua, Ignacio

; APPLICANT: Skokut, Thomas

; APPLICANT: Smith, Doug

; APPLICANT: Hu, Zihua

; APPLICANT: Ruegger, Max

; APPLICANT: Shukla, Vipula

; APPLICANT: Bauer, Teresa

; APPLICANT: Weglarz, Ted

; APPLICANT: Blakslee, Beth

; APPLICANT: Oriedo, Jeremiah

; APPLICANT: Savickas, Philip

; APPLICANT: McCreery, David

; APPLICANT: Miller, Barbara

; APPLICANT: della-Cioppa, Gregory

; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Dwarfism Phenotype

; FILE REFERENCE: DOM-04681

; CURRENT APPLICATION NUMBER: US/10/333,184

; PRIOR FILING DATE: 2003-10-10

; PRIOR APPLICATION NUMBER: 60/219,809

; PRIOR FILING DATE: 2000-07-20

; NUMBER OF SEQ ID NOS: 571

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 54

; LENGTH: 724

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-10-333-184-54

## Alignment Scores:

Pred. No.: 6.86e-22 Length: 724

Score: 207.50 Matches: 47

Percent Similarity: 87.7% Conservative: 3

Best Local Similarity: 82.5% Mismatches: 4

Query Match: 76.6% Indels: 3

DB: 7 Gaps: 2

US-10-628-525A-33 (1-56) x US-10-333-184-54 (1-724)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

Db 43 ATGGCTTCCTCTATGCTCTCTCCCGCGCTGTGGTT-----ACATCCCGGCTCAGGCC 96

QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39

Db 97 ACCATGGTCGCTCCATTACCGGCTTGAAGTCATCCGCTGCATTCGCGTCAACCGCAAG 156

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 157 ACCAACAGGACATCATCTTCATCGCAAGCAACGGGGGAAGAGTTAGCTGC 207

## RESULT 30

US-10-333-184-202

; Sequence 202, Application US/10333184

; Publication No. US20040088762A1

; GENERAL INFORMATION:

; APPLICANT: Reddy, Avutu

; APPLICANT: Larrinua, Ignacio

; APPLICANT: Skokut, Thomas

; APPLICANT: Smith, Doug

; APPLICANT: Hu, Zihua

; APPLICANT: Ruegger, Max

; APPLICANT: Shukla, Vipula

; APPLICANT: Bauer, Teresa

; APPLICANT: Weglarz, Ted

; APPLICANT: Blakslee, Beth

; APPLICANT: Oriedo, Jeremiah  
; APPLICANT: Savickas, Philip  
; APPLICANT: McCreery, David  
; APPLICANT: Miller, Barbara  
; APPLICANT: della-Cioppa, Gregory  
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Dwarfism Phenotype  
; FILE REFERENCE: DOM-04681  
; CURRENT APPLICATION NUMBER: US/10/333,184  
; CURRENT FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: 60/219,809  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 571  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 202  
; LENGTH: 726  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-333-184-202

## Alignment Scores:

Pred. No.: 6.89e-22 Length: 726

Score: 207.50 Matches: 47

Percent Similarity: 87.7% Conservative: 3

Best Local Similarity: 82.5% Mismatches: 4

Query Match: 76.6% Indels: 3

DB: 7 Gaps: 2

US-10-628-525A-33 (1-56) x US-10-333-184-202 (1-726)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20

Db 45 ATGGCTTCCTCTATGCTCTCTCCCGCGCTGTGGTT-----ACATCCCGGCTCAGGCC 98

QY 21 SerMetValAlaProPheThrGlyLeuLys---SerAlaAlaPheProValSerArgLys 39

Db 99 ACCATGGTCGCTCCATTACCGGCTTGAAGTCATCCGCTGCATTCGCGTCAACCGCAAG 158

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

Db 159 ACCAACAGGACATCATCTTCATCGCAAGCAACGGGGGAAGAGTTAGCTGC 209

Search completed: April 2, 2006, 02:04:07

Job time : 268.573 secs



GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 01:09:48 ; Search time 174.864 Seconds  
(without alignments)  
1278.753 Million cell updates/sec

Title: us-10-628-525a-33

Perfect score: 271

Sequence: 1 MASSMLSSAAVATRTNPAQA.....SRQNLDITSIAHGGRVQC 56

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-Q=/abs/ABSWEB.spool/US10628525/runat\_31032006\_095139\_17270/app\_query.fasta.1  
-DB=Published Applications NA.New -OPMT=fastcap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62  
-TRANS=human40.cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=30 -MODS=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abs05h  
-USER=US10628525 @CGN 1.1 2249 @runat\_31032006\_095139\_17270 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -PGAPOP=6 -PGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.New:\*  
1: /SIDSS/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
2: /SIDSS/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /SIDSS/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /SIDSS/ptodata/2/pubpna/PTC\_NEW\_PUB.seq.\*  
5: /SIDSS/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /SIDSS/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
7: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
8: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
9: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
10: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
11: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
12: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
13: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
14: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
15: /SIDSS/ptodata/2/pubpna/US16\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	181.5	67.0	264	8	US-10-840-688-19
2	91	33.6	416	14	US-11-192-801-25

Sequence 30, Appl	416	33.6	91	14	US-11-192-801-30	Sequence 17, Appl
Sequence 17, Appl	3450	33.6	91	14	US-11-192-801-17	Sequence 36, Appl
Sequence 36, Appl	3455	33.6	91	14	US-11-192-801-36	Sequence 13, Appl
Sequence 13, Appl	4149	33.6	91	14	US-11-192-801-13	Sequence 72126, A
Sequence 72126, A	484	24.2	65.5	9	US-10-301-480-72126	Sequence 685535, A
Sequence 685535, A	484	24.2	65.5	10	US-10-301-480-685535	Sequence 61428, A
Sequence 61428, A	201	23.8	64.5	8	US-10-995-561-61428	Sequence 69122, A
Sequence 69122, A	201	23.8	64.5	8	US-10-995-561-69122	Sequence 13406, A
Sequence 13406, A	23803	23.8	64.5	8	US-10-995-561-13406	Sequence 13353, A
Sequence 13353, A	26096	23.8	64.5	8	US-10-995-561-13353	Sequence 9, Appl
Sequence 9, Appl	2024	23.4	63.5	14	US-11-079-122-9	Sequence 10, Appl
Sequence 10, Appl	2024	23.4	63.5	14	US-11-079-122-10	Sequence 14, Appl
Sequence 14, Appl	2024	23.4	63.5	14	US-11-079-122-14	Sequence 46879, A
Sequence 46879, A	1863	23.2	63	8	US-10-750-185-46879	Sequence 46879, A
Sequence 46879, A	1863	23.2	63	8	US-10-750-185-46879	Sequence 47150, A
Sequence 47150, A	573	23.1	62.5	18	US-09-925-065A-47150	Sequence 490520, A
Sequence 490520, A	573	23.1	62.5	18	US-09-925-065A-47150	Sequence 1103929, A
Sequence 1103929, A	589	23.1	62.5	10	US-10-301-480-490520	Sequence 77417, A
Sequence 77417, A	589	23.1	62.5	10	US-10-301-480-1103929	Sequence 941364, A
Sequence 941364, A	885	23.1	62.5	9	US-10-932-182A-77417	Sequence 933859, A
Sequence 933859, A	885	23.1	62.5	9	US-10-932-182A-77417	Sequence 933860, A
Sequence 933860, A	557	22.7	61.5	6	US-09-925-065A-461364	Sequence 921611, A
Sequence 921611, A	557	22.7	61.5	6	US-09-925-065A-461364	Sequence 483931, A
Sequence 483931, A	692	22.7	61.5	6	US-09-925-065A-933859	Sequence 75783, A
Sequence 75783, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 75783, A
Sequence 75783, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 577229, A
Sequence 577229, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 1190638, A
Sequence 1190638, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 94717, A
Sequence 94717, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 94718, A
Sequence 94718, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 94719, A
Sequence 94719, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 708126, A
Sequence 708126, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 708127, A
Sequence 708127, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 708128, A
Sequence 708128, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 944984, A
Sequence 944984, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 34432, A
Sequence 34432, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 1, Appl
Sequence 1, Appl	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 800643, A
Sequence 800643, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 37736, A
Sequence 37736, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 37737, A
Sequence 37737, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 37738, A
Sequence 37738, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 37739, A
Sequence 37739, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 951145, A
Sequence 951145, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 951146, A
Sequence 951146, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 951147, A
Sequence 951147, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 951148, A
Sequence 951148, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 259176, A
Sequence 259176, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 259177, A
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Sequence 259178, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 259179, A
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Sequence 45531, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 42328, A
Sequence 42328, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 42328, A
Sequence 42328, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 442, App
Sequence 442, App	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 442, App
Sequence 442, App	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 61429, A
Sequence 61429, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 61429, A
Sequence 61429, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 503, App
Sequence 503, App	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 410, App
Sequence 410, App	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 13386, A
Sequence 13386, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 302846, A
Sequence 302846, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 916055, A
Sequence 916055, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 216134, A
Sequence 216134, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 635611, A
Sequence 635611, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 354, App
Sequence 354, App	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 559838, A
Sequence 559838, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 1173247, A
Sequence 1173247, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 582739, A
Sequence 582739, A	692	22.7	61.5	6	US-09-925-065A-933860	Sequence 1196148, A
Sequence 1196148, A	692	22.7	61.5	6	US-09-925-065A-933860	



OTHER INFORMATION: ribulose bis-phosphate carboxylase chloroplast  
 OTHER INFORMATION: targeting peptide

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (16)..(162)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (326)..(415)  
 FEATURE:  
 NAME/KEY: intron  
 LOCATION: (163)..(325)  
 OTHER INFORMATION: I-Zm.rbcS

US-11-192-801-25

Alignment Scores:

Pred. No.: 0.148 Length: 416  
 Score: 91.00 Matches: 22  
 Percent Similarity: 64.2% Conservative: 12  
 Best Local Similarity: 41.5% Mismatches: 7  
 Query Match: 33.6% Indels: 12  
 DB: 14 Gaps: 3

US-10-628-525A-33 (1-56) x US-11-192-801-25 (1-416)

Qy 5 MetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAlaSerMetValAla 24  
 Db 31 ATGATGGCCTCGTGGCCACCGCC-----GTGCGT 60  
 Qy 25 ProPheThrGlyLeuLysSer---AlaAlaPheProValSerArgLysGlnAsnLeuAsp 43  
 Db 61 CCGTTCTGGGGCTCAAGTCCACCGCAGCTCCCGTGGCCGCGCTCTCCAGAGC 120  
 Qy 44 IleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 121 CTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

RESULT 3

US-11-192-801-30

Sequence 30, Application US/11192801  
 Publication No. US20050273882A1

GENERAL INFORMATION:

APPLICANT: Romano, Charles P.  
 TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
 FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
 CURRENT APPLICATION NUMBER: US/11/192,801  
 CURRENT FILING DATE: 2005-07-29  
 PRIOR APPLICATION NUMBER: US/10/232,665  
 PRIOR FILING DATE: 2002-08-29  
 PRIOR APPLICATION NUMBER: US/09/377,466  
 PRIOR FILING DATE: 1999-08-19  
 NUMBER OF SEQ ID NOS: 43  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 30

LENGTH: 416

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: modified  
 OTHER INFORMATION: cauliflower mosaic virus promoter AS4

US-11-192-801-30

Alignment Scores:

Pred. No.: 0.148 Length: 416  
 Score: 91.00 Matches: 22  
 Percent Similarity: 64.2% Conservative: 12  
 Best Local Similarity: 41.5% Mismatches: 7  
 Query Match: 33.6% Indels: 12  
 DB: 14 Gaps: 3

US-10-628-525A-33 (1-56) x US-11-192-801-30 (1-416)

Qy 5 MetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAlaSerMetValAla 24  
 Db 31 ATGATGGCCTCGTGGCCACCGCC-----GTGCGT 60

Db 31 ATGATGGCCTCGTGGCCACCGCC-----GTGCGT 60  
 Qy 25 ProPheThrGlyLeuLysSer---AlaAlaPheProValSerArgLysGlnAsnLeuAsp 43  
 Db 61 CCGTTCTGGGGCTCAAGTCCACCGCAGCTCCCGTGGCCGCGCTCTCCAGAGC 120  
 Qy 44 IleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
 Db 121 CTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

RESULT 4

US-11-192-801-17

Sequence 17, Application US/11192801  
 Publication No. US20050273882A1

GENERAL INFORMATION:

APPLICANT: Romano, Charles P.  
 TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
 FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
 CURRENT APPLICATION NUMBER: US/11/192,801  
 CURRENT FILING DATE: 2005-07-29  
 PRIOR APPLICATION NUMBER: US/10/232,665  
 PRIOR FILING DATE: 2002-08-29  
 PRIOR APPLICATION NUMBER: US/09/377,466  
 PRIOR FILING DATE: 1999-08-19  
 NUMBER OF SEQ ID NOS: 43  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 17

LENGTH: 3450

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: expression  
 OTHER INFORMATION: cassette

FEATURE:

NAME/KEY: promoter

LOCATION: (14)..(235)

OTHER INFORMATION: P-CaMV.AS4

FEATURE:

NAME/KEY: 5'UTR

LOCATION: (240)..(304)

OTHER INFORMATION: L-Ta.hcb1

FEATURE:

NAME/KEY: intron

LOCATION: (318)..(805)

OTHER INFORMATION: I-Ob.Act1

FEATURE:

NAME/KEY: transit peptide

LOCATION: (825)..(971)

OTHER INFORMATION: amino terminal TS-Zm.rbcS

FEATURE:

NAME/KEY: intron

LOCATION: (972)..(1134)

OTHER INFORMATION: I-Zm.rbcS

FEATURE:

NAME/KEY: transit peptide

LOCATION: (1135)..(1221)

OTHER INFORMATION: carboxy terminus TS-Zm.rbcS

FEATURE:

NAME/KEY: CDS

LOCATION: (1222)..(3180)

OTHER INFORMATION: Cry3Bb1 variant 11231mv1

FEATURE:

NAME/KEY: terminator

LOCATION: (3198)..(3431)

OTHER INFORMATION: T-Ta.hsp17

US-11-192-801-17

Alignment Scores:

Pred. No.: 1.32 Length: 3450  
 Score: 91.00 Matches: 22  
 Percent Similarity: 64.2% Conservative: 12  
 Best Local Similarity: 41.5% Mismatches: 7  
 Query Match: 33.6% Indels: 12

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US-10-628-525A-33 (1-56) x US-11-192-801-17 (1-3450)
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      |||:||||:||||:|||||
DB      840 ATGATGGCCTCGTGGCCACCGCC-----GTCGCT 869
QY      25 PropThrGlyLeuLysSer---AlaAlaPheProValSerArgLysGlnAsnLeuAsp 43
      |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      870 CCGTTCTCTGGGGCTCAAGTCCACCGCAGCTCCCGTCCCGCGCTCTCCAGAGC 929
QY      44 IleThrSerIleAlaSerAsnGlyArgValGlnCys 56
      ::|:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      930 CTCGGCAACGTC---AGCAACGCGGAGGATCCGGTGC 965

RESULT 5
US-11-192-801-36
; Sequence 36, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; PRIOR FILING DATE: 2005-07-29
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 3455
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: P.CaMV.AS4
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; FEATURE:
; NAME/KEY: intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Ob.Act1
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (825)..(971)
; OTHER INFORMATION: TS-Zm.rbcS amino terminal coding sequence upstream
; FEATURE:
; NAME/KEY: intron
; LOCATION: (972)..(1134)
; OTHER INFORMATION: I-Zm.rbcS
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1135)..(1221)
; OTHER INFORMATION: TS-Zm.rbcS carboxy terminus coding sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1222)..(3180)
; OTHER INFORMATION: variant Cry3BB1 coding sequence encoding v11231
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (3198)..(3431)
; OTHER INFORMATION: T-Ta.hsp17

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US-11-192-801-36
Alignment Scores:
Pred. No.:          1.32          Length:          3455
Score:             91.00         Matches:         22
Percent Similarity: 64.2%        Conservative:    12
Best Local Similarity: 41.5%      Mismatches:      7
Query Match:       33.6%         Indels:          12
DB:                14           Gaps:             3
US-10-628-525A-33 (1-56) x US-11-192-801-36 (1-3455)
QY      5 MetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAlaSerMetValAla 24
      |||:||||:||||:|||||
DB      840 ATGATGGCCTCGTGGCCACCGCC-----GTCGCT 869
QY      25 PropThrGlyLeuLysSer---AlaAlaPheProValSerArgLysGlnAsnLeuAsp 43
      |||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      870 CCGTTCTCTGGGGCTCAAGTCCACCGCAGCTCCCGTCCCGCGCTCTCCAGAGC 929
QY      44 IleThrSerIleAlaSerAsnGlyArgValGlnCys 56
      ::|:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      930 CTCGGCAACGTC---AGCAACGCGGAGGATCCGGTGC 965

RESULT 6
US-11-192-801-13
; Sequence 13, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/11/192,801
; PRIOR FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232,665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4149
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: intron
; LOCATION: (669)..(1472)
; OTHER INFORMATION: I-Zm.Hsp70
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1489)..(1635)
; OTHER INFORMATION: amino terminal TS-Zm.rbcS
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1636)..(1798)
; OTHER INFORMATION: I-Zm.rbcS
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1799)..(1885)
; OTHER INFORMATION: carboxy terminus TS-Zm.rbcS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1885)..(3843)
; OTHER INFORMATION: Cry3Bb1 variant v11231
; FEATURE:
; NAME/KEY: terminator

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Pred. No.: 88.4 Length: 201
Score: 64.50 Matches: 21
Percent Similarity: 51.9% Conservative: 6
Best Local Similarity: 40.4% Mismatches: 17
Query Match: 23.8% Indels: 8
DB: Gaps: 2

US-10-628-525A-33 (1-56) x US-10-995-561-61428 (1-201)

QY 13 ThrArgThrAsnPro---AlaGlnAlaSerMetValAlaProPheThrGlyLeuLysSer 31
Db 46 ACCTCAGATGATCCACGCGCCTCATCTCCCAAAGTGTGGGATTCACAGCATGACCCAC 105
QY 32 AlaAlaPheProValSerArgLysGlnAsnLeuAspIleThrSerIleAla-SerAsn-- 50
Db 106 TGTGCTGCGCTGTATTCTTAACTGAACCTTTCATTACTTCTTTAGCCCAAAAACAG 165
QY 51 -----GlyGlyArgValGlnCys 56
Db 166 GCCTGCTGCATGTACAGGAGGAAGATAGCAATGT 199

RESULT 10
US-10-995-561-69122/c
; Sequence 69122, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69122
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-69122

Alignment Scores:
Pred. No.: 88.4 Length: 201
Score: 64.50 Matches: 21
Percent Similarity: 51.9% Conservative: 6
Best Local Similarity: 40.4% Mismatches: 17
Query Match: 23.8% Indels: 8
DB: Gaps: 2

US-10-628-525A-33 (1-56) x US-10-995-561-69122 (1-201)

QY 13 ThrArgThrAsnPro---AlaGlnAlaSerMetValAlaProPheThrGlyLeuLysSer 31
Db 156 ACCTCAGATGATCCACGCGCCTCATCTCCCAAAGTGTGGGATTCACAGCATGACCCAC 97
QY 32 AlaAlaPheProValSerArgLysGlnAsnLeuAspIleThrSerIleAla-SerAsn-- 50
Db 96 TGTGCTGCGCTGTATTCTTAACTGAACCTTTCATTACTTCTTTAGCCCAAAAACAG 37
QY 51 -----GlyGlyArgValGlnCys 56
Db 36 GCCTGCTGCATGTACAGGAGGAAGATAGCAATGT 3

RESULT 11
US-10-995-561-13406/c
; Sequence 13406, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559

```

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; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13406
; LENGTH: 23803
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13406

Alignment Scores:
Pred. No.: 1.23e+04 Length: 23803
Score: 64.50 Matches: 21
Percent Similarity: 51.9% Conservative: 6
Best Local Similarity: 40.4% Mismatches: 17
Query Match: 23.8% Indels: 8
DB: Gaps: 2

US-10-628-525A-33 (1-56) x US-10-995-561-13406 (1-23803)

QY 13 ThrArgThrAsnPro---AlaGlnAlaSerMetValAlaProPheThrGlyLeuLysSer 31
Db 20502 ACCTCAGATGATCCACGCGCCTCATCTCCCAAAGTGTGGGATTCACAGCATGACCCAC 20443
QY 32 AlaAlaPheProValSerArgLysGlnAsnLeuAspIleThrSerIleAla-SerAsn-- 50
Db 20442 TGTGCTGCGCTGTATTCTTAACTGAACCTTTCATTACTTCTTTAGCCCAAAAACAG 20383
QY 51 -----GlyGlyArgValGlnCys 56
Db 20382 GCCTGCTGCATGTACAGGAGGAAGATAGCAATGT 20349

RESULT 12
US-10-995-561-13353
; Sequence 13353, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13353
; LENGTH: 26096
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13353

Alignment Scores:
Pred. No.: 1.35e+04 Length: 26096
Score: 64.50 Matches: 21
Percent Similarity: 51.9% Conservative: 6
Best Local Similarity: 40.4% Mismatches: 17
Query Match: 23.8% Indels: 8
DB: Gaps: 2

US-10-628-525A-33 (1-56) x US-10-995-561-13353 (1-26096)

QY 13 ThrArgThrAsnPro---AlaGlnAlaSerMetValAlaProPheThrGlyLeuLysSer 31
Db 17808 ACCTCAGATGATCCACGCGCCTCATCTCCCAAAGTGTGGGATTCACAGCATGACCCAC 17867
QY 32 AlaAlaPheProValSerArgLysGlnAsnLeuAspIleThrSerIleAla-SerAsn-- 50
Db 17868 TGTGCTGCGCTGTATTCTTAACTGAACCTTTCATTACTTCTTTAGCCCAAAAACAG 17927
QY 51 -----GlyGlyArgValGlnCys 56
Db 17928 GCCTGCTGCATGTACAGGAGGAAGATAGCAATGT 17961

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QY 34 PheProValSerArgLysGlnAenLeuAspIleThrSerIleAlaSerAenGlyGlyArg 53  
Db 157 CTGCCAGCCTCAGCTCCCAAGGCTGGGATTACAGATGTGAGCCACCAAGCGGCCAA 98

## RESULT 19

US-10-301-480-490520  
; Sequence 490520, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 490520  
; LENGTH: 589  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-490520

Alignment Scores:  
Pred. No.: 460 Length: 589  
Score: 62.50 Matches: 19  
Percent Similarity: 36.2% Conservative: 10  
Best Local Similarity: 23.8% Mismatches: 24  
Query Match: 23.1% Indels: 27  
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-301-480-490520 (1-589)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20  
Db 253 ATGATCTCAGCTTGTCTGGAACCTCTGCCTCTGGTTCAAGAGACTCTCTCGCTCAGCC 312  
QY 21 SerMetValAlaProPheThrGly----- 28  
Db 313 TCYCAAGTAGCTGGGATTACAGGCCACCCACCATCAGCCTGGCTAAGTTTTGTATTTTAA 372  
QY 29 -----LeuLysSerAlaAla 33  
Db 373 GTAGAGATGGAGTTTGGCCACATTGGCCAGGCTGGTCTTGAACCTGCTGACCTCAAGTGAT 432  
QY 34 PheProValSerArgLysGlnAenLeuAspIleThrSerIleAlaSerAenGlyGlyArg 53  
Db 433 CTGCCAGCCTCAGCCTCCCAAGTGTGGGATTACAGATGTGAGCCACCAAGCGGCCAA 492

## RESULT 20

US-10-301-480-1103929  
; Sequence 1103929, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1103929  
; LENGTH: 589  
; TYPE: DNA

; ORGANISM: Homo sapien  
US-10-301-480-1103929  
Alignment Scores:  
Pred. No.: 460 Length: 589  
Score: 62.50 Matches: 19  
Percent Similarity: 36.2% Conservative: 10  
Best Local Similarity: 23.8% Mismatches: 24  
Query Match: 23.1% Indels: 27  
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-301-480-1103929 (1-589)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAenProAlaGlnAla 20  
Db 253 ATGATCTCAGCTTGTCTGGAACCTCTGCCTCTGGTTCAAGAGACTCTCTCGCTCAGCC 312  
QY 21 SerMetValAlaProPheThrGly----- 28  
Db 313 TCYCAAGTAGCTGGGATTACAGGCCACCCACCATCAGCCTGGCTAAGTTTTGTATTTTAA 372  
QY 29 -----LeuLysSerAlaAla 33  
Db 373 GTAGAGATGGAGTTTGGCCACATTGGCCAGGCTGGTCTTGAACCTGCTGACCTCAAGTGAT 432  
QY 34 PheProValSerArgLysGlnAenLeuAspIleThrSerIleAlaSerAenGlyGlyArg 53  
Db 433 CTGCCAGCCTCAGCCTCCCAAGTGTGGGATTACAGATGTGAGCCACCAAGCGGCCAA 492

## RESULT 21

US-10-932-182A-77417  
; Sequence 77417, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77417  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-77417

Alignment Scores:  
Pred. No.: 701 Length: 885  
Score: 62.50 Matches: 16  
Percent Similarity: 52.1% Conservative: 9  
Best Local Similarity: 33.3% Mismatches: 20  
Query Match: 23.1% Indels: 3  
DB: 9 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-932-182A-77417 (1-885)

QY 7 SerSerAlaAlaValAlaThrArgThrAenProAlaGln-----AlaSerMetVal 23  
Db 502 TCTAGCTCTGCTGTAAGCACCATTGCAAGTTCTGCTGAAGTCTCTGTCAGACTCTGTT 561  
QY 24 AlaProPheThrGlyLeuLysSerAlaAlaPheProValSerArgLysGlnAenLeuAap 43  
Db 562 GCAAGCTCTGCTAGTTTTTGGCAATACACAGCTCCAGTTCTTCTACATCTTCTATCTCA 621  
QY 44 IleThrSerIleAlaSerAenGly 51  
Db 622 GTCACTCCAGTGGTCCAAATGGT 645

RESULT 22  
US-10-932-182A-77417  
; Sequence 77417, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; NUMBER OF SEQ ID NOS: 2004-09-02  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 77417  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-77417

Alignment Scores:  
Pred. No.: 701 Length: 885  
Score: 62.50 Matches: 16  
Percent Similarity: 52.1% Conservative: 9  
Best Local Similarity: 33.3% Mismatches: 20  
Query Match: 23.1% Indels: 3  
DB: 9 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-932-182A-77417 (1-885)  
QY 7 SerSerAlaAlaValAlaThrArgThrAsnProAlaGln-----AlaSerMetVal 23  
Db 502 TCTAGCTCGCTGTAAGCACCATTGCAAGTCTCTGCGAAAGTCTGTTGCAAGCTCTGTT 561  
QY 24 AlaProPheThrGlyLeuLysSerAlaAlaPheProValSerArgLysGlnAsnLeuAsp 43  
Db 562 GCAAGCTCGTAGTTTTCGCAATACCACAGCTCCAGTTCTTCTACATCTTCTATCTCA 621  
QY 44 IleThrSerIleAlaSerHengly 51  
Db 622 GTCACTCCAGTGTGTCACAAATGTT 645

RESULT 23  
US-09-925-065A-461364/C  
; Sequence 461364, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 461364  
; LENGTH: 557  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-461364

Alignment Scores:  
Pred. No.: 569 Length: 557  
Score: 61.50 Matches: 19  
Percent Similarity: 50.0% Conservative: 6  
Best Local Similarity: 38.0% Mismatches: 21  
Query Match: 22.7% Indels: 4  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-925-065A-461364 (1-557)  
QY 6 LeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAlaSerMetValAlaPr 25  
Db 264 CTGCCTAGTGAGCTGTGAAGAAAGGCCACCATCTCCAGATGCCAAAATGGTAGCTCC 205  
QY 25 oPheThrGlyLeuLysSerAlaAlaPheProValSerArgLysGlnAsnLeuAspIle 45  
Db 204 ACTGACA-----GCTTGCCACCATGCCCTGGAAAGCCACACACACTCAATACCAG 154  
QY 45 rSerIleAlaSerAsnGlyGlyArgVal 54  
Db 153 CCCATGGAAACAGCTGGGAGGGGGGTG 126

RESULT 24  
US-09-925-065A-933859/C  
; Sequence 933859, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2001-10-24  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 933859  
; LENGTH: 692  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-933859

Alignment Scores:  
Pred. No.: 712 Length: 692  
Score: 61.50 Matches: 18  
Percent Similarity: 52.4% Conservative: 4  
Best Local Similarity: 42.9% Mismatches: 19  
Query Match: 22.7% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-925-065A-933859 (1-692)  
QY 1 MetaIaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 294 ATGGCTTCCCAACAATCTCCAGTGCCTTAATCTCTGCAATTAACCAAGTCCAAG 235  
QY 21 SerMetValAlaProPheThr---GlyLeuLysSerAlaAlaPheProValSerArgLys 39  
Db 234 TCCAAAGTCTCACCTGCACACAGCGCAAGTCCCTTCTGCTGTGAGCCTGTGTAACCAAAA 175  
QY 40 GlnAsn 41  
Db 174 GCAAAAT 169

```
RESULT 25
US-09-925-065A-933860/c
; Sequence 933860, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 933860
; LENGTH: 692
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-933860

Alignment Scores:
Pred. No.: 712          Length: 692
Score: 61.50           Matches: 18
Percent Similarity: 52.4% Conservatives: 4
Best Local Similarity: 42.9% Mismatches: 19
Query Match: 22.7%      Indels: 1
DB: 6                  Gaps: 1

US-10-628-525A-33 (1-56) x US-09-925-065A-933860 (1-692)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAnProAlaGlnAla 20
Db 294 ATGGCTTCCCAACAATTCCTCAGTGCCTTAATTCTCTGCTGATTAACCCAAAGTCCAAG 235
QY 21 SerMetValAlaProPheThr---GlyLeuLysSerAlaAlaPheProValSerArgLys 39
Db 234 TCCAAAGTCTCACCTGACACAGGCAAGTCCCTTCTGCTGTGAGCCTGTAAACCAAAA 175
QY 40 GlnAsn 41
Db 174 GCAAAAT 169

RESULT 26
US-09-925-065A-921611
; Sequence 921611, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 921610
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-921610

Alignment Scores:
Pred. No.: 813          Length: 787
Score: 61.50           Matches: 18
Percent Similarity: 52.4% Conservatives: 4
Best Local Similarity: 42.9% Mismatches: 19
Query Match: 22.7%      Indels: 1
DB: 6                  Gaps: 1

US-10-628-525A-33 (1-56) x US-09-925-065A-921610 (1-787)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThraArgThrAnProAlaGlnAla 20
Db 400 ATGGCTTCCCAACAATTCCTCAGTGCCTTAATTCTCTGCTGATTAACCCAAAGTCCAAG 459
QY 21 SerMetValAlaProPheThr---GlyLeuLysSerAlaAlaPheProValSerArgLys 39
```

```
Db 460 TCACAAAGTCTCACCTGACACAGGCAAGTCCCTTCTGCGCTGTGAGCCTGTGTAACCAAA 519
      ||| |||:| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 40 GlnAsn 41
      ||| |||
Db 520 GCAAA 525
      ||| |||

RESULT 28
US-09-925-065A-483931
; Sequence 483931, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 483931
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-483931

Alignment Scores:
Pred. No.: 657 Length: 562
Score: 61.00 Matches: 20
Percent Similarity: 54.0% Conservative: 7
Best Local Similarity: 40.0% Mismatches: 14
Query Match: 22.5% Indels: 9
DB: 6 Gaps: 1

US-10-628-525A-33 (1-56) x US-09-925-065A-483931 (1-562)
Qy 6 LeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAlaSerMetValAlaPro 25
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 44 CTGACTTCTGTGTGTGTCAGCCACTGCTGCTTCTCTCTGCTGTGATCTTTCTGCGCGAC 103
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 26 PheThrGly-LeuLysSer-----AlaAlaPheProValSe 37
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 104 TTCACCTGGCCCTTCAGCTGTGATCTTCTCTCCAGGCGACCTTCCCTGTTGT 163
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 37 rArgLysGlnAsnLeuAspIleThrSer 46
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 164 GCGATATCAGGCTCTTCCTTGTGCTTCA 191
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 29
US-10-932-182A-75783
; Sequence 75783, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75783
; LENGTH: 4911
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-75783

Alignment Scores:
Pred. No.: 6,18e+03 Length: 4911
Score: 61.00 Matches: 18
Percent Similarity: 54.3% Conservative: 7
Best Local Similarity: 39.1% Mismatches: 19
Query Match: 22.5% Indels: 2
DB: 9 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-932-182A-75783 (1-4911)
Qy 2 AlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAlaSer 21
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 382 GCCTGCTCCACCTTTCTTCAACTGCACAACCTCATAGGACATCTCACCTCTCTCTTCA 441
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 22 MetValAlaProPheThrGlyLeuLysSerAlaAlaPheProValSerArgLysGlnAsn 41
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 442 TTCGAGCTACCACTGCTCCATCATCTCTAGTTTACCGTCTCA-----ACTTCA 495
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 42 LeuAspIleThrSerIle 47
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 TTGACATTTACGTCAGTT 513
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 30
US-10-932-182A-75783
; Sequence 75783, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75783
; LENGTH: 4911
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-75783

Alignment Scores:
Pred. No.: 6,18e+03 Length: 4911
Score: 61.00 Matches: 18
Percent Similarity: 54.3% Conservative: 7
Best Local Similarity: 39.1% Mismatches: 19
Query Match: 22.5% Indels: 2
DB: 9 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-932-182A-75783 (1-4911)
Qy 2 AlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAlaSer 21
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 382 GCCTGCTCCACCTTTCTTCAACTGCACAACCTCATAGGACATCTCACCTCTCTCTTCA 441
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Search completed: April 2, 2006, 01:54:34  
Job time : 182.864 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 20:18:18 ; Search time 1530.93 Seconds  
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Perfect score: 271  
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Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	240.5	88.7	174	33	US-09-854-286-15
3	240.5	88.7	177	6	US-07-662-921C-10
4	240.5	88.7	177	7	US-07-785-566B-12
5	240.5	88.7	177	7	US-07-785-568B-12
6	240.5	88.7	177	7	US-07-785-569A-8
7	240.5	88.7	177	8	US-07-805-061B-12
					Sequence 4, Appl
					Sequence 15, Appl
					Sequence 10, Appl
					Sequence 12, Appl
					Sequence 8, Appl
					Sequence 12, Appl

8	240.5	88.7	177	14	US-08-473-512-12	Sequence 12, Appl	81	218	80.4	806	1	PCT-US02-27882-1093	Sequence 1093, Ap
9	240.5	88.7	204	1	PCT-US01-12928-3	Sequence 3, Appli	82	215	79.3	655	1	PCT-US02-27882-561	Sequence 561, App
10	240.5	88.7	204	61	US-10-758-064-3	Sequence 3, Appli	83	215	79.3	683	3	PCT-US04-33379-126	Sequence 126, App
11	240.5	88.7	297	1	PCT-US02-27884-7209	Sequence 7209, Ap	84	215	79.3	683	3	PCT-US05-36373-126	Sequence 126, App
12	240.5	88.7	297	51	US-10-487-901-7209	Sequence 7209, Ap	85	215	79.3	683	72	US-11-247-587-126	Sequence 126, App
13	240.5	88.7	377	1	PCT-US02-27884-3504	Sequence 3504, Ap	86	215	79.3	683	72	PCT-US02-27884-1716	Sequence 1716, Ap
14	240.5	88.7	377	51	US-10-487-901-3504	Sequence 3504, Ap	87	215	79.3	738	51	US-10-487-901-1716	Sequence 1716, Ap
15	240.5	88.7	489	1	PCT-US02-27884-3503	Sequence 3503, Ap	88	215	79.3	753	1	PCT-US02-27884-5764	Sequence 5764, Ap
16	240.5	88.7	489	51	US-10-487-901-3503	Sequence 3503, Ap	89	215	79.3	753	51	US-10-487-901-5764	Sequence 5764, Ap
17	240.5	88.7	492	1	PCT-US02-27883-1433	Sequence 1433, Ap	90	215	79.3	754	1	PCT-US02-27884-5028	Sequence 5028, Ap
18	240.5	88.7	504	1	PCT-US02-27884-7207	Sequence 7207, Ap	91	215	79.3	754	51	US-10-487-901-5028	Sequence 5028, Ap
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20	240.5	88.7	581	1	PCT-US02-27883-13	Sequence 13, Appl	93	215	79.3	831	1	PCT-US02-27882-226	Sequence 226, App
21	240.5	88.7	608	1	PCT-US02-27883-1213	Sequence 1213, Ap	94	213.5	78.8	399	31	US-09-705-926-16470	Sequence 16470, A
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23	240.5	88.7	615	1	PCT-US02-27883-1218	Sequence 1218, Ap	96	213.5	78.8	546	83	US-60-723-596-46744	Sequence 46744, A
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26	240.5	88.7	718	1	PCT-US02-27884-5765	Sequence 5765, Ap	99	212.5	78.4	323	29	US-09-637-086A-8290	Sequence 8290, Ap
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RESULT 1  
US-08-543-608-4  
; Sequence 4, Application US/08543608  
; GENERAL INFORMATION:  
; APPLICANT: Trulson, Anna J.  
; TITLE OF INVENTION: A Method for Visually Selecting  
; TITLE OF INVENTION: Transformed Plants Cells or Tissues by Carotenoid  
; TITLE OF INVENTION: Pigmentation  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greer, Burns & Crain, Ltd.  
; STREET: 233 South Wacker Drive, Suite 8660, Sears  
; STREET: Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/543,608  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueller, Lisa V.  
; REGISTRATION NUMBER: 38,978  
; REFERENCE/DOCKET NUMBER: PET02  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-993-0080  
; TELEFAX: 312-993-0633  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 171 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..171  
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Query Match: 88.7% Indels: 1  
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Db 121 CAAACCTTGACATCACTTCCATTGCCAGCACGGCGAAGAGTGCAATGC 171  
RESULT 2  
US-09-854-286-15  
; Sequence 15, Application US/09854286  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; APPLICANT: Deheah, Katayoon  
; TITLE OF INVENTION: Plastid Transit Peptide Sequences for Efficient Plastid Targeting  
; FILE REFERENCE: US 60/203,618 38-77(15378)  
; CURRENT APPLICATION NUMBER: US/09/854,286  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/203,618  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 174  
; TYPE: DNA  
; ORGANISM: Pisum sativum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(174)  
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Query Match: 88.7% Indels: 1  
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QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
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QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
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RESULT 3  
US-07-662-921C-10  
; Sequence 10, Application US/07662921C  
; GENERAL INFORMATION:  
; APPLICANT: Ausich, Rodney L  
; APPLICANT: Brinkhaus, Friedhelm L  
; APPLICANT: Mukharji, Indrani  
; APPLICANT: Proffitt, John H  
; APPLICANT: Yarger, James G  
; APPLICANT: Yen, Hwei-Che B  
; TITLE OF INVENTION: Biosynthesis of Zeaxanthin and Glycosylated  
; TITLE OF INVENTION: Zeaxanthin in Genetically Engineered Hosts  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
; STREET: 200 E Randolph St  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60680-0703  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/662,921C  
; FILING DATE: 19910228  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Galloway, Norval B  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-662-921C-10

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Pred. No.: 9,96e-29 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
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Db 1 ATGGCTTCCTCAGTCTTCTCTGAGCAGTTCGCCCGCAGCAATGTTGCTCAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
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QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 171

## RESULT 4

US-07-785-566B-12  
Sequence 12, Application US/07785566B  
GENERAL INFORMATION:  
APPLICANT: Ausich, Rodney L  
APPLICANT: Brinkhaus, Friedhelm L  
APPLICANT: Mukharji, Indrani  
APPLICANT: Proffitt, John H  
APPLICANT: Yarger, James G  
APPLICANT: Yen, Huel-Che B  
TITLE OF INVENTION: Beta-Carotene Biosynthesis in  
TITLE OF INVENTION: Genetically Engineered Hosts  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
STREET: 200 E Randolph St  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60680-0703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/785,566B  
FILING DATE: 19911030  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, Norval B  
TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
US-07-785-566B-12

Alignment Scores:  
Pred. No.: 9,96e-29 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x US-07-785-566B-12 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTCTTCTCTGAGCAGTTCGCCCGCAGCAATGTTGCTCAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGGTGGCGCTTTCATCGCCTTAAGTCAGCTGCCTCATTCCTCTTTCAAGGAAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 171

## RESULT 5

US-07-785-566B-12  
Sequence 12, Application US/07785566B  
GENERAL INFORMATION:  
APPLICANT: Ausich, Rodney L  
APPLICANT: Brinkhaus, Friedhelm L  
APPLICANT: Mukharji, Indrani  
APPLICANT: Proffitt, John H  
APPLICANT: Yarger, James G  
APPLICANT: Yen, Huel-Che B  
TITLE OF INVENTION: Lycopene Biosynthesis in  
TITLE OF INVENTION: Genetically Engineered Hosts  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
STREET: 200 E Randolph St  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60680-0703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/785,566B  
FILING DATE: 19921030  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, Norval B  
TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-785-566B-12

Alignment Scores:  
Pred. No.: 9,96e-29 Length: 177  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1

```
Query Match: 88.7% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x US-07-785-568B-12 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 ATGGCTTCCTCAGTCTCTTCTCTGACAGATTGCCACCGCAGCAATGTTGCTCAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLySerAlaAla---PheProValSerArgLys 39
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 AACATGGTGGCGCTTTCAGTGGCTTAAGTCAGCTGCCTCATTCCTGTTCAAGGAAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 121 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGAAGAGTGCAATGC 171

RESULT 7
US-07-805-061B-12
; Sequence 12, Application US/07805061B
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Hwei-Che B
; TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
; TITLE OF INVENTION: Glycosylated Zeaxanthin in
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/805,061B
; FILING DATE: 19911209
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, Norval B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3128567180
; TELEFAX: 3128564972
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-805-061B-12

Alignment Scores:
Pred. No.: 9,96e-29 Length: 177
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 8 Gaps: 1

US-10-628-525A-33 (1-56) x US-07-805-061B-12 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 ATGGCTTCCTCAGTCTCTTCTCTGACAGATTGCCACCGCAGCAATGTTGCTCAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLySerAlaAla---PheProValSerArgLys 39
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 61 AACATGGTGGCGCTTTCAGTGGCTTAAGTCAGCTGCCTCATTCCTGTTCAAGGAAG 120

QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 121 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGAAGAGTGCAATGC 171

RESULT 6
US-07-785-569A-8
; Sequence 8, Application US/07785569A
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Hwei-Che B
; TITLE OF INVENTION: Phytoene Biosynthesis in
; TITLE OF INVENTION: Genetically Engineered Hosts
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/785,569A
; FILING DATE: 19911030
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, Norval B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3128567180
; TELEFAX: 3128564972
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-785-569A-8

Alignment Scores:
Pred. No.: 9,96e-29 Length: 177
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 7 Gaps: 1

US-10-628-525A-33 (1-56) x US-07-785-569A-8 (1-177)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 ATGGCTTCCTCAGTCTCTTCTCTGACAGATTGCCACCGCAGCAATGTTGCTCAAGCT 60
```



Query Match: 88.7% Indels: 1  
DB: 61 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-758-064-3 (1-204)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 1 ATGGCTTCCTCAGTTCTTTCTCTGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 60  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 61 AACATGTTGCACCTTTCACTGGCCTTAAGTCAGCTGCTCATTCCTCTGTTTCAGGAAG 120  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 121 CAAAACCTTGACATCACTTCATTTGCCAGCAACGGCGGAAGAGTGCATATGC 171

RESULT 11

PCT-US02-27884-7209  
; Sequence 7209, Application PC/TUS0227884  
; GENERAL INFORMATION:  
; APPLICANT: The Dow Chemical Company  
; APPLICANT: Dow Agro Sciences, LLC  
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri  
; FILE REFERENCE: DOW-07611  
; CURRENT APPLICATION NUMBER: PCT/US02/27884  
; CURRENT FILING DATE: 2002-08-30  
; NUMBER OF SEQ ID NOS: 7560  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7209  
; LENGTH: 297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
PCT-US02-27884-7209

Alignment Scores:  
Pred. No.: 2,34e-28 Length: 297  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27884-7209 (1-297)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 97 ATGGCTTCCTCAGTTCTTTCTCTGCAGCAGTTCGCCACCGCAGCAATGTTGCTCAAGCT 156  
Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 157 AACATGTTGCACCTTTCACTGGCCTTAAGTCAGCTGCTCATTCCTCTGTTTCAGGAAG 216  
Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 217 CAAAACCTTGACATCACTTCATTTGCCAGCAACGGCGGAAGAGTGCATATGC 267

RESULT 12

US-10-487-901-7209  
; Sequence 7209, Application US/10487901  
; GENERAL INFORMATION:  
; APPLICANT: Oreido, Jeremiah Vincent  
; APPLICANT: McCreary, David  
; APPLICANT: Peill, Randy  
; APPLICANT: Miller, Barbara  
; APPLICANT: Weglarz, Thaddeus  
; APPLICANT: Gachotte, Daniel  
; APPLICANT: Blakeslee, Beth  
; APPLICANT: Larrinua, Ignacio  
; APPLICANT: Reddy, Avutu  
; APPLICANT: Shukla, Vipula

```
Db 128 AACATGGTTGCACCTTTTCACAGGCTTAAAGTCTGTGCTCCATTCCTCTCAAGTCTTCAAGAAAG 187
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
|||
Db 188 CAAACCTTGCATCATCTTCCATTGCCAGACGGCGGAAGAGTGCAATGC 238

RESULT 14
US-10-487-901-3504
; Sequence 3504, Application US/10487901
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3504
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-3504

Alignment Scores:
Pred. No.: 377 Length: 377
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 51 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-3504 (1-377)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
|||
Db 68 ATGGCTTCTCAGTCTTTCTCCAGCAGCAGTTGCCACCCGCGAGCAATGTTGCTCAAGCT 127
:::
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
:::
Db 128 AACATGGTTGCACCTTTTCACAGGCTTAAAGTCTGTGCTCATTCCTCTCAAGTCTTCAAGAAAG 187
:::
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
|||
Db 188 CAAACCTTGCATCATCTTCCATTGCCAGACGGCGGAAGAGTGCAATGC 238

RESULT 15
PCT-US02-27884-3503
; Sequence 3503, Application PC/TUS0227884
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-07611
; CURRENT APPLICATION NUMBER: PCT/US02/27884
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3503
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27884-3503

Alignment Scores:
Pred. No.: 531e-28 Length: 489
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 51 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27884-3503 (1-489)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
|||
Db 79 ATGGCTTCTCAGTCTTTCTCCAGCAGCAGTTGCCACCCGCGAGCAATGTTGCTCAAGCT 138
:::
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
:::
Db 139 AACATGGTTGCACCTTTTCACAGGCTTAAAGTCTGTGCTCATTCCTCTCAAGTCTTCAAGAAAG 198
:::
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
|||
Db 199 CAAACCTTGCATCATCTTCCATTGCCAGACGGCGGAAGAGTGCAATGC 249

RESULT 16
US-10-487-901-3503
; Sequence 3503, Application US/10487901
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3503
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-3503

Alignment Scores:
Pred. No.: 531e-28 Length: 489
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservative: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 51 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-3503 (1-489)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
|||
Db 79 ATGGCTTCTCAGTCTTTCTCCAGCAGCAGTTGCCACCCGCGAGCAATGTTGCTCAAGCT 138
:::
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
:::
Db 139 AACATGGTTGCACCTTTTCACAGGCTTAAAGTCTGTGCTCATTCCTCTCAAGTCTTCAAGAAAG 198
:::
```

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 199 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGAAGAGTGCATGC 249

RESULT 17  
PCT-US02-27883-1433  
; Sequence 1433, Application PC/TUS0227883  
; GENERAL INFORMATION:  
; APPLICANT: The Dow Chemical Company  
; APPLICANT: Dow Agro Sciences, LLC  
; FILE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance  
; CURRENT FILING DATE: 2002-08-30  
; NUMBER OF SEQ ID NOS: 2324  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1433  
; LENGTH: 492  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
PCT-US02-27883-1433

Alignment Scores:  
Pred. No.: 5.37e-28 Length: 492  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-1433 (1-492)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 66 ATGGCTTCTCAGTCTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 125

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 126 AACATGGTTGCACCTTCTCACTGGTCTTAAGTCTGCTGCCTCATTCCTGTTTCAAGGAAG 185

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 186 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGAAGAGTGCATGC 236

RESULT 18  
PCT-US02-27884-7207  
; Sequence 7207, Application PC/TUS0227884  
; GENERAL INFORMATION:  
; APPLICANT: The Dow Chemical Company  
; APPLICANT: Dow Agro Sciences, LLC  
; FILE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri  
; CURRENT FILING DATE: 2002-08-30  
; NUMBER OF SEQ ID NOS: 7560  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 7207  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
PCT-US02-27884-7207

Alignment Scores:  
Pred. No.: 5.58e-28 Length: 504  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27884-7207 (1-504)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 78 ATGGCTTCTCAGTCTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 137

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 138 AACATGGTTGCACCTTCTCAAGTCTTAAGTCTGCTGCCTCATTCCTGTTTCAAGGAAG 197

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 198 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGAAGAGTGCATGC 248

RESULT 19  
US-10-487-901-7207  
; Sequence 7207, Application US/10487901  
; GENERAL INFORMATION:  
; APPLICANT: Oreido, Jeremiah Vincent  
; APPLICANT: McCreary, David  
; APPLICANT: Pell, Randy  
; APPLICANT: Miller, Barbara  
; APPLICANT: Weglarz, Thaddeus  
; APPLICANT: Gachotte, Daniel  
; APPLICANT: Blakeslee, Beth  
; APPLICANT: Larrinua, Ignacio  
; APPLICANT: Reddy, Avutu  
; APPLICANT: Shukla, Vipula  
; APPLICANT: Crosley, Rodney  
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri  
; FILE REFERENCE: DOW-08552  
; CURRENT APPLICATION NUMBER: US/10/487,901  
; CURRENT FILING DATE: 2004-02-26  
; NUMBER OF SEQ ID NOS: 7560  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 7207  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-487-901-7207

Alignment Scores:  
Pred. No.: 5.58e-28 Length: 504  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-7207 (1-504)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20  
Db 78 ATGGCTTCTCAGTCTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 137

Qy 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39  
Db 138 AACATGGTTGCACCTTCTCAAGTCTTAAGTCTGCTGCCTCATTCCTGTTTCAAGGAAG 197

Qy 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 198 CAAACCTTGACATCACTTCCATTGCCAGCAACGGCGAAGAGTGCATGC 248

RESULT 20  
PCT-US02-27883-13  
; Sequence 13, Application PC/TUS0227883  
; GENERAL INFORMATION:  
; APPLICANT: The Dow Chemical Company  
; APPLICANT: Dow Agro Sciences, LLC  
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance

```
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Nicotiana benthamiana
PCT-US02-27883-13

Alignment Scores:
Pred. No.: 7,06e-28 Length: 581
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-13 (1-581)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 63 ATGGCTTCTCAGTTCTTTCTCAGCAGCAGTGGCCACCCGAGCAATGTTGCTCAAGCT 122
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 123 AACATGGTTGCACCTTTCTACTGGTCTTAAGTCAGCTGCTTCCTCTCTTTCAAGGAAG 182
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 183 CAAAACCTTGACATCATTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 233

RESULT 21
PCT-US02-27883-1213
; Sequence 1213, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1213
; LENGTH: 608
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27883-1213

Alignment Scores:
Pred. No.: 7.6e-28 Length: 608
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-1213 (1-608)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 38 ATGGCTTCTCAGTTCTTTCTCAGCAGCAGTGGCCACCCGAGCAATGTTGCTCAAGCT 97
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 98 AACATGGTTGCACCTTTCTACTGGTCTTAAGTCAGCTGCTTCCTCTCTTTCAAGGAAG 157
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
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Db 158 CAAAACCTTGACATCATTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 208

RESULT 22
PCT-US02-27883-1225
; Sequence 1225, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1225
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27883-1225

Alignment Scores:
Pred. No.: 7.73e-28 Length: 614
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-33 (1-56) x PCT-US02-27883-1225 (1-614)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
Db 46 ATGGCTTCTCAGTTCTTTCTCAGCAGCAGTGGCCACCCGAGCAATGTTGCTCAAGCT 105
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
Db 106 AACATGGTTGCACCTTTCTACTGGTCTTAAGTCAGCTGCTTCCTCTCTTTCAAGGAAG 165
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 166 CAAAACCTTGACATCATTCCATTGCCAGCAACGGCGGAAGAGTGCAATGC 216

RESULT 23
PCT-US02-27883-1218
; Sequence 1218, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1218
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: misc feature
; LOCATION: (490)..(490)
; OTHER INFORMATION: The residue at this position can be any nucleotide.
PCT-US02-27883-1218

Alignment Scores:
Pred. No.: 7.75e-28 Length: 615
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
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Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1
US-10-628-525A-33 (1-56) x PCT-US02-27883-1218 (1-615)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 47 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 106
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 107 AACATGGTTGCACCTTTACAGGCTTTAAGTCTGCTGCTCCTCATTCCTGTTTCAGGAAG 166
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 167 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 217
RESULT 24
PCT-US02-27883-1222
; Sequence 1222, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1222
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27883-1222
Alignment Scores:
Pred. No.: 81e-28 Length: 632
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1
US-10-628-525A-33 (1-56) x PCT-US02-27883-1222 (1-632)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 52 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 111
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 112 AACATGGTTGCACCTTTACAGGCTTTAAGTCTGCTGCTCCTCATTCCTGTTTCAGGAAG 171
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 172 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 222
RESULT 25
PCT-US02-27883-1217
; Sequence 1217, Application PC/TUS0227883
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Disease Resistance
; FILE REFERENCE: DOW-07613
; CURRENT APPLICATION NUMBER: PCT/US02/27883
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 2324
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1217
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27883-1217
Alignment Scores:
Pred. No.: 9.23e-28 Length: 684
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1
US-10-628-525A-33 (1-56) x PCT-US02-27883-1217 (1-684)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 47 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 106
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 107 AACATGGTTGCACCTTTACAGGCTTTAAGTCTGCTGCTCCTCATTCCTGTTTCAGGAAG 166
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 167 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 217
RESULT 26
PCT-US02-27884-5765
; Sequence 5765, Application PC/TUS0227884
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteristics
; FILE REFERENCE: DOW-07611
; CURRENT APPLICATION NUMBER: PCT/US02/27884
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5765
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27884-5765
Alignment Scores:
Pred. No.: 1e-27 Length: 718
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1
US-10-628-525A-33 (1-56) x PCT-US02-27884-5765 (1-718)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 45 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 104
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 105 AACATGGTTGCACCTTTACAGGCTTTAAGTCTGCTGCTCCTCATTCCTGTTTCAGGAAG 164
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 165 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 215
RESULT 27
US-10-487-901-5765
; Sequence 5765, Application US/10487901
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27883-1217
Alignment Scores:
Pred. No.: 9.23e-28 Length: 684
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1
US-10-628-525A-33 (1-56) x PCT-US02-27883-1217 (1-684)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 47 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 106
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 107 AACATGGTTGCACCTTTACAGGCTTTAAGTCTGCTGCTCCTCATTCCTGTTTCAGGAAG 166
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 167 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 217
RESULT 26
PCT-US02-27884-5765
; Sequence 5765, Application PC/TUS0227884
; GENERAL INFORMATION:
; APPLICANT: The Dow Chemical Company
; APPLICANT: Dow Agro Sciences, LLC
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteristics
; FILE REFERENCE: DOW-07611
; CURRENT APPLICATION NUMBER: PCT/US02/27884
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5765
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-27884-5765
Alignment Scores:
Pred. No.: 1e-27 Length: 718
Score: 240.50 Matches: 52
Percent Similarity: 96.5% Conservatives: 3
Best Local Similarity: 91.2% Mismatches: 1
Query Match: 88.7% Indels: 1
DB: 1 Gaps: 1
US-10-628-525A-33 (1-56) x PCT-US02-27884-5765 (1-718)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThrArgThrAsnProAlaGlnAla 20
DB 45 ATGGCTTCCTCAGTTCTTCTCAGCAGCAGTTGCCACCGCAGCAATGTTGCTCAAGCT 104
QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39
DB 105 AACATGGTTGCACCTTTACAGGCTTTAAGTCTGCTGCTCCTCATTCCTGTTTCAGGAAG 164
QY 40 GlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
DB 165 CAAACCTTGACATCACTTCATTGCCAGCAACGGCGGAAGAGTGCAATGC 215
RESULT 27
US-10-487-901-5765
; Sequence 5765, Application US/10487901
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APPLICANT: Croasley, Rodney  
TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Character  
FILE REFERENCE: DOM-08552  
CURRENT APPLICATION NUMBER: US/10/487,901  
CURRENT FILING DATE: 2004-02-26  
NUMBER OF SEQ ID NOS: 7560  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1704  
LENGTH: 736  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-487-901-1704

Alignment Scores:  
Pred. NO.: 1.04e-27 Length: 736  
Score: 240.50 Matches: 52  
Percent Similarity: 96.5% Conservative: 3  
Best Local Similarity: 91.2% Mismatches: 1  
Query Match: 88.7% Indels: 1  
DB: 51 Gaps: 1

US-10-628-525A-33 (1-56) x US-10-487-901-1704 (1-736)

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Qy	21	SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys	39
Db	123	AACATGTTGACCTTTTCATCTGTTTAAAGTCAGTCGCTCCCTGTTTCAAGGAAG	182
Qy	40	GlnAsnLeuAepIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56
Db	183	CAAAACCTTGACATCACTTCATTGCCAGCAACGCGGAGAGTGCAATGC	233

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GenCore version 5.1.7  
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Run on: April 1, 2006, 21:21:57 ; Search time 104.728 Seconds  
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Title: US-10-628-525A-33

Perfect score: 271

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Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	212.5	78.4	323	8	US-11-331-019-8290
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4	212.5	78.4	359	8	US-11-331-019-7156
5	212.5	78.4	369	8	US-11-331-019-37546

375	8	US-11-331-032-18420	Sequence 18420, A
379	8	US-11-331-019-36580	Sequence 36580, A
381	8	US-11-331-019-38462	Sequence 38462, A
381	8	US-11-331-019-38951	Sequence 38951, A
391	8	US-11-331-019-19877	Sequence 19877, A
391	8	US-11-331-019-36843	Sequence 36843, A
399	8	US-11-331-019-36471	Sequence 36471, A
405	8	US-11-331-019-38154	Sequence 38154, A
405	8	US-11-331-019-38762	Sequence 38762, A
411	8	US-11-331-019-36603	Sequence 36603, A
414	8	US-11-331-019-7434	Sequence 7434, Ap
415	8	US-11-331-019-8439	Sequence 8439, Ap
415	8	US-11-331-019-37318	Sequence 37318, A
419	8	US-11-331-019-39124	Sequence 39124, A
420	8	US-11-331-019-40131	Sequence 40131, A
422	8	US-11-331-019-37373	Sequence 37373, A
433	8	US-11-331-019-8542	Sequence 8542, Ap
434	8	US-11-331-019-39634	Sequence 39634, A
435	8	US-11-331-019-37716	Sequence 37716, A
436	8	US-11-331-019-38865	Sequence 38865, A
437	8	US-11-331-019-39767	Sequence 39767, A
440	8	US-11-331-019-39351	Sequence 39351, A
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461	8	US-11-331-019-8383	Sequence 8383, Ap
463	8	US-11-331-019-8391	Sequence 8391, Ap
553	8	US-11-331-019-36740	Sequence 36740, A
562	8	US-11-331-019-36830	Sequence 36830, A
582	8	US-11-331-019-36677	Sequence 36677, A
594	8	US-11-331-019-36653	Sequence 36653, A
622	8	US-11-331-019-36754	Sequence 36754, A
632	8	US-11-331-019-36808	Sequence 36808, A
711	8	US-11-331-019-7368	Sequence 7368, Ap
729	8	US-11-331-019-9010	Sequence 9010, Ap
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735	8	US-11-331-019-9356	Sequence 9356, Ap
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735	8	US-11-331-019-9351	Sequence 9351, Ap
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735	8	US-11-331-019-38514	Sequence 38514, A
735	8	US-11-331-019-39037	Sequence 39037, A
735	8	US-11-331-019-38139	Sequence 38139, A
735	8	US-11-331-019-39105	Sequence 39105, A
735	8	US-11-331-019-37795	Sequence 37795, A
735	8	US-11-331-019-9359	Sequence 9359, Ap
735	8	US-11-331-019-39347	Sequence 39347, A
735	8	US-11-330-364-6351	Sequence 6351, Ap
735	8	US-11-056-3558-49339	Sequence 49339, A
735	7	US-10-953-349-8894	Sequence 8894, Ap
735	8	US-11-056-3558-36037	Sequence 36037, A
735	8	US-11-056-3558-47209	Sequence 47209, A
735	8	US-11-056-3558-97594	Sequence 97594, A
735	8	US-11-056-3558-108833	Sequence 108833, A
735	8	US-11-056-3558-107434	Sequence 107434, A
735	8	US-11-056-3558-118673	Sequence 118673, A
735	12	US-60-752-355-716	Sequence 716, App
735	8	US-11-056-3558-108015	Sequence 108015, A
735	8	US-11-056-3558-119254	Sequence 119254, A
735	8	US-11-331-019-8716	Sequence 8716, Ap
735	8	US-11-331-019-38707	Sequence 38707, A
735	8	US-11-331-019-40760	Sequence 40760, A
735	8	US-11-331-019-36524	Sequence 36524, A
735	8	US-11-331-019-36633	Sequence 36633, A
735	8	US-11-331-019-8985	Sequence 8985, Ap
735	8	US-11-331-019-9070	Sequence 9070, Ap
735	8	US-11-331-019-40770	Sequence 40770, A
735	8	US-11-331-019-9053	Sequence 9053, Ap

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81	207	76.4	342	8	US-11-331-019-39585	Sequence 39585, A
82	207	76.4	343	8	US-11-331-019-6978	Sequence 6978, Ap
83	207	76.4	346	8	US-11-331-019-7826	Sequence 7826, Ap
84	207	76.4	352	8	US-11-331-019-40716	Sequence 40716, A
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86	207	76.4	356	8	US-11-331-019-36496	Sequence 36496, A
87	207	76.4	359	8	US-11-331-019-38246	Sequence 38246, A
88	207	76.4	359	8	US-11-331-019-38704	Sequence 38704, A
89	207	76.4	359	8	US-11-331-019-39045	Sequence 39045, A
90	207	76.4	378	8	US-11-331-019-40754	Sequence 40754, A
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98	207	76.4	398	8	US-11-331-019-36470	Sequence 36470, A
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101	207	76.4	403	8	US-11-331-019-6581	Sequence 6581, Ap
102	207	76.4	403	8	US-11-331-019-38620	Sequence 38620, A
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104	207	76.4	409	8	US-11-331-019-37634	Sequence 37634, A
105	207	76.4	411	8	US-11-331-019-9160	Sequence 9160, Ap
106	207	76.4	411	8	US-11-331-019-39962	Sequence 39962, A
107	207	76.4	415	8	US-11-331-019-40013	Sequence 40013, A
108	207	76.4	416	8	US-11-331-019-40013	Sequence 40013, A
109	207	76.4	417	8	US-11-331-019-38032	Sequence 38032, A
110	207	76.4	417	8	US-11-331-019-39806	Sequence 39806, A
111	207	76.4	419	8	US-11-331-019-37232	Sequence 37232, A
112	207	76.4	421	8	US-11-331-019-6568	Sequence 6568, Ap
113	207	76.4	422	8	US-11-331-019-40171	Sequence 40171, A
114	207	76.4	423	8	US-11-331-019-37817	Sequence 37817, A
115	207	76.4	423	8	US-11-331-019-39410	Sequence 39410, A
116	207	76.4	424	8	US-11-331-019-39419	Sequence 39419, A
117	207	76.4	425	8	US-11-331-019-8186	Sequence 8186, Ap
118	207	76.4	427	8	US-11-331-019-37120	Sequence 37120, A
119	207	76.4	427	8	US-11-331-019-40372	Sequence 40372, A
120	207	76.4	429	8	US-11-331-019-39780	Sequence 39780, A
121	207	76.4	431	8	US-11-331-019-39555	Sequence 39555, A
122	207	76.4	431	8	US-11-331-019-39717	Sequence 39717, A
123	207	76.4	433	8	US-11-331-019-8008	Sequence 8008, Ap
124	207	76.4	433	8	US-11-331-019-37680	Sequence 37680, A
125	207	76.4	435	8	US-11-331-019-39700	Sequence 39700, A
126	207	76.4	435	8	US-11-331-019-39738	Sequence 39738, A
127	207	76.4	437	8	US-11-331-019-40244	Sequence 40244, A
128	207	76.4	439	8	US-11-331-019-39637	Sequence 39637, A
129	207	76.4	439	8	US-11-331-019-40219	Sequence 40219, A
130	207	76.4	441	8	US-11-331-019-40464	Sequence 40464, A
131	207	76.4	442	8	US-11-331-019-39613	Sequence 39613, A
132	207	76.4	442	8	US-11-331-019-39979	Sequence 39979, A
133	207	76.4	446	8	US-11-331-019-36213	Sequence 36213, A
134	207	76.4	448	8	US-11-331-019-39873	Sequence 39873, A
135	207	76.4	451	8	US-11-331-019-6116	Sequence 6116, Ap
136	207	76.4	456	8	US-11-331-019-8531	Sequence 8531, Ap
137	207	76.4	601	8	US-11-331-019-36811	Sequence 36811, A
138	207	76.4	604	8	US-11-331-019-36656	Sequence 36656, A
139	207	76.4	665	8	US-11-331-019-36735	Sequence 36735, A
140	205.5	75.8	666	8	US-11-331-019-36709	Sequence 36709, A
141	205.5	75.8	404	8	US-11-331-019-38120	Sequence 38120, A
142	205.5	75.8	424	8	US-11-331-019-39430	Sequence 39430, A
143	205	75.6	386	8	US-11-331-019-39972	Sequence 39972, A
144	205	75.6	397	8	US-11-331-019-34443	Sequence 34443, A
145	205	75.6	481	8	US-11-331-019-38790	Sequence 38790, A
146	204.5	75.5	285	8	US-11-331-019-36325	Sequence 36325, A
147	204.5	75.5	294	8	US-11-331-019-40747	Sequence 40747, A
148	204.5	75.5	358	8	US-11-331-019-8984	Sequence 8984, Ap
149	204.5	75.5	362	8	US-11-331-019-38912	Sequence 38912, A
150	204.5	75.5	363	8	US-11-331-019-38252	Sequence 38252, A

ALIGNMENTS

RESULT 1

US-11-336-680-33

Sequence 33, Application US/11336680

GENERAL INFORMATION:

APPLICANT: E.I. duPont de Nemours and Company, Inc.

APPLICANT: Meyer, Knut

APPLICANT: Viitanen, Paul

APPLICANT: Flint, Dennis

TITLE OF INVENTION: High Level Production of Arbutin in Green Plants and Microbes

FILE REFERENCE: CL 2155 US NA

CURRENT APPLICATION NUMBER: US/11/336,680

CURRENT FILING DATE: 2006-01-20

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIn version 3.2

SEQ ID NO 33

LENGTH: 684

TYPE: DNA

ORGANISM: Escherichia coli

US-11-336-680-33

Alignment Scores:

Pred. No.: 1.74e-23

Length: 684

Score: 223.50

Matches: 47

Percent Similarity: 93.0%

Conservative: 6

Best Local Similarity: 82.5%

Mismatches: 3

Indels: 1

Query Match: 8

Gaps: 1

DB:

US-10-628-525A-33 (1-56) x US-11-336-680-33 (1-684)

QY 1 MetaSerSerMetLeuSerSerAlaValAlaThrArgThrAsnProAlaGlnAla 20

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 ATGGTCTCTCTGTCTATTTCTTCAGCAGCTGTTCACACGACGAAATGTTACACAAGCT 60

QY 21 SerMetValAlaProPheThrGlyLeuLysSerAlaAla---PheProValSerArgLys 39

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 AGCATGGTTGGACCTTTCAGTGTCTCAATCTTCAGCCACTTCCCTGTTTACAAGAAG 120

QY 40 GlnAsnLeuAapPileThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 121 CAAAACCTTGACATCATCTCCATCTCCTAGCAATGCTGGAAGAGTTAGTGTGC 171

RESULT 2

US-11-331-019-8290

Sequence 8290, Application US/11331019

GENERAL INFORMATION:

APPLICANT: Fincher, Karen L.

APPLICANT: La Rosa, Thomas J.

APPLICANT: McCarter, David W.

APPLICANT: Pear, Julie R.

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

FILE REFERENCE: 16517.359 - 38-21(51375)C/US

CURRENT APPLICATION NUMBER: US/11/331,019

CURRENT FILING DATE: 2006-01-13

PRIOR APPLICATION NUMBER: US 09/637,086

PRIOR FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: US 60/149,881

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 52949

SEQ ID NO 8290

LENGTH: 323

TYPE: DNA

ORGANISM: Gossypium hirsutum

FEATURE:

OTHER INFORMATION: Clone ID: LIB120-031-Q1-K1-D12

US-11-331-019-8290

Alignment Scores:

Pred. No.: 2.62e-22

Length: 323

Score: 212.50 Matches: 46  
Percent Similarity: 89.8% Conservative: 7  
Best Local Similarity: 78.0% Mismatches: 3  
Query Match: 78.4% Indels: 3  
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-8290 (1-323)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
Db 66 ATGGCTCTCTCCATGATCTCATCGCAACCATTCGCCACCGTGAACCGCTCTCCCGGCA 125  
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
Db 126 CAGGCCAACATGTGGGCCCTTACCGGCTCAAAATCTGCCTCTGCTTTCCCAAGTCACC 185  
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 186 AGGAGGCCAACACGACATCACTTCTTGCAGCAACCGTGGGAGAGTGCAATGC 242

## RESULT 3

US-11-331-019-38696  
; Sequence 38696, Application US/11331019

; GENERAL INFORMATION:

; APPLICANT: Fincher, Karen L.

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: McCarter, David W.

; APPLICANT: Pear, Julie R.

; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

; FILE OF INVENTION: Plants

; FILE REFERENCE: 16517.359 - 38-21(51375)C/US

; CURRENT APPLICATION NUMBER: US/11/331.019

; PRIOR FILING DATE: 2006-01-13

; PRIOR APPLICATION NUMBER: US 09/637,086

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: US 60/149,881

; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 52949

; SEQ ID NO 38696

; TYPE: DNA

; ORGANISM: Gossypium hirsutum

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3165-034-P1-K1-H11

US-11-331-019-38696

Alignment Scores:  
Pred. No.: 2,95e-22 Length: 350  
Score: 212.50 Matches: 46  
Percent Similarity: 89.8% Conservative: 7  
Best Local Similarity: 78.0% Mismatches: 3  
Query Match: 78.4% Indels: 3  
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-38696 (1-350)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
Db 66 ATGGCTCTCTCCATGATCTCATCGCAACCATTCGCCACCGTGAACCGCTCTCCCGGCA 125  
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
Db 126 CAGGCCAACATGTGGGCCCTTACCGGCTCAAAATCTGCCTCTGCTTTCCCAAGTCACC 185  
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 186 AGGAGGCCAACACGACATCACTTCTTGCAGCAACCGTGGGAGAGTGCAATGC 242

## RESULT 4

US-11-331-019-7156

; Sequence 7156, Application US/11331019

; GENERAL INFORMATION:

; APPLICANT: Fincher, Karen L.

Alignment Scores:

Pred. No.: 3.19e-22 Length: 369

Score: 212.50 Matches: 46

Percent Similarity: 89.8% Conservative: 7

; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: McCarter, David W.  
; APPLICANT: Pear, Julie R.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US  
; CURRENT APPLICATION NUMBER: US/11/331.019  
; PRIOR FILING DATE: 2006-01-13  
; PRIOR APPLICATION NUMBER: US 09/637,086  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: US 60/149,881  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 52949  
; SEQ ID NO 7156  
; LENGTH: 359  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3120-017-Q1-K1-E2  
US-11-331-019-7156

Alignment Scores:

Pred. No.: 3.07e-22 Length: 359

Score: 212.50 Matches: 46

Percent Similarity: 89.8% Conservative: 7

Best Local Similarity: 78.0% Mismatches: 3

Query Match: 78.4% Indels: 3

DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-7156 (1-359)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
Db 66 ATGGCTCTCTCCATGATCTCATCGCAACCATTCGCCACCGTGAACCGCTCTCCCGGCA 125  
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
Db 126 CAGGCCAACATGTGGGCCCTTACCGGCTCAAAATCTGCCTCTGCTTTCCCAAGTCACC 185  
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56  
Db 186 AGGAGGCCAACACGACATCACTTCTTGCAGCAACCGTGGGAGAGTGCAATGC 242

## RESULT 5

US-11-331-019-37546

; Sequence 37546, Application US/11331019

; GENERAL INFORMATION:

; APPLICANT: Fincher, Karen L.

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: McCarter, David W.

; APPLICANT: Pear, Julie R.

; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

; FILE OF INVENTION: Plants

; FILE REFERENCE: 16517.359 - 38-21(51375)C/US

; CURRENT APPLICATION NUMBER: US/11/331.019

; PRIOR FILING DATE: 2006-01-13

; PRIOR APPLICATION NUMBER: US 09/637,086

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: US 60/149,881

; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 52949

; SEQ ID NO 37546

; LENGTH: 369

; TYPE: DNA

; ORGANISM: Gossypium hirsutum

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3165-018-P1-K1-B9

US-11-331-019-37546

Best Local Similarity:	78.0%	Mismatches:	3
Query Match:	78.4%	Indels:	3
DB:	8	Gaps:	2

US-10-628-525A-33 (1-56) x US-11-331-019-37546 (1-369)

Qy	1	MetAlaSerSerMetLeuSerSerAlaIaValAlaThr-----ArgThrAsnProAla	18
Db	118	ARGGCCTCTCCATGATCATCATCGCAACCATGCAACCGCTCTCTCCCGGCA	177
Qy	19	GlnAlaSerMetValAlaProPhoThrGlyLeuLysSerAla---AlaPheProValSer	37
Db	178	CAGGGCCAACTGGTGGCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC	237
Qy	38	ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56
Db	238	AGGAAGGCCCAACGACATCACTTCTCTCSAAGCAACCGTGGACAGTGCATATGC	294

## RESULT 6

```

US-11-331-032-18420
; Sequence 18420, Application US/11331032
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Xiao, Jinhua
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.361 - 38-21(51462)C/US
; CURRENT APPLICATION NUMBER: US/11/331,032
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/666,355
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 60/155,005
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 25978

```

OTHER INFORMATION: Clone ID: uC-gsflnu33B002b03b1  
US-11-331-032-18420

Alignment Scores:	3.27e-22	Length:	375
Pred. No.:	212.50	Matches:	46
Score:	89.8%	Conservative:	7
Percent Similarity:	78.0%	Mismatches:	3
Best Local Similarity:	78.4%	Indels:	3
Query Match:	8	Gaps:	2
DB:			

US-10-628-525A-33 (1-56) x US-11-331-032-18420 (1-375)

[illegible]

## RESULT 7

```

USC-11-331-019-36580
; Sequence 36580, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.

```

```

/ / TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
/ / TITLE OF INVENTION: Plants
/ / FILE REFERENCE: 16517.359 - 38-21(51375)C/US
/ / CURRENT APPLICATION NUMBER: US/11/331,019
/ / CURRENT FILING DATE: 2006-01-13
/ / PRIOR APPLICATION NUMBER: US 09/637,086
/ / PRIOR FILING DATE: 2000-08-11
/ / PRIOR APPLICATION NUMBER: US 60/149,881
/ / PRIOR FILING DATE: 1999-08-19
/ / NUMBER OF SEQ ID NOS: 52949
/ / SEQ ID NO 36580
/ / LENGTH: 379
/ / TYPE: DNA
/ / ORGANISM: Gossypium hirsutum
/ / FEATURE:
/ / OTHER INFORMATION: Clone ID: LIB3165-006-P1-K1-F12
US-11-331-019-36580

```

**Alignment Scores:**

Pred. No.:	3,320-22	Length:	379
Score:	212.50	Matches:	46
Percent Similarity:	89.8%	Conservative:	7
Best Local Similarity:	78.0%	Mismatches:	3
Query Match:	78.4%	Indels:	3
DB:	8	Gaps:	2

US-10-628-525A-33 (1-56) x US-11-331-019-36580 (1-379)

	QY	1	MetaLaserSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla	18
			:::::	
	Db	64	ATGGCTCCTCCATGATCTCATGGCAACCATTTGCCACCGTGAACCGTCTCTCCCGGCA	123
			:::::	
	QY	19	GlnAlaSerMetValAlaProPheThrGlyLeuLySerAla---AlaPheProValSer	37
			:::::	
	Db	124	CAGGCACAATGTGTGGCCCCCTTCACGGCGCTCAACTTGCTCTGTCTTCCCAGTCACC	183
			:::::	
	QY	38	ArgLyysGlnAnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys	56
			:::::	
	Db	184	AGGAAGGCCAACACGACATCTCTCTGTGCAAGCAAACGGTGGAGAGTGCATGC	240

## RESULT 8

```

US-11-331-019-38462
;
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 38462
; LENGTH: 381

```

Alignment Scores:

Alignment Scores:			
Pred. No.:	3,356-22	Length:	381
Score:	212.50	Matches:	46
Percent Similarity:	89.8%	Conservative:	7
Best Local Similarity:	78.0%	Mismatches:	3
Query Match:	78.4%	Indels:	3
DB:	8	Gaps:	2



```
US-10-628-525A-33 (1-56) x US-11-331-019-38462 (1-381)
Qy 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 66 ATGGCCTCTCCATGATCTCATGGCAACCACTTCCACCGTGAACCGCTCTCTCCCGGCA 125
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 126 CAGGCCAACATGGTGGGCCCCCTTCCCGGCTCAAAATCTGCTCTGCTTTCCCAAGTCACC 185
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 186 AGGAGGCCAACACGACATCTCTTCTTCAAGCAACCGTGGGAGAGTGAATGC 242

RESULT 9
US-11-331-019-38951
; Sequence 38951, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331.019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 38951
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-034-PI-K4-H11
US-11-331-019-38951

Alignment Scores:
Pred. No.: 3,35e-22 Length: 381
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-38951 (1-381)
Qy 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 66 ATGGCCTCTCCATGATCTCATGGCAACCACTTCCACCGTGAACCGCTCTCTCCCGGCA 125
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 126 CAGGCCAACATGGTGGGCCCCCTTCCCGGCTCAAAATCTGCTCTGCTTTCCCAAGTCACC 185
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 186 AGGAGGCCAACACGACATCTCTTCTTCAAGCAACCGTGGGAGAGTGAATGC 242

RESULT 10
US-11-331-019-19877
; Sequence 19877, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331.019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 19877
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-007-PI-K1-B1
US-11-331-019-19877

Alignment Scores:
Pred. No.: 3,48e-22 Length: 391
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-36843 (1-391)
Qy 1 MetAlaSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 30 ATGGCCTCTCCATGATCTCATGGCAACCACTTCCACCGTGAACCGCTCTCTCCCGGCA 89
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 90 CAGGCCAACATGGTGGGCCCCCTTCCCGGCTCAAAATCTGCTCTGCTTTCCCAAGTCACC 149
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 150 AGGAGGCCAACACGACATCTCTTCTTCAAGCAACCGTGGGAGAGTGAATGC 206

RESULT 11
US-11-331-019-36843
; Sequence 36843, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331.019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 36843
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-007-PI-K1-B1
US-11-331-019-36843

Alignment Scores:
Pred. No.: 3,48e-22 Length: 391
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-36843 (1-391)
```



```
Db 48 ATGGCTCTCCATGATCTCATCGCAACCAATTCGCCACCGTGAACCGTCTCTCCCGGCA 107
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 108 CAGGCCAACATGCTGTGGCCCTTCACCGGCTCAATCTGCCTCTGCTTTCCTCCAGTCACC 167
Qy 38 ArgLysGlnAlaSerMetValAlaProPheThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 168 AGGAAGGCCAACACGACATCACTTCTTGTGCAAGCAACGGTGGGAGAGTGCAATGC 224

RESULT 15
US-11-331-019-36603
; Sequence 36603, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 36603
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-006-P1-K1-H5
US-11-331-019-36603

Alignment Scores:
Pred. No.: 3,74e-22 Length: 411
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-36603 (1-411)
Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 95 ATGGCTCTCCATGATCTCATCGCAACCAATTCGCCACCGTGAACCGTCTCTCCCGGCA 154
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 155 CAGGCCAACATGCTGTGGCCCTTCACCGGCTCAATCTGCCTCTGCTTTCCTCCAGTCACC 214
Qy 38 ArgLysGlnAlaSerMetValAlaProPheThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 215 AGGAAGGCCAACACGACATCACTTCTTGTGCAAGCAACGGTGGGAGAGTGCAATGC 271

RESULT 16
US-11-331-019-7434
; Sequence 7434, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
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```
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 7434
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-019-Q1-K1-H9
US-11-331-019-7434

Alignment Scores:
Pred. No.: 3,78e-22 Length: 414
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-7434 (1-414)
Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 39 ATGGCTCTCCATGATCTCATCGCAACCAATTCGCCACCGTGAACCGTCTCTCCCGGCA 98
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 99 CAGGCCAACATGCTGTGGCCCTTCACCGGCTCAATCTGCCTCTGCTTTCCTCCAGTCACC 158
Qy 38 ArgLysGlnAlaSerMetValAlaProPheThrSerIleAlaSerAsnGlyArgValGlnCys 56
Db 159 AGGAAGGCCAACACGACATCACTTCTTGTGCAAGCAACGGTGGGAGAGTGCAATGC 215

RESULT 17
US-11-331-019-8439
; Sequence 8439, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 8439
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-034-Q1-K1-B12
US-11-331-019-8439

Alignment Scores:
Pred. No.: 3,8e-22 Length: 415
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-8439 (1-415)
Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 54 ATGGCTCTCCATGATCTCATCGCAACCAATTCGCCACCGTGAACCGTCTCTCCCGGCA 113
```



```
Db 108 CAGGCCAACATGGTGGCCCCCTTACCGGCTCAAAATCGCTTGTCTTCCCGAGTCACC 167
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 168 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGGTGGGAGAGTGCAATGC 224

RESULT 21
US-11-331-019-37373
; Sequence 37373, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 37373
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-016-P1-K1-B1
US-11-331-019-37373

Alignment Scores:
Pred. No.: 3.86e-22 Length: 420
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservatives: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-37373 (1-420)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 78 ATGGCCCTCTCCATGATCTCATCGCAACCATTTGCCACCGCTCCTCCCGGCA 137
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 138 CAGGCCAACATGGTGGCCCCCTTACCGGCTCAAAATCTGCCTCTTCCCGAGTCACC 197
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 198 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGGTGGGAGAGTGCAATGC 254

RESULT 22
US-11-331-019-39412
; Sequence 39412, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
```

```
; SEQ ID NO 39412
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-039-Q1-K1-F8
US-11-331-019-39412

Alignment Scores:
Pred. No.: 3.89e-22 Length: 422
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservatives: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-39412 (1-422)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 71 ATGGCCCTCTCCATGATCTCATCGCAACCATTTGCCACCGCTCCTCCCGGCA 130
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 131 CAGGCCAACATGGTGGCCCCCTTACCGGCTCAAAATCTGCCTCTTCCCGAGTCACC 190
Qy 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 191 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGGTGGGAGAGTGCAATGC 247

RESULT 23
US-11-331-019-8542
; Sequence 8542, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 8542
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-036-Q1-K1-C2
US-11-331-019-8542

Alignment Scores:
Pred. No.: 4.04e-22 Length: 433
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservatives: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-8542 (1-433)

Qy 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 54 ATGGCCCTCTCCATGATCTCATCGGAGCAACATTTGCCACCGCTCCTCCCGGCA 113
Qy 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
```

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; SEQ ID NO 37716
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-020-P1-K1-E12
US-11-331-019-37716

Alignment Scores:
Pred. No.: 4,07e-22 Length: 435
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-37716 (1-435)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 54 ATGGCTCTCTCATGATCTCATCGGCAACCATTCGACCGTGCACCGCTCTCTCCCGGCA 113
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 114 CAGGCCAACATGCTGGCCCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC 173
QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 174 AGGAAGGCCAACACACGACATCACTTCTCTTGAAGCAACGGTGGGAGAGTGCAATGC 230

RESULT 26
US-11-331-019-38865
; Sequence 38865, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 38865
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-034-P1-K3-H11
US-11-331-019-38865

Alignment Scores:
Pred. No.: 4,08e-22 Length: 436
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-38865 (1-436)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 66 ATGGCTCTCTCATGATCTCATCGGCAACCATTCGACCGTGCACCGCTCTCTCCCGGCA 125
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 126 CAGGCCAACATGCTGGCCCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC 185
```

```

; SEQ ID NO 37716
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-020-P1-K1-E12
US-11-331-019-37716

Alignment Scores:
Pred. No.: 4,07e-22 Length: 435
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-37716 (1-435)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 54 ATGGCTCTCTCATGATCTCATCGGCAACCATTCGACCGTGCACCGCTCTCTCCCGGCA 113
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 114 CAGGCCAACATGCTGGCCCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC 173
QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 174 AGGAAGGCCAACACACGACATCACTTCTCTTGAAGCAACGGTGGGAGAGTGCAATGC 230

RESULT 26
US-11-331-019-38865
; Sequence 38865, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 38865
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-034-P1-K3-H11
US-11-331-019-38865

Alignment Scores:
Pred. No.: 4,08e-22 Length: 436
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-38865 (1-436)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 66 ATGGCTCTCTCATGATCTCATCGGCAACCATTCGACCGTGCACCGCTCTCTCCCGGCA 125
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 126 CAGGCCAACATGCTGGCCCCCTTCACCGGCTCAAAATCTGCCTCTGCTTTCCAGTCACC 185
```

QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56  
 Db 186 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGCTGGGAGAGTGCAATGC 242

## RESULT 27

US-11-331-019-39767  
 ; Sequence 39767, Application US/11331019  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fincher, Karen L.  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: McCarter, David W.  
 ; APPLICANT: Pear, Julie R.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 16517.359 - 38-21(51375)C/US  
 ; CURRENT APPLICATION NUMBER: US/11/331,019  
 ; CURRENT FILING DATE: 2006-01-13  
 ; PRIOR APPLICATION NUMBER: US 09/637,086  
 ; PRIOR FILING DATE: 2000-08-11  
 ; PRIOR APPLICATION NUMBER: US 60/149,881  
 ; PRIOR FILING DATE: 1999-08-19  
 ; NUMBER OF SEQ ID NOS: 52949  
 ; SEQ ID NO 39767  
 ; LENGTH: 437  
 ; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3165-044-Q1-K1-C6  
 US-11-331-019-39767

Alignment Scores:  
 Pred. No.: 4.1e-22 Length: 437  
 Score: 212.50 Matches: 46  
 Percent Similarity: 89.8% Conservative: 7  
 Best Local Similarity: 78.0% Mismatches: 3  
 Query Match: 78.4% Indels: 3  
 DB: Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-39767 (1-437)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
 Db 54 ATGGCTCTCTCCATGATCTCATCGCAACCATGCGCACCGTGAACCGCTCTCTCCCGGCA 113  
 QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
 Db 114 CAGGCCAACATGCTGGGCCCCCTTCAACGGCTCAATCTGCCTCTGCTTCCAGTCACC 173  
 QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56  
 Db 174 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGCTGGGAGAGTGCAATGC 230

## RESULT 28

US-11-331-019-39351  
 ; Sequence 39351, Application US/11331019  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fincher, Karen L.  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: McCarter, David W.  
 ; APPLICANT: Pear, Julie R.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 16517.359 - 38-21(51375)C/US  
 ; CURRENT APPLICATION NUMBER: US/11/331,019  
 ; CURRENT FILING DATE: 2006-01-13  
 ; PRIOR APPLICATION NUMBER: US 09/637,086  
 ; PRIOR FILING DATE: 2000-08-11  
 ; PRIOR APPLICATION NUMBER: US 60/149,881  
 ; PRIOR FILING DATE: 1999-08-19  
 ; NUMBER OF SEQ ID NOS: 52949  
 ; SEQ ID NO 39351  
 ; LENGTH: 440

; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3165-038-Q1-K1-H3  
 US-11-331-019-39351

Alignment Scores:  
 Pred. No.: 4.14e-22 Length: 440  
 Score: 212.50 Matches: 46  
 Percent Similarity: 89.8% Conservative: 7  
 Best Local Similarity: 78.0% Mismatches: 3  
 Query Match: 78.4% Indels: 3  
 DB: Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-39351 (1-440)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
 Db 48 ATGGCTCTCTCCATGATCTCATCGCAACCATGCGCACCGTGAACCGCTCTCTCCCGGCA 107  
 QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
 Db 108 CAGGCCAACATGCTGGGCCCCCTTCAACGGCTCAATCTGCCTCTGCTTCCAGTCACC 167  
 QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56  
 Db 168 AGGAAGGCCAACACGACATCACTTCTTGTCAAGCAACGCTGGGAGAGTGCAATGC 224

## RESULT 29

US-11-331-019-38846  
 ; Sequence 38846, Application US/11331019  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fincher, Karen L.  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: McCarter, David W.  
 ; APPLICANT: Pear, Julie R.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 16517.359 - 38-21(51375)C/US  
 ; CURRENT APPLICATION NUMBER: US/11/331,019  
 ; CURRENT FILING DATE: 2006-01-13  
 ; PRIOR APPLICATION NUMBER: US 09/637,086  
 ; PRIOR FILING DATE: 2000-08-11  
 ; PRIOR APPLICATION NUMBER: US 60/149,881  
 ; PRIOR FILING DATE: 1999-08-19  
 ; NUMBER OF SEQ ID NOS: 52949  
 ; SEQ ID NO 38846  
 ; LENGTH: 456  
 ; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3165-034-P1-K3-P3  
 US-11-331-019-38846

Alignment Scores:  
 Pred. No.: 4.36e-22 Length: 456  
 Score: 212.50 Matches: 46  
 Percent Similarity: 89.8% Conservative: 7  
 Best Local Similarity: 78.0% Mismatches: 3  
 Query Match: 78.4% Indels: 3  
 DB: Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-38846 (1-456)

QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18  
 Db 48 ATGGCTCTCTCCATGATCTCATCGCAACCATGCGCACCGTGAACCGCTCTCTCCCGGCA 107  
 QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37  
 Db 108 CAGGCCAACATGCTGGGCCCCCTTCAACGGCTCAATCTGCCTCTGCTTCCAGTCACC 167  
 QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyArgValGlnCys 56

```
||||| ||| |||||||||:|||||||||
Db 168 AGGAGGCCAACACACATCACTCTCTTGCAAGCAACGGTGGGAGAGTGCAATGC 224

RESULT 30
US-11-331-019-8383
; Sequence 8383, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 8383
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-033-Pl-K1-B2
US-11-331-019-8383

Alignment Scores:
Pred. No.: 4.43e-22 Length: 461
Score: 212.50 Matches: 46
Percent Similarity: 89.8% Conservative: 7
Best Local Similarity: 78.0% Mismatches: 3
Query Match: 78.4% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-33 (1-56) x US-11-331-019-8383 (1-461)
QY 1 MetAlaSerSerMetLeuSerSerAlaAlaValAlaThr-----ArgThrAsnProAla 18
Db 58 ATGGGGTCTCTCCATGATCTCATCGGCAGGCATTCGCCCGCATTCCTCCCGGCA 117
QY 19 GlnAlaSerMetValAlaProPheThrGlyLeuLysSerAla---AlaPheProValSer 37
Db 118 CAGGCCACATGTGTGCCCCCTTCACCGCCTCAAAATCTGCTTCTCTCCAGTCACC 177
QY 38 ArgLysGlnAsnLeuAspIleThrSerIleAlaSerAsnGlyGlyArgValGlnCys 56
Db 178 AGGAGGCCAACACACATCACTCTCTTGCAAGCAACGGTGGGAGAGTGCAATGC 234
```

Search completed: April 2, 2006, 03:51:41  
Job time : 107.728 secs



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OM protein - nucleic search using frame plus p2n model

Run on: April 1, 2006, 04:29:01 ; Search time 1155.21 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MAPTVMAASATATRTNPAQ.....ARRSSRLGNVASNGGRIRC 58

Scoring table:

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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9: gb.ro.\*  
10: gb.sts.\*  
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13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	203.5	72.2	185	6	AR212567 Sequence
3	203.5	72.2	185	6	AR590636 Sequence

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7	203.5	72.2	830	15	ZMRUBSSU
8	203.5	72.2	1648	15	ZMRBCS
9	203.5	72.2	1868	6	Q0828194
10	203.5	72.2	2318	6	BD014494
11	203.5	72.2	5281	6	AR581878
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14	203.5	72.2	5909	6	AX394257
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16	196.5	69.7	415	6	AR229545
17	196.5	69.7	415	6	AR260580
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20	196.5	69.7	3450	6	AR271020
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22	196.5	69.7	4149	6	AR271018
23	196.5	69.7	8349	6	AR260588
24	195.5	69.3	1274	15	ZMRUBSMU
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26	187.5	66.5	195	6	AR577398
27	171.5	60.8	1386	15	STRBCS2C
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32	165.5	58.7	1341	15	LERBCS3C
33	165.5	58.7	1520	15	LERBCS3A
34	164.5	58.3	1314	15	PERBCS11
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36	163.5	58.0	806	15	AY220079
37	162.5	57.6	22574	11	CVE18556
38	161	57.1	808	15	RCCPRBCUA
39	160.5	56.9	591	15	AB020942
40	160.5	56.9	1054	15	LERBCS3B
41	160.5	56.9	4124	15	TOMRBCO
42	159.5	56.6	177	6	I24839
43	159.5	56.6	177	6	I40228
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55	159	56.4	2795	15	NSRUBSSU
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58	156.5	55.5	2242	15	PERBCS08
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85	151.5	53.7	605	15	AB020935	AB020935 Aegilops
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87	151.5	53.7	607	15	AB020938	AB020938 Aegilops
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89	151.5	53.7	724	6	AK364047	AK364047 Sequence
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91	151.5	53.7	726	6	AK364195	AK364195 Sequence
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98	151.5	53.7	787	15	AB020954	AB020954 Triticum
99	151.5	53.7	787	15	AB020955	AB020955 Triticum
c 100	151.5	53.7	83646	15	BT005730	BT005730 Arabidops
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102	151	53.5	546	15	POTRBCS	J03613 Potato (S.t
103	151	53.5	778	15	TOMRBCSD	M15235 Tomato RUBP
104	151	53.5	1032	15	TOMRBCSA	M13542 Tomato (L.e
105	151	53.5	1454	15	LERBCS1	X05982 Tomato rbcs
106	151	53.5	1598	15	STRBCS3	X69763 S.tuberosum
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c 127	150.5	53.4	110000	15	AP008218_100	Continuation (101
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129	150.5	53.4	145890	15	CNS08C70	AL731739 Oryza sat
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131	150	53.2	1337	15	TOMRUBPB	M32420 Tobacco rib
132	149.5	53.0	599	15	TOMRBCSB	M13543 Tomato (L.e
133	149.5	53.0	684	6	AR428736	AR428736 Sequence
134	149.5	53.0	684	6	AR455412	AR455412 Sequence
135	149.5	53.0	684	6	AX329368	AX329368 Sequence
136	149.5	53.0	684	6	AX382258	AX382258 Sequence
137	149.5	53.0	720	15	AY062458	AY062458 Arabidops
138	149.5	53.0	728	15	AY062543	AY062543 Arabidops
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141	149.5	53.0	758	15	AY059939	AY059939 Arabidops
142	149.5	53.0	1097	15	BT013023	BT013023 Lycopersi
143	149.5	53.0	2006	15	BNRBCSF1	X55937 Brassica na
144	149.5	53.0	2776	15	LERBCS2	X05983 Tomato rbcs
145	149.5	53.0	9647	15	AYATSGS	X14564 A.thaliana
146	149	52.8	562	15	AY705444	AY705444 Fagus syl
147	148.5	52.7	586	15	AY093288	AY093288 Arabidops
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LOCUS						AX147212 183 bp DNA linear PAT 08-JUN-2001
DEFINITION						Sequence 1 from Patent WO0136622.
ACCESSION						AX147212
VERSION						AX147212.1 GI:14346383
KEYWORDS						Zea mays
SOURCE						Zea mays
ORGANISM						Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE						Caimi,P.G. and Lightner,J. Fructose polymer synthesis in monocot plastids Patent: WO 0136622-A 1 25-MAY-2001; E.I. DU PONT DE NEMOURS AND COMPANY (US)
AUTHORS						Location/Qualifiers
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QY						21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db						37 -----GCCGTGCTCCGTTCCAGGGGCTTAAGTCCACGCCGAGCTCCCGTCGCCCGC 90
QY						41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db						91 CGCTCTCTAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGAATCGGTGC 141
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LOCUS						AR212567 185 bp DNA linear PAT 20-JUN-2002
DEFINITION						Sequence 14 from patent US 6399861.
ACCESSION						AR212567
VERSION						AR212567.1 GI:21516176
KEYWORDS						Unknown.
SOURCE						Unknown.
ORGANISM						Unclassified.
REFERENCE						1 (bases 1 to 185)
AUTHORS						Anderson,P.C., Flick,C.E., Gordon-Kamm,W.J., Kausch,A.P., Mackey,C.J., Orozco,E.M., Orr,P., Stephens,M.A., Walters,D.A. and Walters,D.S.
TITLE						Methods and compositions for the production of stably transformed, fertile monocot plants and cells thereof
JOURNAL						Patent: US 6399861-A 14 04-JUN-2002;
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Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
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 Db 132 CGGTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 182

RESULT 3  
 AR590636 185 bp DNA linear PAT 15-DEC-2004  
 LOCUS  
 DEFINITION Sequence 14 from patent US 6803499.  
 ACCESSION AR590636  
 VERSION AR590636.1 GI:56638304  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 185)  
 AUTHORS Anderson,P.C., Flick,C.E., Gordon-Kamm,W.J., Kausch,A.P., Mackey,C.J., Orozco,E.M., Orr,P., Stephens,M.A., Walters,D.A. and Walters,D.S.  
 TITLE Methods and compositions for the production of stably transformed, fertile monocot plants and cells thereof  
 JOURNAL Patent: US 6803499-A 14 12-OCT-2004;  
 DeKalb Genetics Corporation; DeKalb, IL

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Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
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 Db 78 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 131

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
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 Db 132 CGGTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 182

RESULT 4  
 A44435 405 bp DNA linear PAT 07-MAR-1997  
 LOCUS  
 DEFINITION Sequence 4 from Patent EP0652286.

ACCESSION A44435  
 VERSION A44435.1 GI:2299261  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1 (bases 1 to 405)  
 AUTHORS Capellades,M., De,R.R., Montoliu,L., Puigdomenech,P., Torres,M.A., Rigau,J. and Uribe,J.  
 TITLE Promoter elements of chimaeric alpha tubulines  
 JOURNAL Patent: EP 0652286-A 4 10-MAY-1995;  
 RHONE POULENC AGROCHIMIE (FR)  
 COMMENT Other publication CN 1121958 960508  
 Other publication ZA 9408826 950717  
 Other publication SK 134094 950607  
 Other publication HU 70464 951030  
 Other publication BG 99169 950728  
 Other publication CZ 9402743 950913  
 Other publication BR 9404562 950620  
 Other publication JP 7184664 950725  
 Other publication PL 305775 950515  
 Other publication FR 2712302 950519  
 Other publication CA 2135461 950511  
 Other publication AU 7775194 950518.

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Alignment Scores:  
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US-10-628-525A-34 (1-58) x A44435 (1-405)

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Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
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 Db 298 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 351

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
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 Db 352 CGGTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 402

RESULT 5  
 I44914 405 bp DNA linear PAT 07-OCT-1997  
 LOCUS  
 DEFINITION Sequence 4 from patent US 5635618.  
 ACCESSION I44914  
 VERSION I44914.1 GI:2469627  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 405)  
 AUTHORS Capellades,M., De Rose,R., Montoliu,L., Puigdomenech,P., Torres,M.A., Uribe,J. and Rigau,J.  
 TITLE Promoter elements of chimeric genes of .alpha.-tubulin  
 JOURNAL Patent: US 5635618-A 4 03-JUN-1997;  
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ORIGIN



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Qy      41  ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgGlyArgCys 58
Db      156 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 206

RESULT 8
ZMRBCS
LOCUS      1648 bp      DNA      linear      PLN 10-FEB-1999
DEFINITION Maize rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase
small subunit (EC 4.1.1.39).
ACCESSION Y00322.1 GI:22464
VERSION   rbcS gene; ribulose bisphosphate carboxylase.
KEYWORDS  Zea mays
SOURCE    Zea mays
ORGANISM  Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1648)
Lebrun, M., Wakeman, G. and Freyssinet, G.
Nucleotide sequence of a gene encoding corn
ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
(rbcS)
JOURNAL   Nucleic Acids Res. 15 (10), 4360 (1987)
PUBMED    3588298
REFERENCE 2 (bases 1 to 1648)
AUTHORS   Freyssinet, G.
TITLE     Direct Submission
JOURNAL   Submitted (16-OCT-1987)
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misc_feature
intron
exon

Alignment Scores:
Pred. No.:      2,83e-09      Length:      1648
Score:          359.362
Percent Similarity: 81.0%
Best Local Similarity: 81.0%
Query Match:    11
DB:             2

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Score:          203.50      Matches:      47
Percent Similarity: 81.0%
Best Local Similarity: 81.0%
Query Match:    11
DB:             2

US-10-628-525A-34 (1-58) x ZMRBCS (1-1648)
Qy      1  MetaAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGln 20
Db      491  ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 526
Qy      21  AlaSerAlaValalaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db      527 -----GCCGTCGCTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 580
Qy      41  ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgGlyArgCys 58
Db      581  CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 631

RESULT 9
CQ828194
LOCUS      1868 bp      DNA      linear      PAT 05-JUL-2004
DEFINITION Sequence 6 from Patent WO2004053135.
ACCESSION CQ828194
VERSION   CQ828194.1 GI:49731677
KEYWORDS  synthetic construct
SOURCE    other sequences; artificial sequences.
ORGANISM  synthetic construct
REFERENCE 1
AUTHORS   Ferullo, J.M., Sailland, A., Schmitt, F. and Paget, E.
TITLE     Expression cassette encoding a hydroxyphenylpyruvate dioxygenase
and herbicide-tolerant plants containing such a gene
JOURNAL   Patent: WO 2004053135-A 6 24-JUN-2004;
Bayer CropScience S.A. (FR)
FEATURES
     source
       1..1868
         /organism="synthetic construct"
         /mol_type="unassigned DNA"
         /db_xref="taxon:32630"
         /note="Cassette d'expression actine intron -OTF-HPPD-tnos"

ORIGIN
Alignment Scores:
Pred. No.:      3.18e-09      Length:      1868
Score:          203.50      Matches:      47
Percent Similarity: 81.0%
Best Local Similarity: 81.0%
Query Match:    11
DB:             2

US-10-628-525A-34 (1-58) x CQ828194 (1-1868)
Qy      1  MetaAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGln 20
Db      234  ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 269
Qy      21  AlaSerAlaValalaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db      270 -----GCCGTCGCTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 323
Qy      41  ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgGlyArgCys 58
Db      324  CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 374

RESULT 10
BD014494
LOCUS      2318 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Transgenic corn and method of detecting recombinant gene from foods
containing the same.
ACCESSION BD014494
VERSION   BD014494.1 GI:22555277

```

KEYWORDS JP 2001136983-A/36.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 2318)  
AUTHORS Hino,A., Matsuoka,T., Kurihara,H., Masatake, Toyota, Aida,Y. and Akiyama,H.  
TITLE Transgenic corn and method of detecting recombinant gene from foods containing the same  
JOURNAL Patent: JP 2001136983-A 36 22-MAY-2001;  
NATL FOOD RES INST, DIRECTOR GENERAL OF NATIONAL INSTITUTE OF HEALTH SCIENCES  
COMMENT OS Artificial Sequence  
PN JP 2001136983-A/36  
PD 22-MAY-2001  
PF 30-AUG-2000 JP 2000261106  
PI AKIHIRO HINO, TAKESHI MATSUOKA, HIDEO KURIHARA, MASATAKE PI TOYOTA, YUKIHIRO AIDA,  
PI HIROSHI AKIYAMA  
PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00  
CC Description of Artificial Sequence: Partial sequence of CC recombinant gene in  
CC genetically modified maize  
FH Key Location/Qualifiers  
FT source 1. .2318  
FT Location/Qualifiers  
FEATURES  
source 1. .2318  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Alignment Scores:  
Pred. No.: 3.9e-09 Length: 2318  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2  
US-10-628-525A-34 (1-58) x BD014494 (1-2318)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAsnProAlaGln 20  
Db 665 ATGGCGCCACCGTGTATGGCTCGTGGCCACC----- 700  
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 701 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 754  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 755 CGCTCTCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 805  
RESULT 11  
AR581878/c  
LOCUS AR581878 5281 bp DNA linear PAT 15-DEC-2004  
DEFINITION Sequence 1 from patent US 6791014.  
ACCESSION AR581878  
VERSION AR581878.1 GI:56613881  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5281)  
AUTHORS Garcon,F. and Pelissier,B.  
TITLE Use of HPPD inhibitors as selection agents in plant transformation  
JOURNAL Patent: US 6791014-A 1 14-SEP-2004;  
Aventis Cropscience, S.A.;;  
FRX;  
FEATURES  
source Location/Qualifiers  
1. .5281

ORIGIN  
Alignment Scores:  
Pred. No.: 8.45e-09 Length: 5281  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2  
US-10-628-525A-34 (1-58) x AR581878 (1-5281)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAsnProAlaGln 20  
Db 4260 ATGGCGCCACCGTGTATGGCTCGTGGCCACC----- 4225  
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 4224 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 4171  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 4170 CGCTCTCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 4120  
RESULT 12  
AR394256/c  
LOCUS AR394256 5281 bp DNA linear PAT 18-MAY-2002  
DEFINITION Sequence 1 from Patent EP1186666.  
ACCESSION AR394256  
VERSION AR394256.1 GI:21065463  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Garcon,F. and Pelissier,B.  
TITLE Use of hppd inhibitors as selection agents in plant transformation  
JOURNAL Patent: EP 1186666-A 1 13-MAR-2002;  
AVENTIS CROPSCIENCE S.A. (FR)  
FEATURES  
source Location/Qualifiers  
1. .5281  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="gene chimere"  
ORIGIN  
Alignment Scores:  
Pred. No.: 8.45e-09 Length: 5281  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2  
US-10-628-525A-34 (1-58) x AX394256 (1-5281)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAsnProAlaGln 20  
Db 4260 ATGGCGCCACCGTGTATGGCTCGTGGCCACC----- 4225  
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 4224 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 4171  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 4170 CGCTCTCTCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 4120  
RESULT 13  
AR581879

LOCUS AR581879 5909 bp DNA linear PAT 15-DEC-2004  
DEFINITION Sequence 2 from patent US 6791014.  
ACCESSION AR581879  
VERSION AR581879.1 GI:56613883  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5909)  
AUTHORS Garcon,F. and Pelissier,B.  
TITLE Use of HPPD inhibitors as selection agents in plant transformation  
JOURNAL Patent: US 6791014-A 2 14-SEP-2004;  
Aventis Croscience, S.A.;;  
FRX;  
FEATURES  
source Location/Qualifiers  
1. .5909  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.39e-09 Length: 5909  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2  
US-10-628-525A-34 (1-58) x AR581879 (1-5909)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 1655 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 1690  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 1691 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 1744  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 1745 CGCTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1795  
RESULT 14  
AX394257  
LOCUS AX394257 5909 bp DNA linear PAT 18-MAY-2002  
DEFINITION Sequence 2 from Patent EP1186666.  
ACCESSION AX394257  
VERSION AX394257.1 GI:21065464  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Garcon,F. and Pelissier,B.  
TITLE Use of hppd inhibitors as selection agents in plant transformation  
JOURNAL Patent: EP 1186666-A 2 13-MAR-2002;  
AVENTIS CROSCIENCE S.A. (FR)  
FEATURES  
source Location/Qualifiers  
1. .5909  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="gene chimere"  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.39e-09 Length: 5909  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AX394257 (1-5909)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 1655 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 1690  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 1691 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 1744  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 1745 CGCTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1795  
RESULT 15  
AR206035  
LOCUS AR206035 415 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 49 from patent US 6372211.  
ACCESSION AR206035  
VERSION AR206035.1 GI:21504517  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 415)  
AUTHORS Isaac,B.G., Greenplate,J.T., Purcell,J.P. and Romano,C.P.  
TITLE Methods and compositions for controlling insects  
JOURNAL Patent: US 6372211-A 49 16-APR-2002;  
FEATURES  
source Location/Qualifiers  
1. .415  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Alignment Scores:  
Pred. No.: 3.33e-09 Length: 415  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 6 Gaps: 2  
US-10-628-525A-34 (1-58) x AR206035 (1-415)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 15 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 50  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 51 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 104  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 105 CGCTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 155  
RESULT 16  
AR229545  
LOCUS AR229545 415 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 13 from patent US 6448476.  
ACCESSION AR229545  
VERSION AR229545.1 GI:27269161  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 415)  
AUTHORS Barry,G.F.  
TITLE Plants and plant cells transformation to express an  
JOURNAL AMPA-N-acetyltransferase  
Patent: US 6448476-A 13 10-SEP-2002;  
Monsanto Technology LLC; St. Louis, MO  
FEATURES  
source Location/Qualifiers

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source 1. .415
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 3.33e-09 Length: 415
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR229545 (1-415)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 15 ATGGCGCCACCGTGATGATGGCTCTGTCGGCCACC----- 50

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 51 -----GCCGTGCTCCGTTCTTGGGGCTCAAGTCACCGCCAGCCTCCCGTCGCCCGC 104

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 105 CGCTCTCTCAGAAAGCCTCGGCAAGCTC---AGCAACGGCGGAAGGATCCGGTGC 155

RESULT 17
AR260580
LOCUS AR260580 415 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6489542.
ACCESSION AR260580
VERSION AR260580.1 GI:27311135
KEYWORDS
SOURCE
ORGANISM
Unkown.
Unclassified.
REFERENCE 1 (bases 1 to 415)
AUTHORS Corbin,D.R. and Romano,C.P.
TITLE Methods for transforming plants to express Cry2ab
JOURNAL .delta.-endotoxins targeted to the plastids
PATENT: US 6489542-A 3 03-DEC-2002;
Monsanto Technology LLC; St. Louis, MO
FEATURES
source 1. .415
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 3.33e-09 Length: 415
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR260580 (1-415)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 15 ATGGCGCCACCGTGATGATGGCTCTGTCGGCCACC----- 50

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 51 -----GCCGTGCTCCGTTCTTGGGGCTCAAGTCACCGCCAGCCTCCCGTCGCCCGC 104

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 105 CGCTCTCTCAGAAAGCCTCGGCAAGCTC---AGCAACGGCGGAAGGATCCGGTGC 155

RESULT 18
AR271024
LOCUS AR271024 416 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 25 from patent US 6501009.
ACCESSION AR271024
VERSION AR271024.1 GI:29702290
KEYWORDS
SOURCE
ORGANISM
Unkown.
Unclassified.
REFERENCE 1 (bases 1 to 416)
AUTHORS Romano,C.P.
TITLE Expression of Cry3B insecticidal protein in plants
JOURNAL Patent: US 6501009-A 25 31-DEC-2002;
Monsanto Technology LLC; St. Louis, MO
FEATURES
source 1. .416
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 3.34e-09 Length: 416
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR271024 (1-416)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 16 ATGGCGCCACCGTGATGATGGCTCTGTCGGCCACC----- 51

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 52 -----GCCGTGCTCCGTTCTTGGGGCTCAAGTCACCGCCAGCCTCCCGTCGCCCGC 105

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 106 CGCTCTCTCAGAAAGCCTCGGCAAGCTC---AGCAACGGCGGAAGGATCCGGTGC 156

RESULT 19
AR271026
LOCUS AR271026 416 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 30 from patent US 6501009.
ACCESSION AR271026
VERSION AR271026.1 GI:29702292
KEYWORDS
SOURCE
ORGANISM
Unkown.
Unclassified.
REFERENCE 1 (bases 1 to 416)
AUTHORS Romano,C.P.
TITLE Expression of Cry3B insecticidal protein in plants
JOURNAL Patent: US 6501009-A 30 31-DEC-2002;
Monsanto Technology LLC; St. Louis, MO
FEATURES
source 1. .416
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 3.34e-09 Length: 416
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR271026 (1-416)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
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Db      16 ATGGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 51
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      52 -----GCCGTGCTCGTTCTCTGGGGCTCAAGTCCACCGCCAGCTCCCGTCGGCCGC 105
Qy      41 ArgSerSerArgSerLeuGlyAanValAlaSerAanGlyGlyArgIleArgCys 58
Db      106 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

RESULT 20
AR271020
LOCUS      AR271020
DEFINITION Sequence 17 from patent US 6501009.
ACCESSION AR271020
VERSION    AR271020.1 GI:29702286
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 3450)
AUTHORS     Romano, C.P.
TITLE       Expression of Cry3B insecticidal protein in plants
JOURNAL     Monsanto Technology LLC; St. Louis, MO
FEATURES    Location/Qualifiers
             source
               1..3450
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      2,44e-08      Length:      3450
Score:          196.50      Matches:      46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:    69.7%      Indels:      11
DB:             6          Gaps:      2

US-10-628-525A-34 (1-58) x AR271020 (1-3450)

Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      825 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 860
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      861 -----GCCGTGCTCGTTCTCTGGGGCTCAAGTCCACCGCCAGCTCCCGTCGGCCGC 914
Qy      41 ArgSerSerArgSerLeuGlyAanValAlaSerAanGlyGlyArgIleArgCys 58
Db      915 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 965

RESULT 21
AR271032
LOCUS      AR271032
DEFINITION Sequence 36 from patent US 6501009.
ACCESSION AR271032
VERSION    AR271032.1 GI:29702298
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 3455)
AUTHORS     Romano, C.P.
TITLE       Expression of Cry3B insecticidal protein in plants
JOURNAL     Monsanto Technology LLC; St. Louis, MO
FEATURES    Location/Qualifiers
             source
               1..3455
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      2,44e-08      Length:      3455
Score:          196.50      Matches:      46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:    69.7%      Indels:      11
DB:             6          Gaps:      2

US-10-628-525A-34 (1-58) x AR271020 (1-3450)

Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      825 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 860
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      861 -----GCCGTGCTCGTTCTCTGGGGCTCAAGTCCACCGCCAGCTCCCGTCGGCCGC 914
Qy      41 ArgSerSerArgSerLeuGlyAanValAlaSerAanGlyGlyArgIleArgCys 58
Db      915 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 965

RESULT 22
AR271018
LOCUS      AR271018
DEFINITION Sequence 13 from patent US 6501009.
ACCESSION AR271018
VERSION    AR271018.1 GI:29702284
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 4149)
AUTHORS     Romano, C.P.
TITLE       Expression of Cry3B insecticidal protein in plants
JOURNAL     Patent: US 6501009-A 13 31-DEC-2002;
             Monsanto Technology LLC; St. Louis, MO
FEATURES    Location/Qualifiers
             source
               1..4149
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      2,9e-08      Length:      4149
Score:          196.50      Matches:      46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:    69.7%      Indels:      11
DB:             6          Gaps:      2

US-10-628-525A-34 (1-58) x AR271018 (1-4149)

Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      1488 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 1523
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      1524 -----GCCGTGCTCGTTCTCTGGGGCTCAAGTCCACCGCCAGCTCCCGTCGGCCGC 1577
Qy      41 ArgSerSerArgSerLeuGlyAanValAlaSerAanGlyGlyArgIleArgCys 58
Db      1578 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1628

RESULT 23
AR260588
LOCUS      AR260588
DEFINITION Sequence 16 from patent US 6489542.
ACCESSION AR260588
VERSION    AR260588.1 GI:27311143

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ORIGIN
Alignment Scores:
Pred. No.:      2,44e-08      Length:      3455
Score:          196.50      Matches:      46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:    69.7%      Indels:      11
DB:             6          Gaps:      2

US-10-628-525A-34 (1-58) x AR271032 (1-3455)

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Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      825 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 860
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      861 -----GCCGTGCTCGTTCTCTGGGGCTCAAGTCCACCGCCAGCTCCCGTCGGCCGC 914
Qy      41 ArgSerSerArgSerLeuGlyAanValAlaSerAanGlyGlyArgIleArgCys 58
Db      915 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 965

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RESULT 22
AR271018
LOCUS      AR271018
DEFINITION Sequence 13 from patent US 6501009.
ACCESSION AR271018
VERSION    AR271018.1 GI:29702284
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 4149)
AUTHORS     Romano, C.P.
TITLE       Expression of Cry3B insecticidal protein in plants
JOURNAL     Patent: US 6501009-A 13 31-DEC-2002;
             Monsanto Technology LLC; St. Louis, MO
FEATURES    Location/Qualifiers
             source
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ORIGIN
Alignment Scores:
Pred. No.:      2,9e-08      Length:      4149
Score:          196.50      Matches:      46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:    69.7%      Indels:      11
DB:             6          Gaps:      2

US-10-628-525A-34 (1-58) x AR271018 (1-4149)

```

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Qy      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      1488 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 1523
Qy      21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db      1524 -----GCCGTGCTCGTTCTCTGGGGCTCAAGTCCACCGCCAGCTCCCGTCGGCCGC 1577
Qy      41 ArgSerSerArgSerLeuGlyAanValAlaSerAanGlyGlyArgIleArgCys 58
Db      1578 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 1628

RESULT 23
AR260588
LOCUS      AR260588
DEFINITION Sequence 16 from patent US 6489542.
ACCESSION AR260588
VERSION    AR260588.1 GI:27311143

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KEYWORDS      .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 8349)
AUTHORS        Corbin,D.R. and Romano,C.P.
TITLE          Methods for transforming plants to express Cry2ab
               .delta.-endotoxins targeted to the plastids
JOURNAL        Patent: US 6489542-A 16 03-DEC-2002;
               Monsanto Technology LLC; St. Louis, MO
FEATURES      Location/Qualifiers
               source
               1..8349
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      5,6e-08      Length:      8349
Score:          196.50      Matches:      46
Percent Similarity: 79.3%      Conservative: 0
Best Local Similarity: 79.3%      Mismatches: 1
Query Match:     69.7%      Indels:      11
DB:              6          Gaps:          2

US-10-628-525A-34 (1-58) x AR260588 (1-8349)

QY      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      ATGGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 3304

QY      21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40
Db      -----GCCGTGCTCCGTTCCTGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCGC 3358

QY      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAenGlyGlyArgIleArgCys 58
Db      CGCTCTCTCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 3409

RESULT 24
ZMRUBSMSU      1274 bp      DNA      linear      PLN 15-NOV-1996
LOCUS          Z.mays rubisco small subunit gene.
DEFINITION     Y09214
ACCESSION      Y09214.1 GI:1673455
VERSION        rubisco small subunit.
KEYWORDS       Zea mays
SOURCE         Zea mays
ORGANISM       Zea mays

REFERENCE      1
AUTHORS        Ewing,R.M.
JOURNAL        Thesis (1996) Department of Plant Sciences, University of Oxford,
               U.K

REFERENCE      2 (bases 1 to 1274)
AUTHORS        Ewing,R.M.
TITLE          Direct Submission
JOURNAL        Submitted (05-NOV-1996) R.M. Ewing, University of Oxford, Plant
               Sciences, South Parks Road, Oxford, OX1 3RB, UK
FEATURES      Location/Qualifiers
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               /chromosome="21"
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CDS

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343..460
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461..826
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exon
intron
exon

ORIGIN
Alignment Scores:
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Score:          195.50      Matches:      45
Percent Similarity: 79.3%      Conservative: 1
Best Local Similarity: 77.6%      Mismatches: 1
Query Match:     69.3%      Indels:      11
DB:              15         Gaps:          2

US-10-628-525A-34 (1-58) x ZMRUBSMSU (1-1274)

QY      1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db      196 ATGGCGCCACCGTGATGATGGCTCGTCGGCAACC----- 231

QY      21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40
Db      -----GCCGTGCGCCCGCTTCAGGGTCTCAAGTCCGCCGAGCTCCCGTCGCCGC 285

QY      41 ArgSerSerArgSerLeuGlyAsnValAlaSerAenGlyGlyArgIleArgCys 58
Db      CGCAGCACCAAGGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 336

RESULT 25
AR088975
LOCUS          AR088975
DEFINITION     Sequence 9 from patent US 5990390.
ACCESSION      AR088975
VERSION        AR088975.1 GI:10015732
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 195)
AUTHORS        Lundquist,R.C., Walters,D.A. and Kiriwara,J.A.
TITLE          Methods and compositions for the production of stably transformed,
               fertile monocot plants and cells thereof
JOURNAL        Patent: US 5990390-A 9 23-NOV-1999;
FEATURES      Location/Qualifiers
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               /organism="unknown"
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Alignment Scores:
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Best Local Similarity: 80.0%      Mismatches: 0
Query Match:     66.5%      Indels:      11
DB:              6          Gaps:          2

US-10-628-525A-34 (1-58) x AR088975 (1-195)

QY      4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAla 23
Db      61 ACCGTGATGATGGCTCGTCGCCACC-----GCC 90

QY      24 ValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArgSerSer 43
Db      91 GTCGCTCGCTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGCGCGGCTCCTCC 150

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Qy 44 ArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
Db 151 AGAAGCCTCGCAACGTC---AGCAACGGCGGAGGATCGGTGC 192

RESULT 26  
AR577398  
LOCUS AR577398 195 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 9 from patent US 6777589.  
ACCESSION AR577398  
VERSION AR577398.1 GI:56579942  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 195)  
AUTHORS Lundquist,R.C. and Walters,D.A.  
TITLE Methods and compositions for the production of stably transformed, fertile monocot plants and cells thereof  
JOURNAL Patent: US 6777589-A 9 17-AUG-2004;  
DeKalb Genetics Corporation; DeKalb, IL

FEATURES  
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ORIGIN  
Alignment Scores:  
Pred. No.: 1.07e-08 Length: 195  
Score: 187.50 Matches: 44  
Percent Similarity: 80.0% Conservative: 0  
Best Local Similarity: 80.0% Mismatches: 0  
Query Match: 66.5% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x AR577398 (1-195)

Qy 4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGlnAlaSerAla 23  
Db 61 ACCGTGATGATGCCCTCGTCCGCCACC-----GCC 90

Qy 24 ValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgArgSerSer 43  
Db 91 GTCGCTCGGTTCAGGGGCTCAGTCCACGCCAGGCTCCCGTCCCGCGGTCTCTCC 150

Qy 44 ArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
Db 151 AGAAGCCTCGCAACGTC---AGCAACGGCGGAGGATCGGTGC 192

RESULT 27  
STRBCS2C  
LOCUS STRBCS2C 1386 bp DNA linear PLN 09-OCT-1996  
DEFINITION S.tuberosum rbcS2c gene for ribulose-(1,5)-bisphosphate carboxylase/oxygenase small subunit.

ACCESSION X69762.1 GI:21568  
VERSION X69762.1  
KEYWORDS chloroplast; gene expression; gene family; photosynthesis; protein transport; rbcS2c gene.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 1386)  
AUTHORS Fritsch,C., Wolter,F.P., Schenkemeyer,V., Herget,T. and Schreier,P.H.  
TITLE The gene family encoding the ribulose-(1,5)-bisphosphate carboxylase/oxygenase (Rubisco) small subunit of potato  
JOURNAL Gene 137 (2), 271-274 (1993)  
PUBMED 829958  
REFERENCE 2 (bases 1 to 1386)  
AUTHORS Schreier,P.H.  
TITLE Direct Submission  
JOURNAL Submitted (01-DEC-1992) P.H. Schreier, Bayer AG, PF-E/FU Gebaeude

6240, 5090 Leverkusen-Bayerwerk, FRG  
Related sequence: Fritsch, C.C., Proc. Natl. Acad. Sci. 88:4458-4462 (1991).

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429..605  
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605..694  
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830..914  
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915..1145  
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Best Local Similarity: 62.1% Mismatches: 11  
Query Match: 60.8% Indels: 1  
DB: 15 Gaps: 1

US-10-628-525A-34 (1-58) x STRBCS2C (1-1386)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGln 20  
Db 429 ATGGCTTCTTCAGTA---ATGTCCTCAGCGCTGTGCCACCGCGCAATGGTGCACAA 485

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 486 GCCAGCATGGTTGCACCTTCACTGGCCTCAAGTCCACCGCTCTTTCCTGTTTCAGG 545

Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
Db 486 GCCAGCATGGTTGCACCTTCACTGGCCTCAAGTCCACCGCTCTTTCCTGTTTCAGG 545

Db	546	AAGCAAAACCTTGACATTACCTCCATTGCTAGCAATGGTGGAGAGTCAGATGC	599
RESULT 28			
SLARBCS			
LOCUS			
DEFINITION	SLARBCS	723 bp mRNA linear	PLN 30-JUN-1995
ACCESSION	U00001.1	GI:556417	
VERSION	U00001.1	GI:556417	
KEYWORDS	ribosome, complete cds.		
SOURCE	ribosome, complete cds.		
ORGANISM	Stellaria longipes		
REFERENCE	1 (bases 1 to 723)		
AUTHORS	Zhang, X.-H., and Chinnappa, C.C.		
TITLE	Characterization and evolution of a cDNA encoding the small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcS) of Stellaria longipes (Caryophyllaceae)		
JOURNAL	Plant Species Biol. 10, 39-51 (1995)		
REFERENCE	2 (bases 1 to 723)		
AUTHORS	Zhang, X.-H.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-OCT-1994) King-Hai Zhang, Department of Biological Sciences, University of Calgary, Alberta, Canada		
COMMENT	Original source text: Stellaria longipes cDNA to mRNA.		
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	/note="putative"		
CDS	33. .575		
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	/note="putative"		
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Query Match:	60.1%	Indels:	1
DB:	15	Gaps:	1
US-10-628-525A-34 (1-58) x SLARBCS (1-723)			
QY	1	MetaAlaProThrValMetMetAlaSerAlaThrAlaThrArgThrAsnProAlaGln	20

Db	33	ATGGCTTCTCAATA---ATGTCATCGGAGCTGTGCTACACGAGCATGGTGTCTCAA	89
QY	21	AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg	40
Db	90	GCTAGCATGGTCGACCCCTTCACCTGGTCTCAAGTCTTAAGGCTTCTTTCTGTTTCAAGG	149
QY	41	ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgLeuArgCys	58
Db	150	AAGACAAACCTTGACATTACCTCCATTGCTAGCAATGGTGGAGAGTCAGATGC	203
RESULT 29			
STRBCS2			
LOCUS			
DEFINITION	S.tuberosum rbcS2	1629 bp DNA linear	PLN 09-OCT-1996
ACCESSION	X69760.1	GI:21564	
VERSION	X69760.1	GI:21564	
KEYWORDS	chloroplast; gene expression; gene family; photosynthesis; protein transport; rbcS2a gene.		
SOURCE	Solanum tuberosum (potato)		
ORGANISM	Solanum tuberosum		
REFERENCE	1 (bases 1 to 1629)		
AUTHORS	Fritz, C.C., Wolter, F.P., Schenkemeyer, V., Herget, T. and Schreier, P.H.		
TITLE	The gene family encoding the ribulose- (1,5)-bisphosphate carboxylase/oxygenase (Rubisco) small subunit of potato		
JOURNAL	Gene 137 (2), 271-274 (1993)		
REFERENCE	2 (bases 1 to 1629)		
AUTHORS	Schreier, P.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-DEC-1992) P.H. Schreier, Bayer AG, PF-E/FU Gebaeude 6240, 5090 Leverkusen-Bayerwerk, FRG		
COMMENT	Related sequence: Fritz, C.C., Proc. Natl. Acad. Sci. 88:4458-4462 (1991).		
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	exon		



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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 00:15:06 ; Search time 136.553 Seconds  
(without alignments)  
2830.777 Million cell updates/sec

Title: US-10-628-525a-34

Perfect score: 282

Sequence: 1 MATVWMASSATATRTNPAQ.....ARRSRSLGNVAGNGRIRC 58

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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13: Geneseqn2004bs:\*  
14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	203.5	72.2	183	10	Aad79096 Corn RUBI
3	203.5	72.2	185	2	Aaq82917 Maize chl
4	203.5	72.2	228	12	Adp57000 Maize car

5	203.5	72.2	229	12	ADP57015
6	203.5	72.2	230	12	ADP57195
7	203.5	72.2	235	12	ADP57010
8	203.5	72.2	236	12	ADP57001
9	203.5	72.2	238	12	ADP56997
10	203.5	72.2	249	12	ADP57002
11	203.5	72.2	264	12	ADP56984
12	203.5	72.2	265	12	ADP56971
13	203.5	72.2	272	12	ADP56976
14	203.5	72.2	276	12	ADP56957
15	203.5	72.2	276	12	ADP56982
16	203.5	72.2	284	12	ADP56963
17	203.5	72.2	286	12	ADP56968
18	203.5	72.2	291	12	ADP56978
19	203.5	72.2	297	12	ADP56945
20	203.5	72.2	298	12	ADP56952
21	203.5	72.2	305	12	ADP56947
22	203.5	72.2	307	12	ADP56960
23	203.5	72.2	309	12	ADP56946
24	203.5	72.2	311	12	ADP56961
25	203.5	72.2	312	12	ADP56999
26	203.5	72.2	315	12	ADP56942
27	203.5	72.2	317	12	ADP56941
28	203.5	72.2	319	12	ADP56935
29	203.5	72.2	344	12	ADP57162
30	203.5	72.2	405	2	AAQ88331
31	203.5	72.2	409	12	ADP57146
32	203.5	72.2	415	12	ADP57175
33	203.5	72.2	438	12	ADP57141
34	203.5	72.2	441	12	ADP57160
35	203.5	72.2	443	12	ADP57156
36	203.5	72.2	1449	3	AAZ36874
37	203.5	72.2	1868	12	ADQ54814
38	203.5	72.2	2318	5	AAH49585
39	203.5	72.2	5281	6	ABL56341
40	203.5	72.2	5909	6	ABL56342
41	202.5	71.8	197	12	ADP57201
42	202.5	71.8	198	12	ADP57030
43	202.5	71.8	258	12	ADP56979
44	202.5	71.8	268	12	ADP56985
45	202.5	71.8	269	12	ADP56993
46	202.5	71.8	276	12	ADP56975
47	202.5	71.8	278	12	ADP56953
48	202.5	71.8	283	12	ADP56962
49	202.5	71.8	286	12	ADP56972
50	202.5	71.8	290	12	ADP56966
51	202.5	71.8	291	12	ADP56980
52	202.5	71.8	291	12	ADP56956
53	202.5	71.8	291	12	ADP56965
54	202.5	71.8	296	12	ADP56969
55	202.5	71.8	310	12	ADP56954
56	202.5	71.8	310	12	ADP56958
57	202.5	71.8	316	12	ADP56940
58	202.5	71.8	381	12	ADP57151
59	202.5	71.8	411	12	ADP57152
60	202.5	71.8	414	12	ADP57144
61	202.5	71.8	433	12	ADP57142
62	202.5	71.8	434	12	ADP57154
63	202.5	71.8	434	12	ADP57155
64	199.5	70.7	283	12	ADP56970
65	198.5	70.4	226	12	ADP57028
66	198.5	70.4	428	12	ADP57148
67	198.5	70.4	453	12	ADP57161
68	197.5	70.0	199	12	ADP57036
69	197.5	70.0	312	12	ADP56973
70	197.5	70.0	382	12	ADP57166
71	196.5	69.7	285	12	ADP57006
72	196.5	69.7	415	3	AAQ01002
73	196.5	69.7	415	3	AAH15557
74	196.5	69.7	415	6	AAH37859
75	196.5	69.7	415	8	ACD29599
76	196.5	69.7	416	3	AAZ51647
77	196.5	69.7	416	3	AAZ51649

Adp57015 Maize car  
Adp57195 Maize car  
Adp57010 Maize car  
Adp57001 Maize car  
Adp56997 Maize car  
Adp57002 Maize car  
Adp56984 Maize car  
Adp56971 Maize car  
Adp56976 Maize car  
Adp56957 Maize car  
Adp56982 Maize car  
Adp56963 Maize car  
Adp56968 Maize car  
Adp56978 Maize car  
Adp56945 Maize car  
Adp56952 Maize car  
Adp56947 Maize car  
Adp56960 Maize car  
Adp56946 Maize car  
Adp56961 Maize car  
Adp56999 Maize car  
Adp56942 Maize car  
Adp56941 Maize car  
Adp56935 Maize car  
Adp57162 Maize car  
Aaq88331 Optimal  
Adp57146 Maize car  
Adp57175 Maize car  
Adp57141 Maize car  
Adp57160 Maize car  
Adp57156 Maize car  
Aaz36874 cDNA enco  
Aad54814 DNA expre  
Aah49585 Partial s  
Abi56341 Nucleotid  
Abi56342 Nucleotid  
Adp57201 Maize car  
Adp57030 Maize car  
Adp56979 Maize car  
Adp56985 Maize car  
Adp56993 Maize car  
Adp56975 Maize car  
Adp56953 Maize car  
Adp56962 Maize car  
Adp56972 Maize car  
Adp56966 Maize car  
Adp56980 Maize car  
Adp56956 Maize car  
Adp56965 Maize car  
Adp56969 Maize car  
Adp56954 Maize car  
Adp56958 Maize car  
Adp56940 Maize car  
Adp57151 Maize car  
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Adp57144 Maize car  
Adp57142 Maize car  
Adp57154 Maize car  
Adp57155 Maize car  
Adp56970 Maize car  
Adp57028 Maize car  
Adp57148 Maize car  
Adp57161 Maize car  
Adp57036 Maize car  
Adp56973 Maize car  
Adp57166 Maize car  
Adp57006 Maize car  
Aad01002 Maize chl  
Aah15557 ZnSSU pla  
Aad37859 Maize mss  
ACD29599 Maize RUB  
Aaz51647 Maize RUB  
Aaz51649 Cauliflow

78	196.5	69.7	416	10	AA61797 Modified
79	196.5	69.7	416	10	AA61795 Zea mays
80	196.5	69.7	416	12	ADJ62838 CamV35S A
81	196.5	69.7	3450	3	AA251643 Bacillus
82	196.5	69.7	3450	10	AA61791 Bt.cry3Bb
83	196.5	69.7	3450	10	ABX95187 B. thurin
84	196.5	69.7	3455	3	AA251655 Bacillus
85	196.5	69.7	3455	10	AA61803 Bt.cry3Bb
86	196.5	69.7	3455	10	ABX95199 B. thurin
87	196.5	69.7	4149	3	AA251641 Bacillus
88	196.5	69.7	4149	10	AA61789 Bt.cry3Bb
89	196.5	69.7	4149	10	ABX95185 B. thurin
90	196.5	69.7	5600	12	ADK98490 B thuring
91	196.5	69.7	7000	12	ADK98485 B thuring
92	196.5	69.7	8349	3	AA15565 pMON30464
93	195.5	69.3	212	12	ADP57021 Maize car
94	195.5	69.3	232	12	ADP57013 Maize car
95	195.5	69.3	241	12	ADP57003 Maize car
96	195.5	69.3	242	12	ADP57012 Maize car
97	195.5	69.3	242	12	ADP57032 Maize car
98	195.5	69.3	244	12	ADP57019 Maize car
99	195.5	69.3	250	12	ADP57197 Maize car
100	195.5	69.3	259	12	ADP57034 Maize car
101	195.5	69.3	265	12	ADP57029 Maize car
102	195.5	69.3	266	12	ADP57023 Maize car
103	195.5	69.3	269	12	ADP57026 Maize car
104	195.5	69.3	270	12	ADP57025 Maize car
105	195.5	69.3	273	12	ADP57020 Maize car
106	195.5	69.3	275	12	ADP57200 Maize car
107	195.5	69.3	275	12	ADP56990 Maize car
108	195.5	69.3	276	12	ADP57022 Maize car
109	195.5	69.3	276	12	ADP57018 Maize car
110	195.5	69.3	279	12	ADP57014 Maize car
111	195.5	69.3	286	12	ADP57017 Maize car
112	195.5	69.3	287	12	ADP57011 Maize car
113	195.5	69.3	289	12	ADP56981 Maize car
114	195.5	69.3	291	12	ADP57009 Maize car
115	195.5	69.3	292	12	ADP57016 Maize car
116	195.5	69.3	294	12	ADP57008 Maize car
117	195.5	69.3	298	12	ADP56992 Maize car
118	195.5	69.3	302	12	ADP56943 Maize car
119	195.5	69.3	307	12	ADP57007 Maize car
120	195.5	69.3	310	12	ADP56938 Maize car
121	195.5	69.3	312	12	ADP56967 Maize car
122	195.5	69.3	312	12	ADP56948 Maize car
123	195.5	69.3	315	12	ADP56955 Maize car
124	195.5	69.3	316	12	ADP57189 Maize car
125	195.5	69.3	322	12	ADP56949 Maize car
126	195.5	69.3	326	12	ADP56974 Maize car
127	195.5	69.3	330	12	ADP56937 Maize car
128	195.5	69.3	364	12	ADP57185 Maize car
129	195.5	69.3	364	12	ADP57183 Maize car
130	195.5	69.3	381	12	ADP57174 Maize car
131	195.5	69.3	399	12	ADP57170 Maize car
132	195.5	69.3	399	12	ADP57176 Maize car
133	195.5	69.3	415	12	ADP57173 Maize car
134	195.5	69.3	421	12	ADP57191 Maize car
135	195.5	69.3	425	12	ADP57168 Maize car
136	195.5	69.3	428	12	ADP57194 Maize car
137	195.5	69.3	446	12	ADP57172 Maize car
138	195.5	69.3	455	12	ADP57163 Maize car
139	195.5	69.3	510	12	ADJ44718 Plant cDN
140	194.5	69.0	261	12	ADP57024 Maize car
141	194.5	69.0	269	12	ADP56994 Maize car
142	194.5	69.0	458	12	ADP57147 Maize car
143	192.5	68.3	265	12	ADP56996 Maize car
144	192.5	68.3	360	12	ADP57171 Maize car
145	191.5	67.9	271	12	ADP57031 Maize car
146	191.5	67.9	325	12	ADP56977 Maize car
147	191.5	67.9	368	12	ADP57178 Maize car
148	191.5	67.9	418	12	ADP57180 Maize car
149	190.5	67.6	303	12	ADP56959 Maize car
150	189.5	67.2	179	12	ADP57040 Maize car

# ALIGNMENTS

RESULT 1  
AAH27499

ID AAH27499 standard; DNA; 183 BP.

XX

AC AAH27499;

XX

DT 21-AUG-2001 (first entry)

XX

DE Small subunit Rubisco chloroplast transit signal partial DNA sequence.

XX

KW Small subunit RuBP-carboxylase chloroplast transit signal; maize;

KW

Rubisco; fructo-oligosaccharide; FOS; ds.

OS

XX Zea mays.

XX

FT Key Location/Qualifiers

FT

1..141

/tag= a

/product= "Maize small subunit RuBP-carboxylase

chloroplast transit signal"

/transl\_except= (pos:52..54,aa=Trp)

/note= "No stop codon given"

XX

FN WO200136622-A2.

XX

PD 25-MAY-2001.

XX

PF 20-NOV-2000; 2000WO-US031788.

XX

PR 18-NOV-1999; 99US-0166268P.

XX

(DUPO ) DU PONT DE NEMOURS & CO E I.

XX

PI Caiimi PG, Lightner J;

XX

WPI; 2001-355631/37.

DR

P-PSDB; AAB98694.

XX

Increasing fructo-oligosaccharide levels in monocots by inserting

recombinant DNA construct having tissue specific promoter linked to

plastid targeting sequence and fructosyltransferase coding sequence, into

monocot cell.

XX

Example 1; Page 35; 35pp; English.

XX

The present invention relates to a method for increasing fructo-

oligosaccharide (FOS) levels in a monocot. The method comprises inserting

into a monocot cell, a recombinant DNA construct comprising a tissue

specific promoter, operably linked to a plastid targeting sequence,

operably linked to a coding sequence for a fructosyltransferase gene, so

that the construct can transform a monocot cell and the transformed

monocot synthesises and accumulates FOS. The present sequence is a

partial coding sequence for the maize small subunit RuBP-carboxylase

(Rubisco) chloroplast transit signal, which was used in an example from

XX

SQ Sequence 183 BP; 31 A; 65 C; 58 G; 29 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 4.6e-14 Length: 183

Score: 203.50 Matches: 47

Percent Similarity: 81.0% Conservative: 0

Best Local Similarity: 81.0% Mismatches: 0

Query Match: 72.2% Indels: 11

DB: 4 Gaps: 2

US-10-628-525A-34 (1-58) x AAH27499 (1-183)

Qy 1 MetaAlaProThrValMetMetAlaSerAlaThrAlaThrArgThrAsnProAlaGln 20



```

Db 1 ATGGCGGCCACCGTGATGATGGCTCTGTCGCCACCC----- 36
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 37 -----GCCGTGCTCCGCTCCAGGGCTTAAGTCCACCGCCAGCCTCCCGTCGCCCGC 90
Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyArgIleArgCys 58
Db 91 CGCTCTCTAGAGCCTCGGCAACGTC---AGCAACGGCGGAGAAATCCGGTGC 141

RESULT 2
ADD79096
ID ADD79096 standard; DNA; 183 BP.
XX
AC ADD79096;
XX
DT 29-JAN-2004 (first entry)
XX
DE Corn RUBISCO gene chloroplast transit signal DNA.
XX
KW Corn; ds; RUBISCO; chloroplast transit signal;
KW RuBP carboxylase small subunit; PTF; fructosyl transferase; SacB; plant;
KW Corn; fructo-oligosaccharide; monocotyledon; plastid targeting sequence;
KW starch-fructo-oligosaccharide blend; food; fructose syrup; plastic;
KW zein promoter.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT 1..141
FT CDS /*tag= a
FT /partial
FT /note= "No stop codon shown"
FT /product= "RUBISCO chloroplast transit signal"
FT /transl_except= (pos:52..54,aa:Trp)

US2003213013-A1.
13-NOV-2003.
07-MAY-2002; 2002US-00140410.
07-MAY-2002; 2002US-00140410.
(CAIM/) CAIMI P G.
(LIGH/) LIGHTNER J E.

Caimi PG, Lightner JE;
WPI; 2003-864895/80.
P-PSDB; ADD79097.

Increasing fructo-oligosaccharide levels in monocotyledon by transforming
monocotyledon cell with DNA construct comprising tissue specific
promoter, operably linked to plastid targeting sequence and
fructosyltransferase gene.

Example 1; SEQ ID NO 1; 21pp; English.

The invention relates to increasing the fructo-oligosaccharide levels in
a monocotyledon, comprising inserting into a monocotyledon cell a
recombinant DNA construct having a tissue specific promoter, operably
linked to a plastid targeting sequence, operably linked to a coding
sequence for a fructosyltransferase (PTF) gene, so that the construct can
transform a monocotyledon cell and the transformed monocotyledon
synthesizes and accumulates fructo-oligosaccharides. Also included are
following a recombinant DNA construct (comprising a tissue specific
promoter, operably linked to a plastid targeting sequence, operably
linked to a coding sequence for a fructosyltransferase gene so that the
construct can transform a monocotyledon cell to obtain the production of
fructo-oligosaccharides in the plastid of the monocotyledon cell), a
monocotyledon transformed with the construct (producing fructo-

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CC oligosaccharides which accumulate in the plastid within cells of the
CC monocotyledon), a seed produced from the transformed monocotyledon and an
CC isolated starch-fructo-oligosaccharide blend (where the rheological
CC properties of pasting temperature and final viscosity are independently
CC altered related to the pasting temperature and final viscosity of a
CC starch solution substantially free of fructo-oligosaccharides, provided
CC that the starch solution comprises substantially the same amount of
CC starch as in the blend). The construct is useful for making a starch
CC fructo-oligosaccharide blend. The construct and the method are useful for
CC increasing fructo-oligosaccharide levels in a monocotyledon such as corn,
CC wheat, rice barley, sorghum, triticale and rye. The transformed plant is
CC useful for producing fructo-oligosaccharides. The method allows for
CC extraction of fructo-oligosaccharide from the transgenic for the purpose
CC of fructo-oligosaccharide production. The fructo-oligosaccharides and
CC fructo-oligosaccharide/starch mixture may be used in food and non-food
CC applications such as human and animal food products, production of
CC fructose syrups and the production of chemicals and plastics either as
CC such or in modified form. A construct of the invention was produced
CC comprising the Bacillus amyloliquefaciens SacB (FTF) gene under the
CC control of the zein promoter as a fusion protein with the corn RUBISCO
CC (RuBP carboxylase small subunit) chloroplast transit peptide. The present
CC sequence encodes the RUBISCO chloroplast transit peptide.
XX
SQ Sequence 183 BP; 31 A; 65 C; 58 G; 29 T; 0 U; 0 Other;

```

```

Alignment Scores:
Pred. No.: 4..6e-14 Length: 183
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 10 Gaps: 2

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US-10-628-525A-34 (1-58) x ADD79096 (1-183)

```

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 1 ATGGCGGCCACCGTGATGATGGCTCTGTCGCCACCC----- 36
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 37 -----GCCGTGCTCCGCTCCAGGGCTTAAGTCCACCGCCAGCCTCCCGTCGCCCGC 90
Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyArgIleArgCys 58
Db 91 CGCTCTCTAGAGCCTCGGCAACGTC---AGCAACGGCGGAGAAATCCGGTGC 141

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# RESULT 3

```

AAQ82917
ID AAQ82917 standard; DNA; 185 BP.
XX
AC AAQ82917;
XX
DT 25-MAR-2003 (revised)
DT 01-NOV-1995 (first entry)
XX
DE Maize chloroplast transit peptide synthetic gene fragment.
XX
KW Bacillus thuringiensis HD1; Bt gene; endotoxin; transgenic maize;
KW insect resistance; maize chloroplast transit peptide; ds.
XX
OS Synthetic.
XX
PN WO9506128-A2.
XX
PD 02-MAR-1995.
XX
PF 24-AUG-1994; 94WO-US009699.
XX
PR 25-AUG-1993; 93US-00113561.
XX
PA (DEKA-) DEKALB GENETICS CORP.
XX

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PI Dams TR, Anderson PC, Daines RJ, Gordon-Kamm WJ, Kausch AP;
PI Mackey CJ, Orozco EM, Orr PM, Stephens MA;
XX WPI; 1995-106857/14.
DR Fertile, transgenic maize plants and their production - useful for crop
XX improvements e.g. improved resistance to insect pests and improved
XX productivity.
XX Example 6; Page 123; 351pp; English.
XX AAQ82917 is a maize chloroplast transit peptide synthetic gene fragment.
CC It was used in the construction of an expression vector for the Bacillus
CC thuringiensis strain HD1 Bt gene endotoxin (AAR65297). The vector was
CC used to transform maize plants, the progeny of which could express the B.
CC thuringiensis endotoxin. This conferred upon the transgenic maize plants
CC the advantage of increased insect resistance, compared to wild type
CC plants. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 185 BP; 34 A; 70 C; 54 G; 27 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,66e-14 Length: 185
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x AAQ82917 (1-185)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 42 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 77
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 78 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCGC 131
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 132 CGGTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 182

RESULT 4
ADP57000
ID ADP57000 standard; cDNA; 228 BP.
XX AC ADP57000;
XX DT 09-SEP-2004 (first entry)
XX DE Maize carbon assimilation pathway enzyme cDNA #69.
XX KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;
XX KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;
XX KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;
XX KW aldolase; fructose-1,6-bisphosphate; transketolase;
XX KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;
XX KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;
XX KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;
XX KW aspartate aminotransferase; alanine aminotransferase;
XX KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;
XX KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;
XX KW plant metabolic pathway; plant breeding.
XX OS Zea mays.
XX XX US2004116682-A1.
XX PN 17-JUN-2004.
XX PD 16-NOV-2001; 2001US-00987899.
XX PF ADP57015
XX ID ADP57015 standard; cDNA; 229 BP.

PR 06-MAR-1998; 98US-0076912P.
PR 04-MAR-1999; 99US-00262979.
XX (CHEI/) CHEIKH N.
PA (MILL/) MILLER P W.
PA (OCON/) O'CONNELL K M.
PA (LIU/) LIU J.
XX Cheikh N, Miller PW, O'connell KM, Liu J;
XX WPI; 2004-498291/47.
XX New substantially purified nucleic acid molecule encoding a maize or
XX soybean carbon assimilation pathway enzyme, useful for gene mapping, gene
XX identification and analysis, plant breeding, and preparation of
XX constructs.
XX Claim 2; SEQ ID NO 69; 196pp; English.
XX The invention relates to a substantially purified nucleic acid molecule
XX that encodes a maize or soybean carbon assimilation pathway enzyme or its
XX fragment. The maize or soybean carbon assimilation pathway enzyme or its
XX fragment is selected from ribulose-bisphosphate carboxylase,
XX phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose
XX phosphate isomerase, aldolase, fructose-1,6-bisphosphate,
XX transketolase, sedoheptulose-1,7-bisphosphate, D-ribulose-5-phosphate-3
XX -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,
XX phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,
XX aspartate aminotransferase, alanine aminotransferase, NADP-dependent
XX malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,
XX phosphate dikinase and pyrophosphatase. The invention also relates to a
XX substantially purified antibody or its fragment which is capable of
XX specifically binding to a specific maize or soybean carbon assimilation
XX pathway enzyme or its fragment, a transformed plant having a nucleic acid
XX molecule comprising an exogenous promoter region which functions in a
XX plant cell to cause the production of an mRNA molecule, and a method of
XX determining a level or pattern in a plant cell of a carbon assimilation
XX pathway enzyme in a plant metabolic pathway. The methods and compositions
XX of the invention are useful for gene mapping, gene identification and
XX analysis, plant breeding and preparation of constructs for use in plant
XX gene expression and transgenic plants. This sequence represents cDNA
XX encoding a maize carbon assimilation pathway enzyme of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html.
XX SQ Sequence 228 BP; 44 A; 83 C; 68 G; 33 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,01e-14 Length: 228
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP57000 (1-228)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 72
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGGTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 177

RESULT 5
ADP57015
ID ADP57015 standard; cDNA; 229 BP.

```



CC The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

SQ Sequence 230 BP; 44 A; 84 C; 68 G; 34 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 6.08e-14 Length: 230  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP57195 (1-230)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 37 ATGGCGCCACCGTGATGCTCGCTCGGCCACCC----- 72  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuValSerThrAlaSerLeuProValAlaArg 40  
 DB 73 -----GCCGTCGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGCTCGGCCCG 126  
 QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgIleArgCys 58  
 DB 127 CGCTCTCTCAGAACGCTCGGCACAGTC---AGCACGGCGGAAGGATCGGTGC 177

RESULT 7

ADP57010

ID ADP57010 standard; cDNA; 235 BP.

XX AC ADP57010;

XX DT 09-SEP-2004 (first entry)

XX DE Maize carbon assimilation pathway enzyme cDNA #79.

XX KW Ribulose-bisphosphate carboxylase; gene; ss; maize; corn;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphatase; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 XX plant metabolic pathway; plant breeding.

OS Zea mays.

XX PN US2004116682-A1.

XX PD 17-JUN-2004.

XX PF 16-NOV-2001; 2001US-00987899.

XX PR 06-MAR-1998; 98US-0076912P.

XX PR 04-MAR-1999; 99US-00262979.

XX (CHEI/) CHEIKH N.

PA (MILL/) MILLER P W.

PA (OCON/) O'CONNELL K M.

PA (LIU/) LIU J.

XX Cheikh N, Miller PW, O'Connell KM, Liu J;

XX WPI; 2004-498291/47.

XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.

XX Claim 2; SEQ ID NO 79; 196pp; English.

XX The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

XX SQ Sequence 235 BP; 49 A; 84 C; 70 G; 32 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.24e-14 Length: 235  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP57010 (1-235)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

DB 47 ATGGCGCCACCGTGATGCTCGCTCGGCCACCC----- 82

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuValSerThrAlaSerLeuProValAlaArg 40

DB 83 -----GCCGTCGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGCTCGGCCCG 136

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
|||  
Db 137 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 187  
RESULT 8  
ADP57001  
ID ADP57001 standard; cDNA; 236 BP.  
XX AC ADP57001;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Maize carbon assimilation pathway enzyme cDNA #70.  
XX  
XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphate; transketolase;  
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX OS Zea mays.  
XX US2004116682-A1.  
XX PD 17-JUN-2004.  
XX PF 16-NOV-2001; 2001US-00987899.  
XX PR 06-MAR-1998; 98US-0076912P.  
XX PR 04-MAR-1999; 99US-00262979.  
XX  
XX (CHEI/) CHEIKH N.  
XX (MILL/) MILLER P W.  
XX (OCON/) O'CONNELL K M.  
XX (LIUJ/) LIU J.  
XX  
XX Cheikh N, Miller PW, O'connell KM, Liu J;  
XX WPI; 2004-498291/47.  
XX  
XX New substantially purified nucleic acid molecule encoding a maize or  
PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
PT identification and analysis, plant breeding, and preparation of  
PT constructs.  
XX  
XX Claim 2; SEQ ID NO 70; 196pp; English.  
XX  
XX The invention relates to a substantially purified nucleic acid molecule  
CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
CC fragment is selected from ribulose-bisphosphate carboxylase,  
CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
CC phosphate isomerase, aldolase, fructose-1,6-bisphosphate, triose  
CC transketolase, sedoheptulose-1,7-bisphosphate, D-ribulose-5-phosphate-3-  
CC epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
CC substantially purified antibody or its fragment which is capable of  
CC specifically binding to a specific maize or soybean carbon assimilation  
CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
CC molecule comprising an exogenous promoter region which functions in a  
CC plant cell to cause the production of an mRNA molecule, and a method of  
CC determining a level or pattern in a plant cell of a carbon assimilation  
CC pathway enzyme in a plant metabolic pathway. The methods and compositions

CC of the invention are useful for gene mapping, gene identification and  
CC analysis, plant breeding and preparation of constructs for use in plant  
CC gene expression and transgenic plants. This sequence represents cDNA  
CC encoding a maize carbon assimilation pathway enzyme of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
XX seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 236 BP; 40 A; 90 C; 72 G; 34 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 6.27e-14 Length: 236  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 12 Gaps: 2  
US-10-628-525A-34 (1-58) x ADP57001 (1-236)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||  
Db 13 ATGGGCCCCACCGTGATGAGCTCGTCGGCCACC----- 48  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
|||  
Db 49 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCGC 102  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
|||  
Db 103 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 153  
RESULT 9  
ADP56997  
ID ADP56997 standard; cDNA; 238 BP.  
XX AC ADP56997;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Maize carbon assimilation pathway enzyme cDNA #66.  
XX  
XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphate; transketolase;  
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX  
XX Zea mays.  
XX OS  
XX US2004116682-A1.  
XX  
XX PD 17-JUN-2004.  
XX PF 16-NOV-2001; 2001US-00987899.  
XX PR 06-MAR-1998; 98US-0076912P.  
XX PR 04-MAR-1999; 99US-00262979.  
XX  
XX (CHEI/) CHEIKH N.  
XX (MILL/) MILLER P W.  
XX (OCON/) O'CONNELL K M.  
XX (LIUJ/) LIU J.  
XX  
XX Cheikh N, Miller PW, O'connell KM, Liu J;  
XX WPI; 2004-498291/47.  
XX

XX New substantially purified nucleic acid molecule encoding a maize or  
PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
PT identification and analysis, plant breeding, and preparation of  
PT constructs.  
XX Claim 2; SEQ ID NO 66; 196pp; English.  
PS  
XX  
CC The invention relates to a substantially purified nucleic acid molecule  
CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
CC fragment is selected from ribulose-bisphosphate carboxylase,  
CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
CC substantially purified antibody or its fragment which is capable of  
CC specifically binding to a specific maize or soybean carbon assimilation  
CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
CC molecule comprising an exogenous promoter region which functions in a  
CC plant cell to cause the production of an mRNA molecule, and a method of  
CC determining a level or pattern in a plant cell of a carbon assimilation  
CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
CC of the invention are useful for gene mapping, gene identification and  
CC analysis, plant breeding and preparation of constructs for use in plant  
CC gene expression and transgenic plants. This sequence represents cDNA  
CC encoding a maize carbon assimilation pathway enzyme of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 238 BP; 41 A; 90 C; 73 G; 34 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 6.34e-14 Length: 238  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 12 Gaps: 2  
US-10-628-525A-34 (1-58) x ADP56997 (1-238)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 14 ATGGCGCCACCGTGATGATGCGCTCGTCCGCCACC----- 49  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuValSerThrAlaSerIeuProValAlaArg 40  
Db 50 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCCGCC 103  
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 104 CGCTCTCCAGAGGCTCGGCACGTC---AGCAACGGCGGAGGATCCGTGTC 154  
RESULT 10  
ADP57002  
ID ADP57002 standard; cDNA; 249 BP.  
XX  
AC ADP57002;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Maize carbon assimilation pathway enzyme cDNA #71.  
XX  
KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphatase; transketolase;

KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX  
XX Zea mays.  
OS  
XX US2004116682-A1.  
PN  
PD 17-JUN-2004.  
XX  
XX 16-NOV-2001; 2001US-00987899.  
PP  
XX 06-MAR-1998; 98US-0076912P.  
PR  
XX 04-MAR-1999; 99US-00262979.  
PR  
XX (CHEI/) CHEIKH N.  
PA (MILL/) MILLER P W.  
PA (OCON/) O'CONNELL K M.  
PA (LIU/) LIU J.  
XX  
XX Cheikh N, Miller PW, O'connell KM, Liu J;  
PI WPI; 2004-498291/47.  
DR  
XX New substantially purified nucleic acid molecule encoding a maize or  
PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
PT identification and analysis, plant breeding, and preparation of  
PT constructs.  
XX  
PS Claim 2; SEQ ID NO 71; 196pp; English.  
XX  
CC The invention relates to a substantially purified nucleic acid molecule  
CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
CC fragment is selected from ribulose-bisphosphate carboxylase,  
CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
CC substantially purified antibody or its fragment which is capable of  
CC specifically binding to a specific maize or soybean carbon assimilation  
CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
CC molecule comprising an exogenous promoter region which functions in a  
CC plant cell to cause the production of an mRNA molecule, and a method of  
CC determining a level or pattern in a plant cell of a carbon assimilation  
CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
CC of the invention are useful for gene mapping, gene identification and  
CC analysis, plant breeding and preparation of constructs for use in plant  
CC gene expression and transgenic plants. This sequence represents cDNA  
CC encoding a maize carbon assimilation pathway enzyme of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 249 BP; 51 A; 91 C; 73 G; 34 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 6.69e-14 Length: 249  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 12 Gaps: 2  
US-10-628-525A-34 (1-58) x ADP57002 (1-249)







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Pred. No.: 7 46e-14 Length: 272
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56976 (1-272)

Qy 1 MetaAlaProThrValMetMetAlaSerSerAlaThraThrArgThrAsnProAlaGln 20
Db 43 ATGGCGCCACCGTGATGATGGCTCGTCCGCCACC----- 78

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40
Db 79 -----GCCGTGCTCGTTCGATTCAGGGGCTCAAGTCCACCGCCAGCTCCCGCTCGGCCGC 132

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 133 CGTCTCTCCAGAGCTTCGCCAACGTC---AGCAACGGCGGAGGATCCGGTGC 183

RESULT 14
ADP56957
ID ADP56957 standard; cDNA; 276 BP.
XX
AC ADP56957;
XX
DT 09-SEP-2004 (first entry)
XX
DE Maize carbon assimilation pathway enzyme cDNA #26.
XX
KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;
KW ribulose-bisphosphate carboxylase; gene; ss; maize; corn;
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;
KW aldolase; fructose-1,6-bisphosphate; transketolase;
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;
KW aspartate aminotransferase; alanine aminotransferase;
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;
KW plant metabolic pathway; plant breeding.
XX
OS Zea mays.
XX
XX US2004116682-A1.
XX
PD 17-JUN-2004.
XX
PF 16-NOV-2001; 2001US-00987899.
XX
PR 06-MAR-1998; 98US-0076912P.
XX
PR 04-MAR-1999; 99US-00262979.
XX
XX (CHEI/) CHEIKH N.
XX (MILL/) MILLER P W.
XX (OCON/) O'CONNELL K M.
XX (LIU/) LIU J.
XX
XX Cheikh N, Miller PW, O'Connell KM, Liu J;
XX WPI; 2004-498291/47.
XX
XX New substantially purified nucleic acid molecule encoding a maize or
XX soybean carbon assimilation pathway enzyme, useful for gene mapping, gene
XX identification and analysis, plant breeding, and preparation of
XX constructs.
XX
XX Claim 2; SEQ ID NO 26; 196pp; English.
XX
XX The invention relates to a substantially purified nucleic acid molecule
XX that encodes a maize or soybean carbon assimilation pathway enzyme or its
XX fragment. The maize or soybean carbon assimilation pathway enzyme or its

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CC fragment is selected from ribulose-bisphosphate carboxylase,
CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose
CC phosphate isomerase, aldolase, fructose-1,6-bisphosphate,
CC transketolase, sedoheptulose-1,7-bisphosphate, D-ribulose-5-phosphate-3-
CC epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,
CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,
CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent
CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,
CC phosphate dikinase and pyrophosphatase. The invention also relates to a
CC substantially purified antibody or its fragment which is capable of
CC specifically binding to a specific maize or soybean carbon assimilation
CC pathway enzyme or its fragment, a transformed plant having a nucleic acid
CC molecule comprising an exogenous promoter region which functions in a
CC plant cell to cause the production of an mRNA molecule, and a method of
CC determining a level or pattern in a plant cell of a carbon assimilation
CC pathway enzyme in a plant metabolic pathway. The methods and compositions
CC of the invention are useful for gene mapping, gene identification and
CC analysis, plant breeding and preparation of constructs for use in plant
CC gene expression and transgenic plants. This sequence represents cDNA
CC encoding a maize carbon assimilation pathway enzyme of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 276 BP; 54 A; 98 C; 84 G; 40 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.: 7 59e-14 Length: 276
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 12 Gaps: 2

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US-10-628-525A-34 (1-58) x ADP56957 (1-276)

```

Qy 1 MetaAlaProThrValMetMetAlaSerSerAlaThraThrArgThrAsnProAlaGln 20
Db 41 ATGGCGCCACCGTGATGATGGCTCGTCCGCCACC----- 76

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40
Db 77 -----GCCGTGCTCGTTCGATTCAGGGGCTCAAGTCCACCGCCAGCTCCCGCTCGGCCGC 130

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 131 CGTCTCTCCAGAGCTTCGCCAACGTC---AGCAACGGCGGAGGATCCGGTGC 181

```

RESULT 15

ADP56982

ID ADP56982 standard; cDNA; 276 BP.

XX

AC ADP56982;

XX

DT 09-SEP-2004 (first entry)

XX

DE Maize carbon assimilation pathway enzyme cDNA #51.

XX

KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;

KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;

KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;

KW aldolase; fructose-1,6-bisphosphate; transketolase;

KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;

KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;

KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;

KW aspartate aminotransferase; alanine aminotransferase;

KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;

KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;

KW plant metabolic pathway; plant breeding.

XX

OS Zea mays.

XX

XX US2004116682-A1.

PN

XX PD 17-JUN-2004.

XX PF 16-NOV-2001; 2001US-00987899.

XX PR 06-MAR-1998; 98US-0076912P.

XX PR 04-MAR-1999; 99US-00262979.

XX PA (CHEI/) CHEIKH N.

XX PA (MILL/) MILLER P W.

XX PA (OCON/) O'CONNELL K M.

XX PA (LIU/) LIU J.

XX PI Cheikh N, Miller PW, O'connell KM, Liu J;

XX DR WPI; 2004-498291/47.

XX PT New substantially purified nucleic acid molecule encoding a maize or

XX PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene

XX PT identification and analysis, plant breeding, and preparation of

XX PT constructs.

XX PS Claim 2; SEQ ID NO 51; 196pp; English.

XX CC The invention relates to a substantially purified nucleic acid molecule

XX CC that encodes a maize or soybean carbon assimilation pathway enzyme or its

XX CC fragment. The maize or soybean carbon assimilation pathway enzyme or its

XX CC fragment is selected from ribulose-bisphosphate carboxylase, triose

XX CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose

XX CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate

XX CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate kinase,

XX CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,

XX CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,

XX CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent

XX CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,

XX CC phosphate dikinase and pyrophosphatase. The invention also relates to a

XX CC substantially purified antibody or its fragment which is capable of

XX CC specifically binding to a specific maize or soybean carbon assimilation

XX CC pathway enzyme or its fragment. A transformed plant having a nucleic acid

XX CC molecule comprising an exogenous promoter region which functions in a

XX CC plant cell to cause the production of an mRNA molecule, and a method of

XX CC determining a level or pattern in a plant cell of a carbon assimilation

XX CC pathway enzyme in a plant metabolic pathway. The methods and compositions

XX CC of the invention are useful for gene mapping, gene identification and

XX CC analysis, plant breeding and preparation of constructs for use in plant

XX CC gene expression and transgenic plants. This sequence represents cDNA

XX CC encoding a maize carbon assimilation pathway enzyme of the invention.

XX CC Note: The sequence data for this patent did not form part of the printed

XX CC specification but was obtained in electronic format from USPTO at

XX CC seqdata.uspto.gov/sequence.html.

XX SQ Sequence 276 BP; 56 A; 97 C; 83 G; 40 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.59e-14	Length:	276
Score:	203.50	Matches:	47
Percent Similarity:	81.0%	Conservative:	0
Best Local Similarity:	81.0%	Mismatches:	0
Query Match:	72.2%	Indels:	11
DB:	12	Gaps:	2

US-10-628-525A-34 (1-58) x ADP56982 (1-276)

Qy 1 MetAlaProThrValMetSerAlaThrAlaThrArgThrAsnProAlaGln 20

Db 46 ARGGGCCGCCGATGATGCGCTCGTCGCCACC----- 81

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40

Db 82 -----GCCGTCGCTCCGTTCCAGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 135

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

|||||

Db 136 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186

RESULT 16

ADP56963

ID ADP56963 standard; cDNA; 284 BP.

XX AC ADP56963;

XX DT 09-SEP-2004 (first entry)

XX DE Maize carbon assimilation pathway enzyme cDNA #32.

XX KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;

XX KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;

XX KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;

XX KW aldolase; fructose-1,6-bisphosphatase; transketolase;

XX KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;

XX KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;

XX KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;

XX KW aspartate aminotransferase; alanine aminotransferase;

XX KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;

XX KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;

XX KW plant metabolic pathway; plant breeding.

XX OS Zea mays.

XX US2004116682-A1.

XX PD 17-JUN-2004.

XX PF 16-NOV-2001; 2001US-00987899.

XX PR 06-MAR-1998; 98US-0076912P.

XX PR 04-MAR-1999; 99US-00262979.

XX (CHEI/) CHEIKH N.

XX (MILL/) MILLER P W.

XX (OCON/) O'CONNELL K M.

XX (LIU/) LIU J.

XX PI Cheikh N, Miller PW, O'connell KM, Liu J;

XX WPI; 2004-498291/47.

XX PT New substantially purified nucleic acid molecule encoding a maize or

XX PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene

XX PT identification and analysis, plant breeding, and preparation of

XX PT constructs.

XX PS Claim 2; SEQ ID NO 32; 196pp; English.

XX CC The invention relates to a substantially purified nucleic acid molecule

XX CC that encodes a maize or soybean carbon assimilation pathway enzyme or its

XX CC fragment. The maize or soybean carbon assimilation pathway enzyme or its

XX CC fragment is selected from ribulose-bisphosphate carboxylase,

XX CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose

XX CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,

XX CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3

XX CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,

XX CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,

XX CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent

XX CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,

XX CC phosphate dikinase and pyrophosphatase. The invention also relates to a

XX CC substantially purified antibody or its fragment which is capable of

XX CC specifically binding to a specific maize or soybean carbon assimilation

XX CC pathway enzyme or its fragment, a transformed plant having a nucleic acid

XX CC molecule comprising an exogenous promoter region which functions in a

XX CC plant cell to cause the production of an mRNA molecule, and a method of

XX CC determining a level or pattern in a plant cell of a carbon assimilation

XX CC pathway enzyme in a plant metabolic pathway. The methods and compositions

XX CC of the invention are useful for gene mapping, gene identification and

XX CC analysis, plant breeding and preparation of constructs for use in plant

XX CC gene expression and transgenic plants. This sequence represents cDNA

CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX

SQ Sequence 284 BP; 58 A; 100 C; 86 G; 40 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 7.86e-14 Length: 284  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56968 (1-284)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 50 ATGGCGCCACCGTGATGGCTCTCGGCCACC----- 85  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 86 -----GCCGTGCTCGCTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCGCCGC 139  
 QY 41 ArgSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgGlyArgCys 58  
 DB 140 CGCTCTCTCCAGAGCCCTCGGCAAGTC---AGCAACGCGGAGGATCCGGTGC 190

#### RESULT 17

ADP56968  
 ID ADP56968 standard; cDNA; 286 BP.

XX AC ADP56968;

XX DT 09-SEP-2004 (first entry)

XX DE Maize carbon assimilation pathway enzyme cDNA #37.

XX KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.

XX OS Zea mays.

XX PN US2004116682-A1.

XX PD 17-JUN-2004.

XX PF 16-NOV-2001; 2001US-00987899.

XX PR 06-MAR-1998; 98US-0076912P.

XX PR 04-MAR-1999; 99US-00262979.

XX PA (CHEI/) CHEIKH N.

XX PA (MILL/) MILLER P W.

XX PA (OCON/) O'CONNELL K M.

XX PA (LIU/) LIU J.

XX PI Cheikh N, Miller PW, O'connell KM, Liu J;

XX DR WPI; 2004-498291/47.

XX PT New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene

PT identification and analysis, plant breeding, and preparation of  
 PT constructs.

XX PS Claim 2; SEQ ID NO 37; 196pp; English.

XX CC The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, transketolase,  
 CC sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3-epimerase,  
 CC ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX

SQ Sequence 286 BP; 58 A; 102 C; 85 G; 41 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 7.93e-14 Length: 286  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56968 (1-286)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

DB 48 ATGGCGCCACCGTGATGGCTCTCGGCCACC----- 83

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40

DB 84 -----GCCGTGCTCGCTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCGCCGC 137

QY 41 ArgSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgGlyArgCys 58

DB 138 CGCTCTCTCAGAGCCCTCGGCAAGTC---AGCAACGCGGAGGATCCGGTGC 188

#### RESULT 18

ADP56978

ID ADP56978 standard; cDNA; 291 BP.

XX AC ADP56978;

XX DT 09-SEP-2004 (first entry)

XX DE Maize carbon assimilation pathway enzyme cDNA #47.

XX KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;

KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX  
OS Zea mays.  
XX US2004116682-A1.  
XX 17-JUN-2004.  
XX  
XX 16-NOV-2001; 2001US-00987899.  
XX  
XX 06-MAR-1998; 98US-0076912P.  
XX 04-MAR-1999; 99US-00262979.  
XX  
XX (CHEI/) CHEIKH N.  
XX (MILL/) MILLER P W.  
XX (OCON/) O'CONNELL K M.  
XX (LIU/) LIU J.  
XX  
XX Cheikh N, Miller PW, O'connell KM, Liu J;  
XX WPI; 2004-498291/47.  
XX  
XX New substantially purified nucleic acid molecule encoding a maize or  
XX soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
XX identification and analysis, plant breeding, and preparation of  
XX constructs.  
XX  
XX Claim 2; SEQ ID NO 47; 196pp; English.  
XX  
XX The invention relates to a substantially purified nucleic acid molecule  
XX that encodes a maize or soybean carbon assimilation pathway enzyme or its  
XX fragment. The maize or soybean carbon assimilation pathway enzyme or its  
XX fragment is selected from ribulose-bisphosphate carboxylase,  
XX phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
XX phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate-3  
XX transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
XX -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
XX phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
XX aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
XX malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
XX substantially purified antibody or its fragment which is capable of  
XX specifically binding to a specific maize or soybean carbon assimilation  
XX pathway enzyme or its fragment, a transformed plant having a nucleic acid  
XX molecule comprising an exogenous promoter region which functions in a  
XX plant cell to cause the production of an mRNA molecule, and a method of  
XX determining a level or pattern in a plant cell of a carbon assimilation  
XX pathway enzyme in a plant metabolic pathway. The methods and compositions  
XX of the invention are useful for gene mapping, gene identification and  
XX analysis, plant breeding and preparation of constructs for use in plant  
XX gene expression and transgenic plants. This sequence represents cDNA  
XX encoding a maize carbon assimilation pathway enzyme of the invention.  
XX Note: The sequence data for this patent did not form part of the printed  
XX specification but was obtained in electronic format from USPTO at  
XX seqdata.uspto.gov/sequence.html.  
XX  
XX SQ Sequence 291 BP; 57 A; 105 C; 88 G; 41 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: Length: 291  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56978 (1-291)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||

Db 57 ATGGCGCCACCGTGATGATGCTCGTCGGCCACC----- 92  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 93 -----GCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 146  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 147 CGCTCTCTCCAGGAGCTCGGCAACGTC-----AGCAACGGCGGAGGATCCGGTGC 197

RESULT 19  
ADP56945  
ID ADP56945 standard; cDNA; 297 BP.  
XX  
XX ADP56945;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Maize carbon assimilation pathway enzyme cDNA #14.  
XX  
XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
XX ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
XX glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
XX aldolase; fructose-1,6-bisphosphatase; transketolase;  
XX sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
XX ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
XX phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
XX aspartate aminotransferase; alanine aminotransferase;  
XX NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
XX PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
XX plant metabolic pathway; plant breeding.  
XX  
XX Zea mays.  
XX  
XX OS US2004116682-A1.  
XX  
XX 17-JUN-2004.  
XX  
XX 16-NOV-2001; 2001US-00987899.  
XX  
XX 06-MAR-1998; 98US-0076912P.  
XX 04-MAR-1999; 99US-00262979.  
XX  
XX (CHEI/) CHEIKH N.  
XX (MILL/) MILLER P W.  
XX (OCON/) O'CONNELL K M.  
XX (LIU/) LIU J.  
XX  
XX Cheikh N, Miller PW, O'connell KM, Liu J;  
XX WPI; 2004-498291/47.  
XX  
XX New substantially purified nucleic acid molecule encoding a maize or  
XX soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
XX identification and analysis, plant breeding, and preparation of  
XX constructs.  
XX  
XX Claim 2; SEQ ID NO 14; 196pp; English.  
XX  
XX The invention relates to a substantially purified nucleic acid molecule  
XX that encodes a maize or soybean carbon assimilation pathway enzyme or its  
XX fragment. The maize or soybean carbon assimilation pathway enzyme or its  
XX fragment is selected from ribulose-bisphosphate carboxylase,  
XX phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
XX phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate-3  
XX transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
XX -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
XX phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
XX aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
XX malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
XX substantially purified antibody or its fragment which is capable of  
XX specifically binding to a specific maize or soybean carbon assimilation

CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

SQ Sequence 297 BP; 51 A; 108 C; 92 G; 46 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.3e-14 Length: 297  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56945 (1-297)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 12 ATGGCGCCCAACCGTGATGATGGCTCGTCGGCCACC----- 47  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 48 -----GCCGTCGCTCGTTCCAGGGGCTCAGTCCACCCGAGCTCCCGTCGCCCGC 101  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgCys 58  
 DB 102 CGCTCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 152

RESULT 20

ADP56952

ID ADP56952 standard; cDNA; 298 BP.

XX AC ADP56952;

XX DT 09-SEP-2004 (first entry)

XX DE Maize carbon assimilation pathway enzyme cDNA #21.

XX KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphate; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxylase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.

XX OS Zea mays.

XX PN US200411682-A1.

XX PD 17-JUN-2004.

XX PF 16-NOV-2001; 2001US-00987899.

XX PR 06-MAR-1998; 98US-0076912P.

XX PR 04-MAR-1999; 99US-00262979.

XX (CHEI/) CHEIKH N.

XX PA (MILL/) MILLER P W.

XX PA (OCON/) O'CONNELL K M.

PA (LIU/) LIU J.

XX PI Cheikh N, Miller PW, O'connell KM, Liu J;

XX WI; 2004-498291/47.

XX PT New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.

XX PS Claim 2; SEQ ID NO 21; 196pp; English.

XX CC The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase, triose  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate kinase,  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxylase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.

SQ Sequence 298 BP; 60 A; 106 C; 90 G; 42 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.33e-14 Length: 298  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56952 (1-298)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

DB 48 ATGGCGCCCAACCGTGATGATGGCTCGTCGGCCACC----- 83

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40

DB 84 -----GCCGTCGCTCGTTCCAGGGGCTCAGTCCACCCGAGCTCCCGTCGCCCGC 137

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgCys 58

DB 138 CGCTCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 188

RESULT 21

ADP56947

ID ADP56947 standard; cDNA; 305 BP.

XX AC ADP56947;

XX DT 09-SEP-2004 (first entry)

XX DE Maize carbon assimilation pathway enzyme cDNA #16.

XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphatase; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX Zea mays.  
 XX US2004116682-A1.  
 XX 17-JUN-2004.  
 XX 16-NOV-2001; 2001US-00987899.  
 XX 06-MAR-1998; 98US-0076912P.  
 XX 04-MAR-1999; 99US-00262979.  
 XX (CHEI/) CHEIKH N.  
 XX (MILL/) MILLER P W.  
 XX (OCON/) O'CONNELL K M.  
 XX (LIU/) LIU J.  
 XX Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 XX Claim 2; SEQ ID NO 16; 196pp; English.  
 XX The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate-3-  
 CC epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: the sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX Sequence 305 BP; 59 A; 109 C; 92 G; 45 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8,578-14 Length: 305  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0

Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2  
 US-10-628-525A-34 (1-58) x ADP56947 (1-305)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 42 ATGGCGCCACCGTGATGATGCGCTCGTGGCCACC-----  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 DB 78 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCGCGC 131  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
 DB 132 CGCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 182  
 RESULT 22  
 ADP56960  
 ID ADP56960 standard; cDNA; 307 BP.  
 XX  
 AC ADP56960;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Maize carbon assimilation pathway enzyme cDNA #29.  
 XX  
 KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphatase; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.  
 XX Zea mays.  
 XX US2004116682-A1.  
 XX 17-JUN-2004.  
 XX 16-NOV-2001; 2001US-00987899.  
 XX 06-MAR-1998; 98US-0076912P.  
 XX 04-MAR-1999; 99US-00262979.  
 XX (CHEI/) CHEIKH N.  
 XX (MILL/) MILLER P W.  
 XX (OCON/) O'CONNELL K M.  
 XX (LIU/) LIU J.  
 XX Cheikh N, Miller PW, O'connell KM, Liu J;  
 XX WPI; 2004-498291/47.  
 XX New substantially purified nucleic acid molecule encoding a maize or  
 PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 XX Claim 2; SEQ ID NO 29; 196pp; English.  
 XX The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase, D-ribulose-5-phosphate-3-  
 CC epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: the sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX Sequence 305 BP; 59 A; 109 C; 92 G; 45 T; 0 U; 0 Other;

transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3-epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase, phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase, aspartate aminotransferase, alanine aminotransferase, NADP-dependent malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate, phosphate dikinase and pyrophosphatase. The invention also relates to a substantially purified antibody or its fragment which is capable of specifically binding to a specific maize or soybean carbon assimilation pathway enzyme or its fragment, a transformed plant having a nucleic acid molecule comprising an exogenous promoter region which functions in a plant cell to cause the production of an mRNA molecule, and a method of determining a level or pattern in a plant cell of a carbon assimilation pathway enzyme in a plant metabolic pathway. The methods and compositions of the invention are useful for gene mapping, gene identification and analysis, plant breeding and preparation of constructs for use in plant gene expression and transgenic plants. This sequence represents cDNA encoding a maize carbon assimilation pathway enzyme of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 307 BP; 63 A; 107 C; 93 G; 44 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.64e-14 Length: 307  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56946 (1-307)

QY 1 MetaAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 50 ATGGCGCCACCGTGTATGGCTCGTCGCCACC----- 85  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40  
 DB 86 -----GCCGTCTCGTCTCCAGGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 139  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 DB 140 CGCTCTCCAGAGCCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

RESULT 23

ID ADP56946 standard; cDNA; 309 BP.

AC ADP56946;

XX 09-SEP-2004 (first entry)

XX Maize carbon assimilation pathway enzyme cDNA #15.

XX Carbon assimilation pathway enzyme; Gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
 KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 KW aldolase; fructose-1,6-bisphosphatase; transketolase;  
 KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 KW aspartate aminotransferase; alanine aminotransferase;  
 KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 KW plant metabolic pathway; plant breeding.

XX Zea mays.

XX US2004116682-A1.

XX 17-JUN-2004.

XX

PF 16-NOV-2001; 2001US-00987899.

XX 06-MAR-1998; 98US-0076912P.

PR 04-MAR-1999; 99US-00262979.

XX (CHEI/) CHEIKH N.

PA (MILL/) MILLER P W.

PA (OCON/) O'CONNELL K M.

PA (LIUJ/) LIU J.

PI Cheikh N, Miller PW, O'Connell KM, Liu J;

XX WPI; 2004-498291/47.

DR

XX

PT New substantially purified nucleic acid molecule encoding a maize or

PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene

PT identification and analysis, plant breeding, and preparation of

PT constructs.

XX

PF Claim 2; SEQ ID NO 15; 196pp; English.

XX

CC The invention relates to a substantially purified nucleic acid molecule

CC that encodes a maize or soybean carbon assimilation pathway enzyme or its

CC fragment. The maize or soybean carbon assimilation pathway enzyme or its

CC fragment is selected from ribulose-bisphosphate carboxylase,

CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose

CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,

CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3

CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,

CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,

CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent

CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,

CC phosphate dikinase and pyrophosphatase. The invention also relates to a

CC substantially purified antibody or its fragment which is capable of

CC specifically binding to a specific maize or soybean carbon assimilation

CC pathway enzyme or its fragment, a transformed plant having a nucleic acid

CC molecule comprising an exogenous promoter region which functions in a

CC plant cell to cause the production of an mRNA molecule, and a method of

CC determining a level or pattern in a plant cell of a carbon assimilation

CC pathway enzyme in a plant metabolic pathway. The methods and compositions

CC of the invention are useful for gene mapping, gene identification and

CC analysis, plant breeding and preparation of constructs for use in plant

CC gene expression and transgenic plants. This sequence represents cDNA

CC encoding a maize carbon assimilation pathway enzyme of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 309 BP; 62 A; 110 C; 92 G; 45 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.71e-14 Length: 309

Score: 203.50 Matches: 47

Percent Similarity: 81.0% Conservative: 0

Best Local Similarity: 81.0% Mismatches: 0

Query Match: 72.2% Indels: 11

DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56946 (1-309)

QY 1 MetaAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

DB 48 ATGGCGCCACCGTGTATGGCTCGTCGCCACC----- 83

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40

DB 84 -----GCCGTCTCGTCTCCAGGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 137

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

DB 138 CGCTCTCCAGAGCCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 188

RESULT 24

ADP56961  
ID ADP56961 standard; cDNA; 311 BP.  
AC ADP56961;  
XX  
XX  
DT 09-SEP-2004 (first entry)  
XX  
XX  
DE Maize carbon assimilation pathway enzyme cDNA #30.  
XX  
XX  
KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphate; transketolase;  
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX  
XX  
OS Zea mays.  
XX  
XX  
PN US2004116682-A1.  
XX  
XX  
PD 17-JUN-2004.  
XX  
XX  
PF 16-NOV-2001; 2001US-00987899.  
XX  
XX  
PR 06-MAR-1998; 98US-0076912P.  
XX  
PR 04-MAR-1999; 99US-00262979.  
XX  
XX  
PA (CHEI/) CHEIKH N.  
PA (MILL/) MILLER P W.  
PA (OCON/) O'CONNELL K M.  
PA (LIU/) LIU J.  
XX  
XX  
PI Cheikh N, Miller PW, O'connell KM, Liu J;  
XX  
XX  
DR WPI; 2004-498291/47.  
XX  
XX  
PT New substantially purified nucleic acid molecule encoding a maize or  
PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
PT identification and analysis, plant breeding, and preparation of  
PT constructs.  
XX  
XX  
PS Claim 2; SEQ ID NO 30; 196pp; English.  
XX  
XX  
CC The invention relates to a substantially purified nucleic acid molecule  
CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
CC fragment is selected from ribulose-bisphosphate carboxylase,  
CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
CC phosphate isomerase, aldolase, fructose-1,6-bisphosphate,  
CC transketolase, sedoheptulose-1,7-bisphosphate, D-ribulose-5-phosphate-3  
CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
CC substantially purified antibody or its fragment which is capable of  
CC specifically binding to a specific maize or soybean carbon assimilation  
CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
CC molecule comprising an exogenous promoter region which functions in a  
CC plant cell to cause the production of an mRNA molecule, and a method of  
CC determining a level or pattern in a plant cell of a carbon assimilation  
CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
CC of the invention are useful for gene mapping, gene identification and  
CC analysis, plant breeding and preparation of constructs for use in plant  
CC gene expression and transgenic plants. This sequence represents cDNA  
CC encoding a maize carbon assimilation pathway enzyme of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 311 BP; 60 A; 113 C; 93 G; 45 T; 0 U; 0 Other;  
XX  
XX  
Alignment Scores:  
Pred. No.: 8,78e-14 Length: 311  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 12 Gaps: 2  
XX  
XX  
US-10-628-525A-34 (1-58) x ADP56961 (1-311)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 42 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 77  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 78 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTGGCCGC 131  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgLeuArgCys 58  
DB 132 CGCTCTCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 182  
XX  
XX  
RESULT 25  
ADP56999  
ID ADP56999 standard; cDNA; 312 BP.  
XX  
XX  
AC ADP56999;  
XX  
XX  
DT 09-SEP-2004 (first entry)  
XX  
XX  
DE Maize carbon assimilation pathway enzyme cDNA #68.  
XX  
XX  
KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphate; transketolase;  
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX  
XX  
OS Zea mays.  
XX  
XX  
PN US2004116682-A1.  
XX  
XX  
PD 17-JUN-2004.  
XX  
XX  
PF 16-NOV-2001; 2001US-00987899.  
XX  
PR 06-MAR-1998; 98US-0076912P.  
XX  
PR 04-MAR-1999; 99US-00262979.  
XX  
XX  
PA (CHEI/) CHEIKH N.  
PA (MILL/) MILLER P W.  
PA (OCON/) O'CONNELL K M.  
PA (LIU/) LIU J.  
XX  
XX  
PI Cheikh N, Miller PW, O'connell KM, Liu J;  
XX  
XX  
DR WPI; 2004-498291/47.  
XX  
XX  
PT New substantially purified nucleic acid molecule encoding a maize or  
PT soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
PT identification and analysis, plant breeding, and preparation of  
PT constructs.  
XX  
XX



PS Claim 2; SEQ ID NO 68; 196pp; English.

XX The invention relates to a substantially purified nucleic acid molecule

CC that encodes a maize or soybean carbon assimilation pathway enzyme or its

CC fragment. The maize or soybean carbon assimilation pathway enzyme or its

CC fragment is selected from ribulose-bisphosphate carboxylase,

CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose

CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,

CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3

CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,

CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,

CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent

CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,

CC phosphate dikinase and pyrophosphatase. The invention also relates to a

CC substantially purified antibody or its fragment which is capable of

CC specifically binding to a specific maize or soybean carbon assimilation

CC pathway enzyme or its fragment, a transformed plant having a nucleic acid

CC molecule comprising an exogenous promoter region which functions in a

CC plant cell to cause the production of an mRNA molecule, and a method of

CC determining a level or pattern in a plant cell of a carbon assimilation

CC pathway enzyme in a plant metabolic pathway. The methods and compositions

CC of the invention are useful for gene mapping, gene identification and

CC analysis, plant breeding and preparation of constructs for use in plant

CC gene expression and transgenic plants. This sequence represents cDNA

CC encoding a maize carbon assimilation pathway enzyme of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 312 BP; 63 A; 105 C; 92 G; 49 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.:	8.91e-14	Length:	312
Score:	203.50	Matches:	47
Percent Similarity:	81.0%	Conservative:	0
Best Local Similarity:	81.0%	Mismatches:	0
Query Match:	72.2%	Indels:	11
DB:	12	Gaps:	2

US-10-628-525A-34 (1-58) x ADP56999 (1-312)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

DB 43 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 78

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40

DB 79 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCCGC 132

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyCys 58

DB 133 CGCTCTCCAGAGCCTCGGCACGTC---AGCAACGGCGGAGGATCGGTGC 183

RESULT 26

ADP56942

ID ADP56942 standard; cDNA; 315 BP.

XX

AC ADP56942;

XX

DT 09-SEP-2004 (first entry)

XX

DE Maize carbon assimilation pathway enzyme cDNA #11.

XX

XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;

KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;

KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;

KW aldolase; fructose-1,6-bisphosphatase; transketolase;

KW sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;

KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;

KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;

KW aspartate aminotransferase; alanine aminotransferase;

KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;

KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;

plant metabolic pathway; plant breeding.

Zea mays.

US2004116682-A1.

17-JUN-2004.

16-NOV-2001; 2001US-00987899.

06-MAR-1998; 98US-0076912P.

04-MAR-1999; 99US-00262979.

(CHEI/) CHEIKH N.

(MILL/) MILLER P W.

(OCON/) O'CONNELL K M.

(LIUJ/) LIU J.

Cheikh N, Miller PW, O'Connell KM, Liu J;

WPI; 2004-498291/47.

New substantially purified nucleic acid molecule encoding a maize or

soybean carbon assimilation pathway enzyme, useful for gene mapping, gene

identification and analysis, plant breeding, and preparation of

constructs.

Claim 2; SEQ ID NO 11; 196pp; English.

The invention relates to a substantially purified nucleic acid molecule

that encodes a maize or soybean carbon assimilation pathway enzyme or its

fragment. The maize or soybean carbon assimilation pathway enzyme or its

fragment is selected from ribulose-bisphosphate carboxylase,

phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose

phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,

transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3

-epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,

phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,

aspartate aminotransferase, alanine aminotransferase, NADP-dependent

malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,

phosphate dikinase and pyrophosphatase. The invention also relates to a

substantially purified antibody or its fragment which is capable of

specifically binding to a specific maize or soybean carbon assimilation

pathway enzyme or its fragment, a transformed plant having a nucleic acid

molecule comprising an exogenous promoter region which functions in a

plant cell to cause the production of an mRNA molecule, and a method of

determining a level or pattern in a plant cell of a carbon assimilation

pathway enzyme in a plant metabolic pathway. The methods and compositions

of the invention are useful for gene mapping, gene identification and

analysis, plant breeding and preparation of constructs for use in plant

gene expression and transgenic plants. This sequence represents cDNA

encoding a maize carbon assimilation pathway enzyme of the invention.

Note: The sequence data for this patent did not form part of the printed

specification but was obtained in electronic format from USPTO at

seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 315 BP; 62 A; 113 C; 94 G; 46 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.92e-14	Length:	315
Score:	203.50	Matches:	47
Percent Similarity:	81.0%	Conservative:	0
Best Local Similarity:	81.0%	Mismatches:	0
Query Match:	72.2%	Indels:	11
DB:	12	Gaps:	2

US-10-628-525A-34 (1-58) x ADP56942 (1-315)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

DB 48 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 83

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40

Db 84 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCGCCGC 137  
QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 138 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 188  
RESULT 27  
ADP56941  
ID ADP56941 standard; cDNA; 317 BP.  
XX ADP56941;  
XX  
XX 09-SEP-2004 (first entry)  
XX  
XX Maize carbon assimilation pathway enzyme cDNA #10.  
XX  
KW Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphate; transketolase;  
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.  
XX  
OS Zea mays.  
XX  
XX US2004116682-A1.  
XX  
XX 17-JUN-2004.  
XX  
XX 16-NOV-2001; 2001US-00987899.  
XX  
XX 06-MAR-1998; 98US-0076912P.  
XX  
XX 04-MAR-1999; 99US-00262979.  
XX  
XX (CHEI//) CHEIKH N.  
XX (MILL//) MILLER P W.  
XX (OCON//) O'CONNELL K M.  
XX (LIUJ//) LIU J.  
XX  
XX Cheikh N, Miller PW, O'connell KM, Liu J;  
XX  
XX WPI; 2004-498291/47.  
XX  
XX New substantially purified nucleic acid molecule encoding a maize or  
XX soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
XX identification and analysis, plant breeding, and preparation of  
XX constructs.  
XX  
XX Claim 2; SEQ ID NO 10; 196pp; English.  
XX  
XX The invention relates to a substantially purified nucleic acid molecule  
XX that encodes a maize or soybean carbon assimilation pathway enzyme or its  
XX fragment. The maize or soybean carbon assimilation pathway enzyme or its  
XX fragment is selected from ribulose-bisphosphate carboxylase,  
XX phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
XX phosphate isomerase, aldolase, fructose-1,6-bisphosphate,  
XX transketolase, sedoheptulose-1,7-bisphosphate, D-ribulose-5-phosphate-3-  
XX epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
XX phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
XX aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
XX malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
XX phosphate dikinase and pyrophosphatase. The invention also relates to a  
XX substantially purified antibody or its fragment which is capable of  
XX specifically binding to a specific maize or soybean carbon assimilation  
XX pathway enzyme or its fragment, a transformed plant having a nucleic acid  
XX molecule comprising an exogenous promoter region which functions in a  
XX plant cell to cause the production of an mRNA molecule, and a method of

CC determining a level or pattern in a plant cell of a carbon assimilation  
CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
CC of the invention are useful for gene mapping, gene identification and  
CC analysis, plant breeding and preparation of constructs for use in plant  
CC gene expression and transgenic plants. This sequence represents cDNA  
CC encoding a maize carbon assimilation pathway enzyme of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX

SQ Sequence 317 BP; 63 A; 113 C; 95 G; 46 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 8,99e-14 Length: 317  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservatives: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP56941 (1-317)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 50 ATGGCGCCACCGTGTATGATGGCTTCGTGGCCACC----- 85  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40  
Db 86 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCGCCGC 139  
QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 140 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

#### RESULT 28

ADP56935

ID ADP56935 standard; cDNA; 319 BP.

AC ADP56935;

XX 09-SEP-2004 (first entry)

DE Maize carbon assimilation pathway enzyme cDNA #4.

XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;  
KW glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
KW aldolase; fructose-1,6-bisphosphate; transketolase;  
KW sedoheptulose-1,7-bisphosphate; D-ribulose-5-phosphate-3-epimerase;  
KW ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
KW phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
KW aspartate aminotransferase; alanine aminotransferase;  
KW NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
KW PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
KW plant metabolic pathway; plant breeding.

XX Zea mays.

OS US2004116682-A1.

XX 17-JUN-2004.

XX 16-NOV-2001; 2001US-00987899.

XX 06-MAR-1998; 98US-0076912P.

PR 04-MAR-1999; 99US-00262979.

XX (CHEI//) CHEIKH N.

PA (MILL//) MILLER P W.

PA (OCON//) O'CONNELL K M.

PA (LIUJ//) LIU J.

XX Cheikh N, Miller PW, O'connell KM, Liu J;

PI

XX WPI; 2004-498291/47.  
 XX  
 DR New substantially purified nucleic acid molecule encoding a maize or  
 XX soybean carbon assimilation pathway enzyme, useful for gene mapping, gene  
 PT identification and analysis, plant breeding, and preparation of  
 PT constructs.  
 PT  
 XX  
 XX Claim 2; SEQ ID NO 4; 196pp; English.  
 PS  
 XX The invention relates to a substantially purified nucleic acid molecule  
 CC that encodes a maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment. The maize or soybean carbon assimilation pathway enzyme or its  
 CC fragment is selected from ribulose-bisphosphate carboxylase,  
 CC phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose  
 CC phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,  
 CC transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3  
 CC -epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,  
 CC phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,  
 CC aspartate aminotransferase, alanine aminotransferase, NADP-dependent  
 CC malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,  
 CC phosphate dikinase and pyrophosphatase. The invention also relates to a  
 CC substantially purified antibody or its fragment which is capable of  
 CC specifically binding to a specific maize or soybean carbon assimilation  
 CC pathway enzyme or its fragment, a transformed plant having a nucleic acid  
 CC molecule comprising an exogenous promoter region which functions in a  
 CC plant cell to cause the production of an mRNA molecule, and a method of  
 CC determining a level or pattern in a plant cell of a carbon assimilation  
 CC pathway enzyme in a plant metabolic pathway. The methods and compositions  
 CC of the invention are useful for gene mapping, gene identification and  
 CC analysis, plant breeding and preparation of constructs for use in plant  
 CC gene expression and transgenic plants. This sequence represents cDNA  
 CC encoding a maize carbon assimilation pathway enzyme of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 319 BP; 63 A; 112 C; 96 G; 48 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9,05e-14 Length: 319  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservatives: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 12 Gaps: 2  
 US-10-628-525A-34 (1-58) x ADP56935 (1-319)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 DB 41 ATGGCGCCACCCTGATGATGGCTCGTGGCCACC----- 76  
 QY 21 AlaSerAlaValAlaProHeGInGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 DB 77 -----GCCGTGCTCGTCTCCAGGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 130  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyAlaArgCys 58  
 DB 131 CGCTCTCCAGAGCTTCGGACAGTC---AGCACGGCGGAGGATCCGGTGC 181  
 RESULT 29  
 ADP57162  
 ID ADP57162 standard; cDNA; 344 BP.  
 XX  
 AC ADP57162;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Maize carbon assimilation pathway enzyme cDNA #231.  
 DE  
 XX Carbon assimilation pathway enzyme; gene; ss; maize; corn;  
 KW ribulose-bisphosphate carboxylase; phosphoglycerate kinase;

glyceraldehyde 3-phosphate dehydrogenase; triose phosphate isomerase;  
 aldolase; fructose-1,6-bisphosphatase; transketolase;  
 sedoheptulose-1,7-bisphosphatase; D-ribulose-5-phosphate-3-epimerase;  
 ribose-5-phosphate isomerase; ribose-5-phosphate kinase;  
 phosphoenolpyruvate carboxylase; NADP-dependent malate dehydrogenase;  
 aspartate aminotransferase; alanine aminotransferase;  
 NADP-dependent malic enzyme; NAD-dependent malic enzyme;  
 PEP carboxykinase; pyruvate; phosphate dikinase; pyrophosphatase;  
 plant metabolic pathway; plant breeding.

Zea mays.

US2004116682-A1.

17-JUN-2004.

16-NOV-2001; 2001US-00987899.

06-MAR-1998; 98US-0076912P.

04-MAR-1999; 99US-00262979.

(CHEI/) CHEIKH N.

(MILL/) MILLER P W.

(OCON/) O'CONNELL K M.

(LIU/) LIU J.

Cheikh N, Miller PW, O'Connell KM, Liu J;

WPI; 2004-498291/47.

New substantially purified nucleic acid molecule encoding a maize or

soybean carbon assimilation pathway enzyme, useful for gene mapping, gene

identification and analysis, plant breeding, and preparation of

constructs.

Claim 2; SEQ ID NO 231; 196pp; English.

The invention relates to a substantially purified nucleic acid molecule

that encodes a maize or soybean carbon assimilation pathway enzyme or its

fragment. The maize or soybean carbon assimilation pathway enzyme or its

fragment is selected from ribulose-bisphosphate carboxylase,

phosphoglycerate kinase, glyceraldehyde 3-phosphate dehydrogenase, triose

phosphate isomerase, aldolase, fructose-1,6-bisphosphatase,

transketolase, sedoheptulose-1,7-bisphosphatase, D-ribulose-5-phosphate-3

-epimerase, ribose-5-phosphate isomerase, ribose-5-phosphate kinase,

phosphoenolpyruvate carboxylase, NADP-dependent malate dehydrogenase,

aspartate aminotransferase, alanine aminotransferase, NADP-dependent

malic enzyme, NAD-dependent malic enzyme, PEP carboxykinase, pyruvate,

phosphate dikinase and pyrophosphatase. The invention also relates to a

substantially purified antibody or its fragment which is capable of

specifically binding to a specific maize or soybean carbon assimilation

pathway enzyme or its fragment, a transformed plant having a nucleic acid

molecule comprising an exogenous promoter region which functions in a

plant cell to cause the production of an mRNA molecule, and a method of

determining a level or pattern in a plant cell of a carbon assimilation

pathway enzyme in a plant metabolic pathway. The methods and compositions

of the invention are useful for gene mapping, gene identification and

analysis, plant breeding and preparation of constructs for use in plant

gene expression and transgenic plants. This sequence represents cDNA

encoding a maize carbon assimilation pathway enzyme of the invention.

Note: The sequence data for this patent did not form part of the printed

specification but was obtained in electronic format from USPTO at

seqdata.uspto.gov/sequence.html.

Sequence 344 BP; 67 A; 120 C; 104 G; 53 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9,93e-14 Length: 344

Score: 203.50 Matches: 47

Percent Similarity: 81.0% Conservatives: 0

Best Local Similarity: 81.0% Mismatches: 0

Query Match: 72.2% Indels: 11

DB: 12 Gaps: 2

US-10-628-525A-34 (1-58) x ADP57162 (1-344)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 46 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 81  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 82 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 135  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
 Db 136 CGCTCTCTCAGAAGCGCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186

RESULT 30

AAQ88331  
 ID AAQ88331 standard; DNA; 405 BP.

XX AC AAQ88331;

DT 11-JAN-1996 (first entry)

XX Optimised transit peptide coding sequence.

DE Plant promoter; root; meristem; pollen; immature embryo;

KW upstream regulatory element; alpha tubulin gene; transit peptide; ss.

XX OS Synthetic.

XX PN EP652286-A1.

XX PD 10-MAY-1995.

XX PF 09-NOV-1994; 94EP-00420306.

XX PR 10-NOV-1993; 93PR-00013684.

XX PA (RHON ) RHONE POULENC AGROCHIMIE.

XX PI Capallades M, De Rose R, Montoliu L, Puigdomenech P, Torres MA;

XX PI Rigau J, Uribe J;

XX DR WPI; 1995-171922/23.

PT New maize alpha-tubulin promoters - and chimeric genes comprising  
 PT promoter and heterologous gene for prodn. of transgenic plants.

XX PS Example 4; Page 18; 24pp; French.

XX Upstream regulatory elements (UREs) from maize alpha-tubulin genes (esp.  
 CC the alpha 1, 2 or 3 genes, see AAQ88328-Q88330) can be used for  
 CC controlling specific expression of (heterologous) genes in root,  
 CC meristem, pollen and/or immature embryos. Transgenic plants able to  
 CC express a heterologous gene can be generated using the different promoter  
 CC regions, in partic. herbicide-resistant plants. In an example, the maize  
 CC tub-alpha-1 regulatory element was incorporated into a plasmid which also  
 CC contained an optimised transit peptide coding sequence (AAQ88331), the  
 CC aroA gene and the nos terminator. Tobacco leaf discs were transformed  
 CC with the plasmid (via A.tumefaciens) and plants regenerated from the  
 CC discs showed increased tolerance to glyphosate

XX SQ Sequence 405 BP; 79 A; 148 C; 106 G; 72 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.21e-13	Length:	405
Score:	203.50	Matches:	47
Percent Similarity:	81.0%	Conservative:	0
Best Local Similarity:	81.0%	Mismatches:	0
Query Match:	72.2%	Indels:	11
DB:	2	Gaps:	2

US-10-628-525A-34 (1-58) x AAQ88331 (1-405)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 262 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 297  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 298 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCTCCCGTCGCCCGC 351  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
 Db 352 CGCTCTCTCAGAAGCGCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 402

Search completed: April 1, 2006, 04:28:44  
 Job time : 139.553 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 935.32 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

Title: US-10-628-525A-34  
Perfect score: 282  
Sequence: 1 MAPTVWASSATATRNPAQ.....ARRSSRLGNVASNGGRIC 58

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DRV=xlh  
-Q/-abes/ABSSWB spool/US10628525/runat\_31032006\_095118\_16742/app\_query.fasta\_1  
-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOCALIGN=200 -THR\_SCORE=oct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes06h  
-USER=US10628525 @CGN\_1\_11098 -runat\_31032006\_095118\_16742 -NCPU=6 -ICPU=3  
-NO\_WMAP -NEG\_SCORES=0 -WAIT -DSPELLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gsa1:\*  
10: gb\_gsa2:\*  
11: gb\_gsa3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	203.5	72.2	171	AW438072	AW438072 707072C09
2	203.5	72.2	281	B1430868	B1430868 949062B09
3	203.5	72.2	320	CD988795	CD988795 QAR1a03.y
4	203.5	72.2	369	A1372109	A1372109 am78b09.x
5	203.5	72.2	428	BZ647531	BZ647531 OGCBJ16NC
6	203.5	72.2	476	BG458793	BG458793 947054D04
7	203.5	72.2	481	DR826659	DR826659 ZM_BFB006

C	8	203.5	72.2	481	9	CC168222	CC168222 i183b10.g
	9	203.5	72.2	487	2	BG550311	BG550311 947039E03
	10	203.5	72.2	513	3	B1431142	B1431142 949059C09
C	11	203.5	72.2	525	9	CC616048	CC616048 OGUKH26TH
	12	203.5	72.2	544	2	BG349334	BG349334 947028A12
	13	203.5	72.2	545	6	CF025689	CF025689 QCAie07.y
	14	203.5	72.2	569	6	CD998700	CD998700 QBF15C08.
	15	203.5	72.2	608	6	CF025518	CF025518 QCA18a04.
	16	203.5	72.2	619	6	CD990730	CD990730 QAY3f06.y
	17	203.5	72.2	622	2	BG458523	BG458523 947045B08
	18	203.5	72.2	652	1	AW352495	AW352495 707050B11
	19	203.5	72.2	657	7	CO523152	CO523152 3530_1_15
C	20	203.5	72.2	660	2	BG320791	BG320791 Zm04_10c0
	21	203.5	72.2	660	7	CO532595	CO532595 3530_1_21
	22	203.5	72.2	671	6	CD990623	CD990623 QAY2d03.y
	23	203.5	72.2	711	7	CO533682	CO533682 3530_1_22
	24	203.5	72.2	712	6	CD991089	CD991089 QAZ4b01.y
	25	203.5	72.2	769	8	DR822461	DR822461 ZM_BFB006
	26	203.5	72.2	773	8	DR824125	DR824125 ZM_BFB006
	27	203.5	72.2	777	10	CG094731	CG094731 FUKDK52TD
	28	203.5	72.2	779	8	DR829152	DR829152 ZM_BFB007
	29	203.5	72.2	800	9	CC641056	CC641056 OGICD30TV
	30	203.5	72.2	802	8	DR797511	DR797511 ZM_BFB001
	31	203.5	72.2	808	10	CG447685	CG447685 OGATAT65TV
	32	203.5	72.2	817	1	AA979879	AA979879 MEST2-G2.
	33	203.5	72.2	821	8	DR826660	DR826660 ZM_BFB006
	34	203.5	72.2	825	8	DR798785	DR798785 ZM_BFB002
C	35	203.5	72.2	831	2	BG319747	BG319747 Zm03_05b0
	36	203.5	72.2	853	8	DR802699	DR802699 ZM_BFB002
C	37	203.5	72.2	870	10	CG094728	CG094728 FUKDK52TB
	38	203.5	72.2	885	8	DR819095	DR819095 ZM_BFB005
	39	203.5	72.2	890	10	CG262745	CG262745 OGOFV03TH
C	40	203.5	72.2	918	8	CG262755	CG262755 OGOFV03TV
	41	203.5	72.2	929	8	DR820791	DR820791 ZM_BFB005
	42	203.5	72.2	939	10	CG461924	CG461924 PUFIC04TD
C	43	203.5	72.2	1041	10	CG461884	CG461884 PUFIC04TB
	44	200.5	71.1	318	8	DR820790	DR820790 ZM_BFB005
	45	198.5	70.4	670	6	CD990729	CD990729 QAY3f05.y
C	46	197.5	70.0	320	6	CD988611	CD988611 QAY2d11.y
	47	196.5	69.7	574	2	BG517358	BG517358 947061E01
C	48	195.5	69.3	289	1	A1967090	A1967090 496021F11
	49	195.5	69.3	325	6	CD989002	CD989002 QAR3f11.y
	50	195.5	69.3	379	1	AW600621	AW600621 707104A10
	51	195.5	69.3	411	1	AW331399	AW331399 707012E03
	52	195.5	69.3	412	2	BG462689	BG462689 947059C04
	53	195.5	69.3	438	2	BG317226	BG317226 947026G02
	54	195.5	69.3	445	3	B1325424	B1325424 949038G09
	55	195.5	69.3	485	6	CD998181	CD998181 QBF10a04.
	56	195.5	69.3	486	3	B1430769	CD998218 QBF10d10.
	57	195.5	69.3	486	6	CD998218	CD998218 QBF10d10.
	58	195.5	69.3	487	6	CF005221	CF005221 QBH9b04.x
	59	195.5	69.3	507	6	CF003569	CF003569 QBH21b06.
	60	195.5	69.3	558	3	B1643315	B1643315 949077G05
	61	195.5	69.3	563	3	B1644173	B1644173 949022F06
	62	195.5	69.3	586	6	CD999712	CD999712 QBF8b11.x
	63	195.5	69.3	591	6	CD999712	CD999712 QBF8b11.x
	64	195.5	69.3	717	8	CO530543	CO530543 3530_1_20
	65	195.5	69.3	727	7	DR969955	DR969955 ZM_BFB009
C	66	195.5	69.3	732	3	BM080707	BM080707 MEST112-C
	67	195.5	69.3	745	2	BG842572	BG842572 MEST13-80
	68	195.5	69.3	858	8	DR823021	DR823021 ZM_BFB006
	69	195.5	69.3	866	8	DR788406	DR788406 ZM_BFB000
C	70	195.5	69.3	880	2	BG837797	BG837797 Zm10_0400
	71	195.5	69.3	1004	10	CG242767	CG242767 OG0Q81TV
	72	195.5	69.3	1172	4	AV103730	AV103730 Zea_mays
C	73	194.5	69.0	262	2	BG316752	BG316752 947026E07
	74	194.5	69.0	619	3	B1430981	B1430981 949063F09
C	75	194.5	69.0	705	2	BG320451	BG320451 Zm03_10f0
C	76	191.5	67.9	320	6	CD988645	CD988645 QAO2f07.y
	77	191.5	67.9	563	6	CF021885	CF021885 QBPF611.x
	78	190.5	67.6	587	2	BG320894	BG320894 Zm04_09g0
	79	188.5	66.8	723	6	CF014053	CF014053 QBL12g12.
	80	185.5	65.8	529	6	CD998557	CD998557 QBFL3f09.

81	183.5	65.1	467	2	BG517862	BG517862	947071H03
82	183	64.9	351	2	BG549043	BG549043	947072E03
83	182.5	64.7	214	2	BG549870	BG549870	947076D05
84	180.5	64.0	147	3	BI325456	BI325456	949039C04
85	178.5	63.3	234	3	BI430730	BI430730	949060C01
86	178.5	63.3	505	6	CF005283	CF005283	QBH9F03.X
87	178.5	63.3	565	6	CF021641	CF021641	QB3C05.X
88	177.5	62.9	509	2	BG462181	BG462181	947047G02
89	176.5	62.6	426	2	BG517870	BG517870	947071H10
90	175.5	62.2	580	3	BI674933	BI674933	949076E10
91	175.5	62.2	915	2	BG837761	BG837761	2m10_05R10
92	174.5	61.9	271	2	BG317210	BG317210	947026E07
93	172	61.0	549	1	AW398998	AW398998	EST309498
94	171.5	60.8	441	3	BI434512	BI434512	EST37273
95	171.5	60.8	478	1	AW618854	AW618854	EST320843
96	171.5	60.8	526	1	AW399256	AW399256	EST309756
97	171.5	60.8	557	2	BG097016	BG097016	EST461535
98	171.5	60.8	559	2	AW618743	AW618743	EST320729
99	171.5	60.8	611	1	AW398171	AW398171	EST297934
100	171.5	60.8	641	1	AW160224	AW160224	EST290082
101	171.5	60.8	674	7	CK863768	CK863768	35047_In
102	171.5	60.8	703	3	BI432231	BI432231	EST34992
103	170	60.3	341	3	BI433582	BI433582	EST356343
104	170	60.3	595	1	AW618741	AW618741	EST320727
105	170	60.3	634	2	BG589314	BG589314	EST497156
106	170	60.3	667	3	BQ113678	BQ113678	EST599254
107	170	60.3	693	3	BI432899	BI432899	EST535660
108	170	60.3	697	2	BG590013	BG590013	EST497855
109	170	60.3	699	3	BM404997	BM404997	EST579334
110	170	60.3	834	3	BI434599	BI434599	EST537360
111	169.5	60.1	140	3	BI325462	BI325462	949039D04
112	169.5	60.1	414	3	BI434313	BI434313	EST537074
113	169.5	60.1	515	1	AI483371	AI483371	EST243348
114	169	59.9	407	2	BG097139	BG097139	EST461658
115	169	59.9	409	3	BP745218	BP745218	BP745218
116	169	59.9	563	7	CN599952	EG-A11_00	
117	169	59.9	629	3	BM407356	BM407356	EST581683
118	169	59.9	634	3	BM113573	BM113573	EST561109
119	169	59.9	687	3	BM405149	BM405149	EST579476
120	169	59.9	743	7	CV504514	CV504514	71064.1_M
121	168.5	59.8	521	3	BI595975	BI595975	949075C03
122	168.5	59.8	528	1	AW039394	AW039394	EST281651
123	168.5	59.8	578	3	BI396085	BI396085	949048B04
124	168.5	59.8	614	1	AW443539	AW443539	EST308469
125	168	59.6	461	6	CA117824	CA117824	SCBGLR104
126	168	59.6	461	6	CA273397	CA273397	SCBPSD100
127	168	59.6	556	6	CA281255	CA281255	SCBPSD102
128	168	59.6	665	6	CA282404	CA282404	SCCCLV100
129	168	59.6	671	6	CA297496	CA297496	SCCSD100
130	168	59.6	684	6	DN238298	DN238298	MUC4LH100
131	168	59.6	712	8	CF574544	CF574544	MUC4L16G0
132	168	59.6	715	6	DN240065	DN240065	MUC4L1C101
133	168	59.6	744	8	DN239801	DN239801	MUC4L1C101
134	168	59.6	756	8	CA208714	CA208714	SCACSB111
135	168	59.6	764	6	CA208645	CA208645	SCACSB111
136	168	59.6	771	6	CA282815	CA282815	SCOGSD104
137	168	59.6	951	6	BE924621	BE924621	SCBPSD103
138	167.5	59.4	200	2	CA324830	CA324830	EST428390
139	167.5	59.4	555	1	AW443028	AW443028	EST307958
140	167.5	59.4	560	1	AI772337	AI772337	EST253437
141	167	59.2	522	6	CA276409	CA276409	SCBPSD200
142	167	59.2	532	6	CA169255	CA169255	SCJFSB101
143	167	59.2	538	1	AI484172	AI484172	EST249325
144	167	59.2	571	1	AW399318	AW399318	EST309818
145	167	59.2	572	6	CA274801	CA274801	SCBPSD103
146	167	59.2	580	1	AW443497	AW443497	EST308427
147	167	59.2	598	1	AW399017	AW399017	EST309517
148	167	59.2	599	6	CA210512	CA210512	SCBPSB112
149	167	59.2	604	6	CA110175	CA110175	SCVPHR108
150	167	59.2	608	6	CA295185	CA295185	SCACLV102

RESULT 1

LOCUS

DEFINITION

AW438072

mays cDNA, mRNA sequence.

171 bp

mRNA

linear

EST 14-FEB-2000

EST 14-FEB-2000

WALBOT LAB (SK) ZEA

AW438072

GI:6973378

KEYWORDS

EST.

ORGANISM

Zea mays

REFERENCE

1 (bases 1 to 171)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford University

Unpublished (1999)

CONTACT: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 707072 row: C column: 09.

LOCATION/QUALIFIERS

1. 171

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="W23"

/db\_xref="taxon:4577"

/tissue\_type="tassel, kernel, silk, husk, root, leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="707 - Mixed adult tissues from Walbot lab (SK)"

/note="Organ: tassel, kernel, silk, husk, root, leaf; Vector: pGAD10; Site: 1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."

ORIGIN

Alignment Scores:

Pred. No.: 1.27e-13

Length: 171

Score: 203.50

Matches: 47

Conservative: 0

Percent Similarity: 81.0%

Mismatches: 0

Best Local Similarity: 81.0%

Indels: 11

Query Match: 72.2%

DB: 1

Gaps: 2

US-10-628-525A-34 (1-58) x AW438072 (1-171)

Qy 1 MetAlaProThrValMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

Db 18 ATGGGCCCCCGGATGATGGCTTCGTCGCCACC----- 53

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYssSerThrAlaSerLeuProValAlaArg 40

Db 54 -----GCCGTCGCTCCCTTCAGGGGCTCAAGTCCACGCCGCGCTCCCGTCGCCGC 107

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAlaSerAlaGlyGlyArgCys 58

Db 108 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 158

RESULT 2

LOCUS

DEFINITION

BI430868

Zea mays cDNA, mRNA sequence.

281 bp

mRNA

linear

EST 17-AUG-2001

EST 17-AUG-2001

WALBOT LAB (SK) ZEA

BI430868

GI:6973378

KEYWORDS

EST.

ORGANISM

Zea mays

REFERENCE

1 (bases 1 to 171)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford University

Unpublished (1999)

CONTACT: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 707072 row: C column: 09.

LOCATION/QUALIFIERS

1. 171

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="W23"

/db\_xref="taxon:4577"

/tissue\_type="tassel, kernel, silk, husk, root, leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="707 - Mixed adult tissues from Walbot lab (SK)"

/note="Organ: tassel, kernel, silk, husk, root, leaf; Vector: pGAD10; Site: 1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."

ORIGIN

Alignment Scores:

Pred. No.: 1.27e-13

Length: 171

Score: 203.50

Matches: 47

Conservative: 0

Percent Similarity: 81.0%

Mismatches: 0

Best Local Similarity: 81.0%

Indels: 11

Query Match: 72.2%

DB: 1

Gaps: 2

US-10-628-525A-34 (1-58) x AW438072 (1-171)

Qy 1 MetAlaProThrValMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

Db 18 ATGGGCCCCCGGATGATGGCTTCGTCGCCACC----- 53

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYssSerThrAlaSerLeuProValAlaArg 40

Db 54 -----GCCGTCGCTCCCTTCAGGGGCTCAAGTCCACGCCGCGCTCCCGTCGCCGC 107

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAlaSerAlaGlyGlyArgCys 58

Db 108 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 158

RESULT 2

LOCUS

DEFINITION

BI430868

Zea mays cDNA, mRNA sequence.

281 bp

mRNA

linear

EST 17-AUG-2001

EST 17-AUG-2001

WALBOT LAB (SK) ZEA

BI430868

GI:6973378

KEYWORDS

EST.

ORGANISM

Zea mays

REFERENCE

1 (bases 1 to 171)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford University

Unpublished (1999)

CONTACT: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 707072 row: C column: 09.

LOCATION/QUALIFIERS

1. 171

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="W23"

/db\_xref="taxon:4577"

/tissue\_type="tassel, kernel, silk, husk, root, leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="707 - Mixed adult tissues from Walbot lab (SK)"

/note="Organ: tassel, kernel, silk, husk, root, leaf; Vector: pGAD10; Site: 1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."

ORIGIN

Alignment Scores:

Pred. No.: 1.27e-13

Length: 171

Score: 203.50

Matches: 47

Conservative: 0

Percent Similarity: 81.0%

Mismatches: 0

Best Local Similarity: 81.0%

Indels: 11

Query Match: 72.2%

DB: 1

Gaps: 2

US-10-628-525A-34 (1-58) x AW438072 (1-171)

Qy 1 MetAlaProThrValMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

Db 18 ATGGGCCCCCGGATGATGGCTTCGTCGCCACC----- 53

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuYssSerThrAlaSerLeuProValAlaArg 40

Db 54 -----GCCGTCGCTCCCTTCAGGGGCTCAAGTCCACGCCGCGCTCCCGTCGCCGC 107

Qy 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAlaSerAlaGlyGlyArgCys 58

Db 108 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 158

**BT430868.1** GI:15208984  
**VERSION**  
**KEYWORDS**  
**SOURCE**  
**ORGANISM**  
 Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**  
**COMMENT**  
 Maize ESTs from various cDNA libraries sequenced at Stanford University  
 Unpublished (1999)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 949062 row: B column: 09.  
**FEATURES**  
 Location/Qualifiers  
 1..281  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="W64A"  
 /db\_xref="taxon:4577"  
 /tissue\_type="immature leaf primordium and vegetative meristem"  
 /dev\_stage="4 stages from 3-13 days after imbibing"  
 /lab\_host="E. coli XL0LR"  
 /clone\_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"  
 /note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, poly(A<sup>+</sup>) RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda HybriZap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 2,3e-13 Length: 281  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 3 Gaps: 2  
 US-10-628-525A-34 (1-58) x BT430868 (1-281)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20  
 Db 15 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 50  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 51 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTGGCCGC 104  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
 Db 105 CGCTCTCCAGAGGCTCGGCAACGTC---AGCAACGCGGAGGATCCGGTGC 155  
**RESULT 3**  
**LOCUS**  
**DEFINITION**  
 QAR1a03.yg QAR Zea mays cDNA clone QAR1a03 mRNA sequence.  
 CD988795 320 bp mRNA linear EST 16-JUL-2003  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 2,68e-13 Length: 320  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2  
 US-10-628-525A-34 (1-58) x CD988795 (1-320)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20  
 Db 29 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 64  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 65 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTGGCCGC 118  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
 Db 119 CGCTCTCCAGAGGCTCGGCAACGTC---AGCAACGCGGAGGATCCGGTGC 169  
**RESULT 4**  
**LOCUS**  
**DEFINITION**  
 am78b09.xl maize ear glume library Zea mays cDNA clone am78b09 5',  
 CD988795 369 bp mRNA linear EST 12-JAN-1999  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 2,68e-13 Length: 320  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2  
 US-10-628-525A-34 (1-58) x CD988795 (1-320)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20  
 Db 29 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 64  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 65 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTGGCCGC 118  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
 Db 119 CGCTCTCCAGAGGCTCGGCAACGTC---AGCAACGCGGAGGATCCGGTGC 169  
**RESULT 4**  
**LOCUS**  
**DEFINITION**  
 am78b09.xl maize ear glume library Zea mays cDNA clone am78b09 5',  
 CD988795 369 bp mRNA linear EST 12-JAN-1999  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 2,68e-13 Length: 320  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2  
 US-10-628-525A-34 (1-58) x CD988795 (1-320)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20  
 Db 29 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 64  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 65 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTGGCCGC 118  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
 Db 119 CGCTCTCCAGAGGCTCGGCAACGTC---AGCAACGCGGAGGATCCGGTGC 169  
**RESULT 4**  
**LOCUS**  
**DEFINITION**  
 am78b09.xl maize ear glume library Zea mays cDNA clone am78b09 5',  
 CD988795 369 bp mRNA linear EST 12-JAN-1999  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 2,68e-13 Length: 320  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2  
 US-10-628-525A-34 (1-58) x CD988795 (1-320)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20  
 Db 29 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 64  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 65 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTGGCCGC 118  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
 Db 119 CGCTCTCCAGAGGCTCGGCAACGTC---AGCAACGCGGAGGATCCGGTGC 169  
**RESULT 4**  
**LOCUS**  
**DEFINITION**  
 am78b09.xl maize ear glume library Zea mays cDNA clone am78b09 5',  
 CD988795 369 bp mRNA linear EST 12-JAN-1999  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 2,68e-13 Length: 320  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2  
 US-10-628-525A-34 (1-58) x CD988795 (1-320)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20  
 Db 29 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 64  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 65 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTGGCCGC 118  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
 Db 119 CGCTCTCCAGAGGCTCGGCAACGTC---AGCAACGCGGAGGATCCGGTGC 169  
**RESULT 4**  
**LOCUS**  
**DEFINITION**  
 am78b09.xl maize ear glume library Zea mays cDNA clone am78b09 5',  
 CD988795 369 bp mRNA linear EST 12-JAN-1999  
**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 2,68e-13 Length: 320  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2  
 US-10-628-525A-34 (1-58) x CD988795 (1-320)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20  
 Db 29 ATGGCGCCACCGTATGATGCGCTCGTGGCCACC----- 64  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 65 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCGTGGCCGC 118  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyG

## COMMENT

Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org  
Plate: am78 row: b column: 09  
Seq primer: M13 reverse universal  
High quality sequence stop: 369.

## FEATURES

source

1..369  
/organism="Zea mays"  
/mol\_type="mRNA"  
/db\_xref="taxon:4577"  
/clone="am78b03"  
/tissue\_type="glume ear 2 weeks post-pollination"  
/cell\_line="W22-TGA"  
/clone\_lib="maize ear glume library"  
/note="Vector: pBLUESCRIPT SK+ (X52325); Site 1: XhoI;  
Site 2: EcoRI; This library was supplied by John Doebley  
(Univ. of Minnesota). cDNAs are directionally cloned into  
the XhoI and EcoRI sites; XhoI is near the polyA tail.  
Most reads from this library are made with the reverse  
universal M13 primer and are 5' in direction. Additional  
information on this library as well as ftp access to all  
sequences can be found at  
http://www.cshl.org/maizegenome"

## ORIGIN

Alignment Scores:  
Pred. No.: 3,18e-13 Length: 369  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 1 Gaps: 2

US-10-628-525A-34 (1-58) x AJ372109 (1-369)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAsnProAlaGln 20  
|||||  
Db 54 ATGGCGCCACCGTGATGCGCTCGTGGCCACC----- 89

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
|||||  
Db 90 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCCGCGC 143

QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGileArgCys 58  
|||||  
Db 144 CGCTCTCCAGAGCTCGGCAACGTC---AGCAACGGTGGAGGATCCGGTGC 194

RESULT 5  
BZ647531  
LOCUS BZ647531 428 bp DNA linear GSS 29-JAN-2003  
DEFINITION OGCBJ16TC ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0133D08,  
genomic survey sequence.  
ACCESSION BZ647531  
VERSION BZ647531.1 GI:28110542  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 428)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OGCBJ16TM  
Contact: Cathy Whitelaw

## TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TF  
Class: methylation filtered.

## FEATURES

source

1..428  
Location/Qualifiers  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBMA0133D08"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

## ORIGIN

Alignment Scores:  
Pred. No.: 3,79e-13 Length: 428  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 9 Gaps: 2

US-10-628-525A-34 (1-58) x BZ647531 (1-428)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAsnProAlaGln 20  
|||||  
Db 84 ATGGCGCCACCGTGATGCGCTCGTGGCCACC----- 119

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
|||||  
Db 120 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCCCGCGC 173

QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGileArgCys 58  
|||||  
Db 174 CGCTCTCCAGAGCTCGGCAACGTC---AGCAACGGGAGGATCCGGTGC 224

RESULT 6  
BG458793  
LOCUS BG458793 476 bp mRNA linear EST 19-MAR-2001  
DEFINITION 947054D04.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA  
sequence.  
ACCESSION BG458793  
VERSION BG458793.1 GI:13382118  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 476)  
Walbot, V.  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 947054 row: D column: 04.

## FEATURES

source

1..476  
Location/Qualifiers  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"



/tissue types="leaf and stem, including leaf base"  
 /dev\_stage="2 week old seedling (3 leaves)"  
 /lab\_host="XLI-Blue"  
 /clone\_lib="947 - 2 week shoot from Barkan lab"  
 /notes="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);  
 Site 1: EcoRI; Site 2: XhoI; Directionally cloned using  
 Stratagene's Unizap XR cDNA cloning kit with the 5' end  
 at the EcoRI site. The library represents 8 x 10e5  
 independent recombinant phage. The plants were greenhouse  
 grown."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,31e-13 Length: 476  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservatives: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x BG458793 (1-476)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 9 ATGGGCGCCACCGTGTATGGCTCTCGTGGCCACC----- 44  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 45 -----GCCGTCGCTCGTCTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 98  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgGlyArgCys 58  
 |||||  
 Db 99 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 149

## RESULT 7

DR826659 481 bp mRNA linear EST 28-JUL-2005  
 LOCUS ZM\_BFB0069110.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.  
 DEFINITION DR826659

ACCESSION DR826659.1 GI:71445609  
 VERSION  
 KEYWORDS EST.

SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 481)  
 Kim.H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,  
 Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.  
 Maize Full-length cDNA Project

Unpublished (2005)

CONTACT: Yeisoo Yu  
 Arizona Genomics Institute  
 The University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plates: 0069 row: I column: 10.

Location/Qualifiers

1. .481

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev\_stage="varies by tissue"

/lab\_host="PH10B T1 phage resistant"

/clone\_lib="ZM BFB"

/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,36e-13 Length: 481  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservatives: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x DR826659 (1-481)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 42 ATGGCGCCACCGTGTATGGCTCTCGTGGCCACC----- 77

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 78 -----GCCGTCGCTCGTCTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 131

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgGlyArgCys 58  
 |||||

Db 132 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 182

## RESULT 8

CC168222/c

LOCUS

DEFINITION

CC168222

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CC168222

CC168222

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

husks, ears, pollen, shoot tips, leaf, root tips, whole  
 seed, embryo. This is a Gateway compatible vector,  
 permitting clone movement to new vector backbones for  
 expression in diverse host cells using recombination  
 rather than restriction enzymes. poly(A)+ mRNA was  
 prepared by invitrogen, and equimolar amounts of RNA from  
 each of the 12 tissue samples were mixed together for  
 selection of mRNA with a 5' cap. After synthesis of cDNA,  
 a normalization step was conducted against the mixture of  
 RNA sources. Tissues prepared: 1. just emerging silks; 2.  
 inner husks from ears of sample #1; 3. 20 dap aleurone; 4.  
 immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to  
 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from  
 15 day old seedlings; all leaves with an expanded or  
 partially expanded sheath were removed; 8. mature leaf  
 tissue; 9. 0.5 cm long root tips from 15 day old  
 seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and  
 embryo; 12. 17 dap endosperm and embryo. All of the  
 sequenced clones in Maize Full-length cDNA Project will be  
 archived at the University of Arizona. Clones, high  
 density filters and amplified library can be ordered from  
 the University of Arizona  
 (http://www.genome.arizona.edu/orders/)."

CC168222 481 bp DNA linear GSS 29-APR-2003  
 iJ83b10.g1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone  
 iJ83b10.g1 genomic survey sequence.

CC168222

CC168222

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

CC168222.1

Plate: ij83 row: b column: 10  
Seq primer: -21M13UnivRev  
Class: shotgun  
High quality sequence stop: 481.  
Location/Qualifiers

FEATURES  
source

1..481  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="i183b10"  
/lab\_host="DH5a"  
/clone\_lib="WGS-ZmaysF (DH5a methyl filtered)"  
/note="Organ: immature ears; Site\_1: Xba I; Site\_2: Xba I;  
The vector was digested with XbaI and one nucleotide was  
added by fill in the recessive 3' end. The genomic DNA  
was rebligated, end repaired, adaptor ligated and size  
fractionated using sephadex. The resulting fragments were  
between 0.8 and 3 kb and were cloned into the vector (.x/y  
reads in M13mp19, .b/g reads in pUC19). The same ligation  
was transformed into DH5a."

ORIGIN

Alignment Scores:  
Pred. No.: 4,36e-13 Length: 481  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 9 Gaps: 2

US-10-628-525A-34 (1-58) x CCI68222 (1-481)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
DB 245 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 210  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
|||||  
DB 209 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCAGCCGAGCTCCCGTCGCCGC 156  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
|||||  
DB 155 CGCTCTCCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 105

RESULT 9  
BG550311

LOCUS BG550311 487 bp mRNA linear EST 05-APR-2001  
DEFINITION 947039B03.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA  
sequence.  
ACCESSION BG550311  
VERSION BG550311.1 GI:13558956  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 487)

REFERENCE  
AUTHORS

TITLE Walbot.V.  
JOURNAL Zea mays  
COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

FEATURES  
source

1..487  
Location/Qualifiers

/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf and stem, including leaf base"  
/dev\_stage="2 week old seedling (3 leaves)"  
/lab\_host="XL1-Blue"  
/clone\_lib="947 - 2 week shoot from Barkan lab"  
/note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);  
Site\_1: EcoRI; Site\_2: XhoI; Directionally cloned using  
Stratagene's UniZap XR cDNA cloning kit with the 5' end  
at the EcoRI site. The library represents 8 x 10<sup>5</sup>  
independent recombinant phage. The plants were greenhouse  
grown."

ORIGIN

Alignment Scores:  
Pred. No.: 4,43e-13 Length: 487  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x BG550311 (1-487)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
DB 18 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 53  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
|||||  
DB 54 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCAGCCGAGCTCCCGTCGCCGC 107  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
|||||  
DB 108 CGCTCTCCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 158

RESULT 10  
BI431142

LOCUS BI431142 513 bp mRNA linear EST 20-AUG-2001  
DEFINITION 949059C09.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose  
Zea mays cDNA, mRNA sequence.  
ACCESSION BI431142  
VERSION BI431142.1 GI:15215043  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 513)

REFERENCE  
AUTHORS

TITLE Walbot.V.  
JOURNAL Zea mays  
COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

FEATURES  
source

1..513  
Location/Qualifiers  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W64A"  
/db\_xref="taxon:4577"  
/tissue\_type="immature leaf primordium and vegetative  
meristem"  
/dev\_stage="4 stages from 3-13 days after imbibing"

/lab\_host="E. coli XL0LR"  
 /clone\_lib="949 - juvenile leaf and shoot cDNA from Steve  
 Moose"  
 /notes="Organ: juvenile vegetative shoots; Vector:  
 pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts  
 of total RNA by weight from 4 tissue sources (see below)  
 were pooled, polyA+ RNA isolated, and cDNA synthesized for  
 EcoRI (5') and XhoI (3') directional cloning into lambda  
 HybriZap vector from Stratagene. Tissue Sources: 1. Whole  
 shoots 3 days after sowing/imbibing in wet soil. 2. Basal  
 1.5 cm shoots 6 days after sowing - includes yellow  
 portions of developing leaves 1-5, primordia from 6-8, and  
 the vegetative apex. 3. Non-green portions of developing  
 leaves 4-5 and the vegetative apex, including adult leaf  
 primordia, 9 days after sowing. 4. Partially expanded and  
 greening leaves 4-5 at 13 days after sowing."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,71e-13 Length: 513  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x BI431142 (1-513)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAanProAlaGln 20  
 |||||  
 Db 2 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 37  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 38 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 91  
 QY 41 ArgSerSerArgSerLeuGlyAanValAlaSerAanGlyGlyArgIleArgCys 58  
 |||||  
 Db 92 CGCTCTCTCAGAAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 142

RESULT 11  
 CC616048/c  
 LOCUS  
 DEFINITION  
 CC616048 525 bp DNA linear GSS 18-JUN-2003  
 genomic survey sequence.

ACCESSION  
 VERSION  
 CC616048.1 GI:31977469  
 GSS.

SOURCE  
 Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

1 (bases 1 to 525)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: OGUKH26TV

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: methylation filtered.

Location/Qualifiers

1..525

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

## FEATURES

source

/db\_xref="taxon:4577"  
 /clone\_lib="ZMBMa0460P04"  
 /clone\_lib="ZM 0.7 1.5 KB"  
 /note="Vector: pBCSK- Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,84e-13 Length: 525  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 9 Gaps: 2

US-10-628-525A-34 (1-58) x CC616048 (1-525)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAanProAlaGln 20  
 |||||  
 Db 306 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 271  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 270 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 217  
 QY 41 ArgSerSerArgSerLeuGlyAanValAlaSerAanGlyGlyArgIleArgCys 58  
 |||||  
 Db 216 CGCTCTCTCAGAAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 166

## RESULT 12

BG349334

LOCUS

DEFINITION

BG349334

ACCESSION

VERSION

BG349334.1 GI:13178076

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

1 (bases 1 to 544)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 947028 row: A column: 12.

Location/Qualifiers

1..544

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="leaf and stem, including leaf base"

/dev\_stage="2 week old seedling (3 leaves)"

/lab\_host="XL1-Blue"

/clone\_lib="947 - 2 week shoot from Barkan lab"

/note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-);

Site 1: EcoRI; Site 2: XhoI; Directionally cloned using

Stratagene's Unizap XR cDNA cloning kit with the 5' end

at the EcoRI site. The library represents 8 x 10<sup>5</sup>

independent recombinant phage. The plants were greenhouse

grown."

## ORIGIN

```

Alignment Scores:
Pred. No.: 5.05e-13 Length: 544
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x BG349334 (1-544)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20
Db 44 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 79
QY 21 AlaSerAlaValaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 80 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCAGGATCCCGTCGCCGC 133
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 134 CGCTCTCTCAGAGGCTCGGCAACGTC---AGCAACGGCGAAGGATCCGGTGC 184

RESULT 13
CF025689
LOCUS 545 bp mRNA linear EST 17-JUL-2003
DEFINITION QCA1e07.yg QCA Zea mays cDNA clone QCA1e07, mRNA sequence.
ACCESSION CF025689
VERSION CF025689.1 GI:32920877
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE Clade; Panicoidae; Andropogoneae; Zea.
JOURNAL 1 (bases 1 to 545)
COMMENT Genoplatante, a major partnership french program in plant genomics
Contact: Genoplatante
Unpublished (2003)
Genoplatante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatante' (http://www.genoplatante.com
and http://genoplatante-info.infobiogen.fr).

FEATURES
source
1..545
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="f334"
/db_xref="taxon:4577"
/clone="QCA1e07"
/tissue_type="3rd adult leaf"
/clone_lib="QCA"

ORIGIN
Alignment Scores:
Pred. No.: 5.06e-13 Length: 545
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CF025689 (1-545)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20
Db 29 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 64
QY 21 AlaSerAlaValaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40

```

---

```

Db 65 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCAGGCTCCCGTCGCCGC 118
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 119 CGCTCTCTCAGAGGCTCGGCAACGTC---AGCAACGGCGAAGGATCCGGTGC 169

RESULT 14
CD998700
LOCUS 569 bp mRNA linear EST 16-JUL-2003
DEFINITION QBF15C08.yg QBF Zea mays cDNA clone QBF15C08, mRNA sequence.
ACCESSION CD998700
VERSION CD998700.1 GI:32859019
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE Clade; Panicoidae; Andropogoneae; Zea.
JOURNAL 1 (bases 1 to 569)
COMMENT Genoplatante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplatante
Genoplatante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatante' (http://www.genoplatante.com
and http://genoplatante-info.infobiogen.fr).

FEATURES
source
1..569
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QBF15C08"
/tissue_type="ear leaf"
/clone_lib="QBF"

ORIGIN
Alignment Scores:
Pred. No.: 5.33e-13 Length: 569
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CD998700 (1-569)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraAlaThraArgThrAsnProAlaGln 20
Db 57 ATGGCGCCACCGTGATGCTCGTCCGCCACC----- 92
QY 21 AlaSerAlaValaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 93 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCAGGATCCCGTCGCCGC 146
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 147 CGCTCTCTCAGAGGCTCGGCAACGTC---AGCAACGGCGAAGGATCCGGTGC 197

RESULT 15
CF025518
LOCUS 608 bp mRNA linear EST 17-JUL-2003
DEFINITION QCA18e04.yg QCA Zea mays cDNA clone QCA18e04, mRNA sequence.
ACCESSION CF025518
VERSION CF025518.1 GI:32920706
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

# REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 608)

Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (<http://www.genoplante.com>

and <http://genoplante-info.infobiogen.fr>).

## FEATURES

source

1..608

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="F334"

/db\_xref="taxon:4577"

/clone="QCA18e04"

/tissue\_type="3rd adult leaf"

/clone\_lib="QCA"

## ORIGIN

Alignment Scores:  
Pred. No.: 5,76e-13 Length: 608  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CF025518 (1-608)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 29 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 64  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 65 -----GCCGTGCTCGTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 118  
QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 119 CGCTCTCCAGAGCGCTCGGCAACGTC---AGCAACGGCGAAGGATCGGTGC 169

## RESULT 16

CD990730

LOCUS

QAY3f06.Yg QAY Zea mays cDNA clone QAY3f06, mRNA linear EST 16-JUL-2003

ACCESSION

CD990730.1 GI:32851049

VERSION

CD990730.1

KEYWORDS

EST.

Ze mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 619)

Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (<http://www.genoplante.com>

and <http://genoplante-info.infobiogen.fr>).

## FEATURES

source

1..619

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/clone="QAY3f06"

/tissue\_type="aerial, root, whole plant"

/clone\_lib="QAY"

/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="QAY3f06"  
/tissue\_type="aerial, root, whole plant"  
/clone\_lib="QAY"

## ORIGIN

Alignment Scores:

Pred. No.: 5,89e-13 Length: 619  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CD990730 (1-619)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 62 ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 97  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 98 -----GCCGTGCTCGTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 151  
QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 152 CGCTCTCCAGAGCGCTCGGCAACGTC---AGCAACGGCGAAGGATCGGTGC 202

## RESULT 17

BG458523

LOCUS

947045808.y1 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA

DEFINITION

sequence.

ACCESSION

BG458523

VERSION

BG458523.1 GI:13381848

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 622)

Walbot V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 947045 row: B column: 08.

Location/Qualifiers

1..622

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="leaf and stem, including leaf base"

/dev\_stage="2 week old seedling (3 leaves)"

/lab\_host="XLI-Blue"

/clone\_lib="947 - 2 week shoot from Barkan lab"

/note="Organ: shoot; Vector: Lambda ZAP (pBluescript SK-);

Site 1: EcoRI; Site 2: XhoI; Directionally cloned using

Stratagene's Unizap-XR cDNA cloning kit with the 5' end

at the EcoRI site. The library represents 8 x 10e5

independent recombinant phage. The plants were greenhouse

grown."

## ORIGIN

## Alignment Scores:

Pred. No.: 5,92e-13 Length: 622  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 2 Gaps: 2

US-10-628-525A-34 (1-58) x BG458523 (1-622)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 31 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 66  
 |||||  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerIeuProValAlaArg 40  
 |||||  
 Db 67 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 120  
 |||||  
 QY 41 ArgSerSerArgSerIeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 |||||  
 Db 121 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGT 171  
 |||||

## RESULT 18

AW352495

LOCUS AW352495 652 bp mRNA linear EST 02-FEB-2000  
 DEFINITION 707050811.y1 707 - Mixed adult tissues from Walbot lab (SK) Zea  
 mays cDNA, mRNA sequence.

ACCESSION AW352495  
 VERSION AW352495.1 GI:6851485

## KEYWORDS

EST.

## SOURCE

Zea mays

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 652)

Walbot V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 707050 row: B column: 11.

Location/Qualifiers

1..652

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="W23"

/db\_xref="taxon:4577"

/tissue\_type="tassel, kernel, silk, husk, root, leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="707 - Mixed adult tissues from Walbot lab

(SK)"

/note="Organ: tassel, kernel, silk, husk, root, leaf;

Vector: pGAD10; Site 1: EcoRI; cDNA library from fully

differentiated maize tissues from an active Mutator

plant. tissue ratio is 4/2/1/1/1 (tassel, kernel, silk,

husk, root, leaf). Unidirectionally cloned."

## ORIGIN

## Alignment Scores:

Pred. No.: 6,27e-13 Length: 652  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0

## Query Match:

DB: 72.2% Indels: 11  
 1 Gaps: 2

US-10-628-525A-34 (1-58) x AW352495 (1-652)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 74 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 109  
 |||||  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerIeuProValAlaArg 40  
 |||||  
 Db 110 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 163  
 |||||  
 QY 41 ArgSerSerArgSerIeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 |||||  
 Db 164 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGT 214  
 |||||

## RESULT 19

COS23152

LOCUS COS23152 657 bp mRNA linear EST 15-JUL-2004  
 DEFINITION 3530.1\_153.1\_B03.y.1 3530 - Full length cDNA library created by  
 Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.

ACCESSION COS23152

VERSION COS23152.1 GI:50328026

## KEYWORDS

EST.

## SOURCE

Zea mays

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 657)

Walbot V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 3530.1\_153.1 row: B column: 03.

Location/Qualifiers

1..657

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="multiple"

/dev\_stage="varies by tissue"

/lab\_host="DH10B"

/clone\_lib="3530 - Full length cDNA library created by

Invitrogen from multiple tissues"

/note="Organ: silks, husks, ears, pollen, shoot tips,

leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT

6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery

Project contracted with Invitrogen to produce a

normalized, full length library in a pSPORT vector. This

is a Gateway compatible vector, permitting clone movement

to new vector backbones for expression in diverse host

cells using recombination rather than restriction enzymes.

Details of the vector and sequencing primers are available

at ZmDB in the EST library description tables. poly(A)+

mRNA was prepared by Invitrogen, and equimolar amounts of

RNA from each of the 12 tissue samples were mixed together

for selection of mRNA with a 5' cap. After synthesis of

cDNA, a normalization step was conducted against the

mixture of RNA sources. This step effected a 20X to 80X

reduction in common transcript types. Tissues prepared: 1.

just emerging silks; 2. inner husks from ears of sample

#1; 3. 20 dap aleurone; 4. immature tassels, stages from

1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm

vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.32e-13 Length: 657  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 2  
 Gaps: 2

US-10-628-525A-34 (1-58) x COS23152 (1-657)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThrAlaThraThrArgThrAsnProAlaGln 20  
 |||||  
 Db 54 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 89  
 |||||  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 90 -----GCCGTCTCCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGCGCGCC 143  
 |||||  
 QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgileArgCys 58  
 |||||  
 Db 144 CGCTCTCCAGAGCTCGGCAAGTC---AGCACGGCGGAGGATCCGGTGC 194  
 |||||

## RESULT 20

## BG320791/c

LOCUS Zm04\_10c04\_R Zm04\_AAPC\_ECORC cold stressed\_maize\_seedlings Zea mays  
 DEFINITION cDNA clone Zm04\_10c04, mRNA sequence.

ACCESSION BG320791.1 GI:13150469  
 VERSION EST.  
 KEYWORDS Zea mays

## SOURCE

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 660)

Singh, J.A., Wakui, K., Couroux, P., De Moors, A., Harris, L.J.,  
 Hattori, J.I., Ouellet, T., Robert, L.S., Spott, D., and Tinker, N.A.  
 Expressed Sequence Tags from Cold-Stressed Maize Seedlings  
 Unpublished (2001)

## TITLE

## JOURNAL

## COMMENT

Contact: Singh, J.A.  
 Eastern Cereal and Oilseed Research Centre  
 Agriculture and Agri-food Canada  
 KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A  
 OC6, Canada  
 Tel: (613) 759-1662  
 Fax: (613) 759-1701  
 Email: singhja@agr.gc.ca.

## FEATURES

## source

1. .660  
 /location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="CO328"  
 /db\_xref="taxon:4577"  
 /clone="Zm04\_10c04"  
 /tissue\_type="Leaf, crown"  
 /clone\_lib="Zm04\_AAPC\_ECORC cold stressed\_maize\_seedlings"  
 /note="Vector: Bluescript SK-/XhoI-EcoRI; Site\_1: Eco RI;

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.36e-13 Length: 660  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 2  
 Gaps: 2

US-10-628-525A-34 (1-58) x BG320791 (1-660)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThrAlaThraThrArgThrAsnProAlaGln 20  
 |||||  
 Db 623 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC----- 588  
 |||||  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 587 -----GCCGTCTCCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGCGCGCC 534  
 |||||  
 QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgileArgCys 58  
 |||||  
 Db 533 CGCTCTCCAGAGCTCGGCAAGTC---AGCACGGCGGAGGATCCGGTGC 483  
 |||||

## RESULT 21

## COS32595

## LOCUS

DEFINITION 3530\_1\_214\_1\_E03.Y\_1\_3530 - Full length cDNA library created by  
 Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.

ACCESSION COS32595

VERSION COS32595.1 GI:50337469

## KEYWORDS

## SOURCE

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 660)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot, V.

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 3530\_1\_214\_1 row: E column: 03.

## FEATURES

## source

1. .660  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="multiple"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B"  
 /clone\_lib="3530 - Full length cDNA library created by  
 Invitrogen from multiple tissues"  
 /note="Organ: silks, husks, ears, pollen, shoot tips,  
 leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT  
 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery  
 Project contracted with Invitrogen to produce a  
 normalized, full length library in a pSPORT vector. This  
 is a Gateway compatible vector, permitting clone movement  
 to new vector backbones for expression in diverse host

Site 2: Xho I; Lower temperature 50 C / hour from 22 to  
 120C; bring to 50 in 1 hour from 120C. Leave at 50C 2  
 days, photoperiod 16 hours. Light intensity was 125 uE-1.  
 Library prepared by in vivo mass excision from amplified  
 library."

cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,36e-13 Length: 660  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 7 Gaps: 2

US-10-628-525A-34 (1-58) x COS32595 (1-660)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 47 ATGGGCGCCACCGTATGATGGCTCGTCGGCCACC----- 82  
 |||||  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 83 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 136  
 |||||  
 QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyVArgIleArgCys 58  
 |||||  
 Db 137 CGCTCTCTCAGAAGCGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 187

RESULT 22  
 CD990623  
 LOCUS CD990623 671 bp mRNA linear EST 16-JUL-2003  
 DEFINITION QAY2d03.yg QAY Zea mays cDNA clone QAY2d03, mRNA sequence.  
 ACCESSION CD990623  
 VERSION CD990623.1 GI:32850942  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 671)  
 AUTHORS Genoplante.  
 TITLE Genoplante, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french plant genomics programme 'genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr/>.

FEATURES  
 source

Location/Qualifiers  
 1..671  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="P2"  
 /db\_xref="taxon:4577"  
 /clone="QAY2d03"  
 /tissue\_type="aerial, root, whole plant"  
 /clone\_lib="QAY"

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,48e-13 Length: 671  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CD990623 (1-671)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 114 ATGGGCGCCACCGTATGATGGCTCGTCGGCCACC----- 149  
 |||||  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 150 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 203  
 |||||  
 QY 41 ArgSerSerArgSerLeuGlyValAlaSerAsnGlyGlyVArgIleArgCys 58  
 |||||  
 Db 204 CGCTCTCTCAGAAGCGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 254

## RESULT 23

COS33682  
 LOCUS COS33682 711 bp mRNA linear EST 15-JUL-2004  
 DEFINITION 3530.1.221.1.H01.Y.1 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.  
 ACCESSION COS33682  
 VERSION COS33682.1 GI:50338556  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 711)  
 AUTHORS Walbot,V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

UNPUBLISHED (1999)  
 CONTACT: Walbot V  
 DEPARTMENT OF Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 3530.1.221.1 row: H column: 01.  
 Location/Qualifiers  
 1..711

FEATURES  
 source

Location/Qualifiers  
 1..711  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="multiple"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B"  
 /clone\_lib="3530 - Full length cDNA library created by Invitrogen from multiple tissues"  
 /note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site\_2: NotI; Maize Gene Discovery



Project contracted with Invitrogen to produce a normalized, full length library in a pSport vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 day aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 day whole seed; 11. 12 day endosperm and embryo; 12. 17 day endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery RST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,95e-13 Length: 711  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 7 Gaps: 2

US-10-628-525A-34 (1-58) x COS33682 (1-711)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 54 ATGGCCGCCACCGTGATGGCTCGTCGGCCACC----- 89  
 QY 21 AlaSerAlaValaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 90 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 143  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
 |||||  
 Db 144 CGCTCCTCCAGAGCCCTCGGCAACGTC---AGCACGGCGGAAGGATCCGGTGC 194

## RESULT 24

CD991089  
 LOCUS CD991089 712 bp mRNA linear EST 16-JUL-2003  
 DEFINITION QAZ4b01.yg QAZ Zea mays cDNA clone QAZ4b01, mRNA sequence.  
 ACCESSION CD991089  
 VERSION CD991089.1 GI:32851408  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 712)  
 Genoplante.  
 Genoplante, a major partnership french program in plant genomics  
 Unpublished (2003)  
 JOURNAL  
 COMMENT  
 CONTACT: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES  
 source

Location/Qualifiers  
 1..712  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /clone="QAZ4b01"  
 /tissue\_type="aerial, root, whole plant"  
 /clone\_lib="QAZ"

## ORIGIN

Alignment Scores:  
 Pred. No.: 6,96e-13 Length: 712  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 6 Gaps: 2

US-10-628-525A-34 (1-58) x CD991089 (1-712)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 64 ATGGCCGCCACCGTGATGGCTCGTCGGCCACC----- 99  
 QY 21 AlaSerAlaValaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 100 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 153  
 QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAsnGlyGlyArgIleArgCys 58  
 |||||  
 Db 154 CGCTCCTCCAGAGCCCTCGGCAACGTC---AGCACGGCGGAAGGATCCGGTGC 204

## RESULT 25

DR822461  
 LOCUS ZM\_BPB0062L05.r ZM\_BPB Zea mays cDNA 5', mRNA sequence.  
 ACCESSION DR822461  
 VERSION DR822461.1 GI:71441411  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 769)  
 Kim H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.  
 Maize Full-length cDNA Project  
 Unpublished (2005)  
 CONTACT: Yeisoo Yu  
 Arizona Genomics Institute  
 The University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9585  
 Fax: 520 621 1259  
 Email: yeisoo@genome.arizona.edu  
 Plate: 0062 row: L column: 05.

Location/Qualifiers  
 1..769  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="ZM\_BPB"

FEATURES  
 source

Location/Qualifiers  
 1..769  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="ZM\_BPB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(http://www.genome.arizona.edu/orders/)."

## ORIGIN

Alignment Scores:  
Pred. No.: 7,63e-13 Length: 769  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x DR822461 (1-769)

QY 1 MetalProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 54 ATGGCGCCACCGTGATGCGCTCGTGGCCACC----- 89  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 90 -----GCCGTGCTCCGTTCAGGGGCTCAAGTCCAGCGCAGCTCCCGTCCCGCGC 143  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 144 CGCTCCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 194

## RESULT 26

DR824125  
LOCUS ZM\_BFB0065M08.r ZM\_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005

DEFINITION ZM\_BFB0065M08.r Zea mays cDNA 5', mRNA sequence.

ACCESSION DR824125

VERSION DR824125.1 GI:71443075

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 773)

Kim, H., Collura, K., Wisotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project

Unpublished (2005)

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CG094731

PURDK52TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBta0794107,

genomic survey sequence.

CG094731

CG094731.1 GI:33977025

GSS.

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Zea mays

Email: yeisoo@genome.arizona.edu  
Plate: 0065 row: M column: 08.

## FEATURES

source

1..773

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"

/dev\_stage="varies by tissue"

/lab\_host="DH10B T1 phage resistant"

/clone\_lib="ZM\_BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(http://www.genome.arizona.edu/orders/)."

## ORIGIN

Alignment Scores:  
Pred. No.: 7,67e-13 Length: 773  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x DR824125 (1-773)

QY 1 MetalProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

DB 54 ATGGCGCCACCGTGATGCGCTCGTGGCCACC----- 89

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40

DB 90 -----GCCGTGCTCCGTTCAGGGGCTCAAGTCCAGCGCAGCTCCCGTCCCGCGC 143

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

DB 144 CGCTCCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 194

## RESULT 27

CG094731

LOCUS

DEFINITION

CG094731

CG094731.1 GI:33977025

GSS.

KEYWORDS Zea mays

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.

#### REFERENCE AUTHORS

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Reenick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.

#### TITLE JOURNAL COMMENT

Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PURDKS2TB  
Contact: Cathy Whitelaw  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@cigr.org

Seq primer: TF

Class: sheared ends.

#### FEATURES source

Location/Qualifiers

1..777

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZM87A0794107"

/clone\_lib="ZM 0.6-1.0 kb"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high  
cot selected genomic DNA library"

#### ORIGIN

Alignment Scores:  
Pred. No.: 7,72e-13 Length: 777  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 10 Gaps: 2

US-10-628-525A-34 (1-58) x CG094731 (1-777)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraAlaThraArgThrAenProAlaGln 20  
DB 610 ATGGCGCCACCGTGATGATGGCTCTGTCGCCACCC----- 645  
QY 21 AlaSerAlaValaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
DB 646 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 699  
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
DB 700 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 750

#### RESULT 28

DR829152 ZM\_BFB0074M16.r ZM\_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005

LOCUS DR829152

DEFINITION DR829152

ACCESSION DR829152.1 GI:71448102

VERSION EST.

KEYWORDS Zea mays

SOURCE Zea mays

#### ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 775)

Kim H., Collura, K., Wisotski, M., Smart, D., Kudrna, D., Muller, C.,

Rao, K., Haller, K., Wang, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project

Unpublished (2005)

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0074 row: M column: 16.

#### FEATURES source

Location/Qualifiers

1..775

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev\_stage="varies by tissue"

/lab\_host="DH10B T1 phage resistant"

/clone\_lib="ZM BFB"

/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector,

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination

rather than restriction enzymes. poly(A)+ mRNA was

prepared by Invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for

selection of mRNA with a 5' cap. After synthesis of cDNA,

a normalization step was conducted against the mixture of

RNA sources. Tissues prepared: 1. just emerging silks; 2.

inner husks from ears of sample #1; 3. 20 dap aleurone; 4.

immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from

15 day old seedlings; all leaves with an expanded or

partially expanded sheath were removed; 8. mature leaf

tissue; 9. 0.5 cm long root tips from 15 day old

seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and

embryo; 12. 17 dap endosperm and embryo. All of the

sequenced clones in Maize Full-length cDNA Project will be

archived at the University of Arizona. Clones, high

density filters and amplified library can be ordered from

the University of Arizona

(http://www.genome.arizona.edu/orders/).

#### ORIGIN

Alignment Scores:  
Pred. No.: 7,74e-13 Length: 779  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x DR829152 (1-779)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraAlaThraArgThrAenProAlaGln 20  
DB 49 ATGGCGCCACCGTGATGATGGCTCTGTCGCCACCC----- 84  
QY 21 AlaSerAlaValaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
DB 85 -----GCCGTCGCTCGGTCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 138  
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
DB 139 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 189

#### RESULT 29

CC641056

LOCUS CC641056

DEFINITION OGLCD30TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0320P12,

genomic survey sequence.

ACCESSION CC641056

VERSION CC641056.1 GI:32024778

KEYWORDS GSS.

SOURCE  
ORGANISM  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
AUTHORS  
1 (bases 1 to 800)  
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OGLCD30TH  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TF  
Class: methylation filtered.  
FEATURES  
source  
1..800  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZM\_BFB"0320F12"  
/clone\_lib="ZM\_0.7.1.5\_KB"  
/note="Vector: pBGSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"  
ORIGIN  
Alignment Scores:  
Pred. No.: 7,99e-13 Length: 800  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 9 Gaps: 2  
US-10-628-525A-34 (1-58) x CC641056 (1-800)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db ATGGCGCCACCGTGCATGATGCGCTCGTGGCCACC----- 105  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCGCTCCCGTCCGCCGC 159  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db CGCTCCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 210  
RESULT 30  
DR797511  
LOCUS ZM\_BFB0019K07.r ZM\_BFB Zea mays cDNA 5', mRNA linear EST 27-JUL-2005  
DEFINITION DR797511  
ACCESSION DR797511.1 GI:71321661  
VERSION DR797511.1  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
AUTHORS  
1 (bases 1 to 802)  
Kim,H., Collura,K., Wisseotski,M., Smart,D., Kudrna,D., Muller,C.,  
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.  
Maize Full-length cDNA Project  
Unpublished (2005)  
Contact: Yeisoo Yu  
Arizona Genomics Institute

The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: yeisoo@genome.arizona.edu  
Plate: 0019 row: K column: 07.  
Location/Qualifiers  
1..802  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot  
tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM BFB"  
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:  
NotI; Maize Full length cDNA library (3530 library)  
created by Invitrogen from multiple tissues; Organ: silks,  
husks, ears, pollen, shoot tips, leaf, root tips, whole  
seed, embryo. This is a Gateway compatible vector,  
permitting clone movement to new vector backbones for  
expression in diverse host cells using recombination  
rather than restriction enzymes. poly(A)+ mRNA was  
prepared by Invitrogen, and equimolar amounts of RNA from  
each of the 12 tissue samples were mixed together for  
selection of mRNA with a 5' cap. After synthesis of cDNA,  
a normalization step was conducted against the mixture of  
RNA sources. Tissues prepared: 1. just emerging silks; 2.  
inner husks from ears of sample #1; 3. 20 day aleurone; 4.  
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to  
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from  
15 day old seedlings; all leaves with an expanded or  
partially expanded sheath were removed; 8. mature leaf  
tissue; 9. 0.5 cm long root tips from 15 day old  
seedlings; 10. 10 day whole seed; 11. 12 day endosperm and  
embryo; 12. 17 day endosperm and embryo. All of the  
sequenced clones in Maize Full-length cDNA Project will be  
archived at the University of Arizona. Clones, high  
density filters and amplified library can be ordered from  
the University of Arizona  
(http://www.genome.arizona.edu/orders/)."  
ORIGIN  
Alignment Scores:  
Pred. No.: 8.02e-13 Length: 802  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2  
US-10-628-525A-34 (1-58) x DR797511 (1-802)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db ATGGCGCCACCGTGCATGATGCGCTCGTGGCCACC----- 68  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCGCTCCCGTCCGCCGC 122  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db CGCTCCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 173  
Search completed: April 1, 2006, 19:23:32  
Job time : 937.32 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 31, 2006, 22:47:42 ; Search time 77.568 Seconds  
(without alignments)  
1329.139 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MATVMASSATATRNPAQ.....ARRSSRLGNVASNGRIIRC 58

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlp  
-Q=abss/ABSSWEB spool/US10628525/runat\_31032006\_095123\_16858/app\_query.fasta\_1  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=150 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abs02p -USER=US10628525 @CGN 1 1.855 @runat\_31032006\_095123\_16858  
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	203.5	72.2	405	2	US-08-336-778-4
4	203.5	72.2	5281	3	US-09-921-263-1
5	203.5	72.2	5909	3	US-09-921-263-2
6	196.5	69.7	415	3	US-09-063-733A-49
7	196.5	69.7	415	3	US-09-441-340-13
8	196.5	69.7	415	3	US-09-186-002-3
9	196.5	69.7	415	3	US-09-377-466B-25

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13	196.5	69.7	3450	3	US-09-377-466B-17	Sequence 17, Appl
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22	187.5	66.5	195	3	US-09-122-399-9	Sequence 9, Appl
23	187.5	66.5	195	3	US-08-440-646A-9	Sequence 9, Appl
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25	159.5	56.6	177	2	US-08-096-043-12	Sequence 12, Appl
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130 71 25.2 885 3 US-09-902-540-5770 Sequence 5770, Ap
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137 70 24.8 13145 3 US-09-949-016-13083 Sequence 13083, A
138 70 24.8 28791 3 US-09-949-016-15396 Sequence 15396, A
139 69 24.3 2787 3 US-09-624-693A-16 Sequence 16, Appl
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## ALIGNMENTS

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US-08-447-985-14
; Sequence 14, Application US/08447985
; Patent No. 6399861
; GENERAL INFORMATION:
; APPLICANT: Adams, Thomas R. et al.
; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants
and Cells Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/447,985
APPLICATION NUMBER: 08/113,561
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: DEKM:055/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 713/789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-447-985-14
Alignment Scores:
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Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2
US-10-628-525A-34 (1-58) x US-08-447-985-14 (1-185)
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QY 41 ArgSerSerArgSerIeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
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US-08-852-340-14
; Sequence 14, Application US/08852340
; Patent No. 6803499
; GENERAL INFORMATION:
; APPLICANT: Adams, Thomas R., et al.
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PRODUCTION OF STABLY TRANSFORMED, FERTILE MONOCOT PLANTS  
TITLE OF INVENTION: AND CELLS THEREOF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/852,340  
FILING DATE: 07-MAY-1997  
CLASSIFICATION: 504  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/113,561  
FILING DATE: 25-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: DEKM:146/WIM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-852-340-14

Alignment Scores:  
Pred. No.: 2,25e-15 Length: 185  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-08-852-340-14 (1-185)

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QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
Db 132 CGGTCCTCCAGAGCTCGGCAAGTC---AGCAACGGCGGAGGATCGGTGC 182

RESULT 3  
US-08-336-778-4  
Sequence 4, Application US/08336778  
Patent No. 5635618  
GENERAL INFORMATION:  
APPLICANT: Capellades, Montserrat  
APPLICANT: DeRose, Richard  
APPLICANT: Montoliu, Lluís  
APPLICANT: Puigdomenech, Pedro  
APPLICANT: Torres, Miguel  
APPLICANT: Uribe, Javier  
APPLICANT: Rigau, Juan  
TITLE OF INVENTION: PROMOTER ELEMENTS OF CHIMERIC GENES

TITLE OF INVENTION: OF ALPHA-TUBULIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Preseer  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,778  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9487  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 405 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-336-778-4

Alignment Scores:  
Pred. No.: 6.08e-15 Length: 405  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 2 Gaps: 2

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Db 262 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 297

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
Db 298 -----GCCGTCGCTCGTTCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCGC 351

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58  
Db 352 CGGTCCTCCAGAGCTCGGCAAGTC---AGCAACGGCGGAGGATCGGTGC 402

RESULT 4  
US-09-921-263-1/c  
Sequence 1, Application US/09921263  
Patent No. 6791014  
GENERAL INFORMATION:  
APPLICANT: Aventis CropScience S.A.  
TITLE OF INVENTION: Use of HPPD inhibitors as selection agents in the transformation of plants  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/921,263  
CURRENT FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1  
LENGTH: 5281  
TYPE: DNA  
ORGANISM: Artificial sequence





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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 415
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; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: N region
; LOCATION: (15)..(163)
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; LOCATION: (164)..(322)
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; NAME/KEY: C region
; LOCATION: (323)..(411)
US-09-441-340-13

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Pred. No.: 4.02e-14 Length: 415
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservatives: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
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US-10-628-525A-34 (1-58) x US-09-441-340-13 (1-415)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 15 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 50
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 51 -----GCCGTGCTCGTTCTTGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 104
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
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RESULT 8
US-09-186-002-3
; Sequence 3, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: delta-Endotoxins
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Zea mays
US-09-186-002-3

Alignment Scores:
Pred. No.: 4.02e-14 Length: 415
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservatives: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-186-002-3 (1-415)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 15 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 50
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 51 -----GCCGTGCTCGTTCTTGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 104
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 105 CGTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 155
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Db 51 -----GCCGTGCTCGTTCTTGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 104
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 105 CGTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 155

RESULT 9
US-09-377-466B-25
; Sequence 25, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: non-naturally
; OTHER INFORMATION: occurring nucleotide sequence encoding Zea mays
; OTHER INFORMATION: ribulose bis-phosphate carboxylase chloroplast
; OTHER INFORMATION: targeting peptide
; NAME/KEY: CDS
; LOCATION: (16)..(162)
; NAME/KEY: CDS
; LOCATION: (326)..(415)
; NAME/KEY: intron
; LOCATION: (163)..(325)
; OTHER INFORMATION: I-Zm.rbcS
US-09-377-466B-25

Alignment Scores:
Pred. No.: 4.03e-14 Length: 416
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservatives: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-377-466B-25 (1-416)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 16 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 51
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 52 -----GCCGTGCTCGTTCTTGGGGCTCAAGTCCACCGCCAGCTCCCGTGGCCGC 105
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 106 CGTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 156

RESULT 10
US-09-377-466B-30
; Sequence 30, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry2Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 416
```

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: modified  
; OTHER INFORMATION: cauliflower mosaic virus promoter AS4  
US-09-377-466B-30

Alignment Scores:  
Pred. No.: 4,03e-14 Length: 416  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-377-466B-30 (1-416)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 16 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 51  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 52 -----GCCGTGCTCCGTTCCTGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 105  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 106 CGCTCTCTCAGAAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

#### RESULT 11

US-10-232-665-25  
; Sequence 25, Application US/10232665  
; Patent No. 6943281  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/10/232,665  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 416  
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: non-naturally  
; OTHER INFORMATION: occurring nucleotide sequence encoding Zea mays  
; OTHER INFORMATION: ribulose bis-phosphate carboxylase chloroplast  
; OTHER INFORMATION: targeting peptide

; NAME/KEY: CDS  
; LOCATION: (16)..(162)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (326)..(415)  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (163)..(325)  
; OTHER INFORMATION: I-Zm.rbcS  
US-10-232-665-25

Alignment Scores:  
Pred. No.: 4,03e-14 Length: 416  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-10-232-665-25 (1-416)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 16 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 51  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 52 -----GCCGTGCTCCGTTCCTGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 105  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 106 CGCTCTCTCAGAAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

#### RESULT 12

US-10-232-665-30  
; Sequence 30, Application US/10232665  
; Patent No. 6943281  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/10/232,665  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 30  
; LENGTH: 416  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: modified  
; OTHER INFORMATION: cauliflower mosaic virus promoter AS4  
US-10-232-665-30

#### Alignment Scores:

Pred. No.: 4,03e-14 Length: 416  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-10-232-665-30 (1-416)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 16 ATGGCGCCACCGTGATGGCTCGTCGGCCACC----- 51  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 52 -----GCCGTGCTCCGTTCCTGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 105  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 106 CGCTCTCTCAGAAAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 156

#### RESULT 13

US-09-377-466B-17  
; Sequence 17, Application US/09377466B  
; Patent No. 6501009  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/09/377,466B  
; CURRENT FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 3450  
; TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
NAME/KEY: promoter  
LOCATION: (14)..(235)  
OTHER INFORMATION: P-CaMV.AS4  
NAME/KEY: 5'UTR  
LOCATION: (240)..(304)  
OTHER INFORMATION: L-Ta.hcb1  
NAME/KEY: intron  
LOCATION: (318)..(805)  
OTHER INFORMATION: I-Os.Act1  
NAME/KEY: transit\_peptide  
LOCATION: (825)..(971)  
OTHER INFORMATION: amino terminal TS-Zm.rbcs  
NAME/KEY: intron  
LOCATION: (972)..(1134)  
OTHER INFORMATION: I-Zm.rbcs  
NAME/KEY: transit\_peptide  
LOCATION: (1135)..(1221)  
OTHER INFORMATION: carboxy terminus TS-Zm.rbcs  
NAME/KEY: CDS  
LOCATION: (1222)..(3180)  
OTHER INFORMATION: Cry3Bb1 variant 11231mv1  
NAME/KEY: terminator  
LOCATION: (3198)..(3431)  
OTHER INFORMATION: T-Ta.hsp17  
US-09-377-466B-17

Alignment Scores:  
Pred. No.: 5.89e-13 Length: 3450  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-377-466B-17 (1-3450)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 825 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 860  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 861 -----GCCGTCGCTCGTTCTCTGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCGC 914  
QY 41 ArgSerSerArgSerLeuGlyAnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 915 CGCTCTCCAGAACGCTCGCAACGTC---AGCACGGCGGAAGGATCCGGTGC 965

RESULT 14  
US-10-232-665-17  
Sequence 17, Application US/10232665  
Patent No. 6943281  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/10/232,665  
PRIOR FILING DATE: 2002-08-29  
PRIORITY APPLICATION NUMBER: US/09/377,466  
PRIOR FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 17  
LENGTH: 3450  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette

FEATURE:  
NAME/KEY: promoter  
LOCATION: (14)..(235)  
OTHER INFORMATION: P-CaMV.AS4  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: (240)..(304)  
OTHER INFORMATION: L-Ta.hcb1  
FEATURE:  
NAME/KEY: intron  
LOCATION: (318)..(805)  
OTHER INFORMATION: I-Os.Act1  
FEATURE:  
NAME/KEY: transit\_peptide  
LOCATION: (825)..(971)  
OTHER INFORMATION: amino terminal TS-Zm.rbcs  
FEATURE:  
NAME/KEY: intron  
LOCATION: (972)..(1134)  
OTHER INFORMATION: I-Zm.rbcs  
FEATURE:  
NAME/KEY: transit\_peptide  
LOCATION: (1135)..(1221)  
OTHER INFORMATION: carboxy terminus TS-Zm.rbcs  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1222)..(3180)  
OTHER INFORMATION: Cry3Bb1 variant 11231mv1  
FEATURE:  
NAME/KEY: terminator  
LOCATION: (3198)..(3431)  
OTHER INFORMATION: T-Ta.hsp17  
US-10-232-665-17

Alignment Scores:  
Pred. No.: 5.89e-13 Length: 3450  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservative: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-10-232-665-17 (1-3450)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
DB 825 ATGGCGCCACCGTGATGGCTCGTGGCCACC----- 860  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
DB 861 -----GCCGTCGCTCGTTCTCTGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCGC 914  
QY 41 ArgSerSerArgSerLeuGlyAnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 915 CGCTCTCCAGAACGCTCGCAACGTC---AGCACGGCGGAAGGATCCGGTGC 965

RESULT 15  
US-09-377-466B-36  
Sequence 36, Application US/09377466B  
Patent No. 6501009  
GENERAL INFORMATION:  
APPLICANT: Romano, Charles P.  
TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
CURRENT APPLICATION NUMBER: US/09/377,466B  
CURRENT FILING DATE: 1999-08-19  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 3455  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: expression  
OTHER INFORMATION: cassette

```

; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: cassette
; LOCATION: (14)..(235)
; OTHER INFORMATION: P.CaMV.AS4
; NAME/KEY: 5'UTR
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; NAME/KEY: intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; NAME/KEY: transit_peptide
; LOCATION: (825)..(971)
; OTHER INFORMATION: TS-Zm.rbcS amino terminal coding sequence upstream
; OTHER INFORMATION: of Zea mays rbcS intron
; NAME/KEY: intron
; LOCATION: (972)..(1134)
; OTHER INFORMATION: I-Zm.rbcS
; NAME/KEY: transit_peptide
; LOCATION: (1135)..(1221)
; OTHER INFORMATION: TS-Zm.rbcS carboxy terminus coding sequence
; OTHER INFORMATION: downstream of Zea mays rbcS intron
; NAME/KEY: CDS
; LOCATION: (1222)..(3180)
; OTHER INFORMATION: variant Cry3BB1 coding sequence encoding v11231
; NAME/KEY: terminator
; LOCATION: (3198)..(3431)
; OTHER INFORMATION: T-Ta.hsp17
US-09-377-466B-36

```

```

Alignment Scores:
Pred. No.: 5,9e-13 Length: 3455
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

```

US-10-628-525A-34 (1-58) x US-09-377-466B-36 (1-3455)

```

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThAlaThrArgThrAsnProAlaGln 20
Db 825 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 860

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 861 -----GCCGTGCTCCGTTCTCGGGGCTCAAGTCCACCGCAGCCTCCCGTCGCCCGC 914

QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyValGileArgCys 58
Db 915 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGGGGAAGGATCCGGTGC 965

```

```

RESULT 16
US-10-232-665-36
; Sequence 36, Application US/10232665
; Patent No. 6943281
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/10/232,665
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36
; LENGTH: 3455
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette

```

```

; FEATURE:
; NAME/KEY: promoter
; LOCATION: (14)..(235)
; OTHER INFORMATION: P.CaMV.AS4
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (240)..(304)
; OTHER INFORMATION: L-Ta.hcb1
; FEATURE:
; NAME/KEY: intron
; LOCATION: (318)..(805)
; OTHER INFORMATION: I-Os.Act1
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (825)..(971)
; OTHER INFORMATION: TS-Zm.rbcS amino terminal coding sequence upstream
; OTHER INFORMATION: of Zea mays rbcS intron
; FEATURE:
; NAME/KEY: intron
; LOCATION: (972)..(1134)
; OTHER INFORMATION: I-Zm.rbcS
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1135)..(1221)
; OTHER INFORMATION: TS-Zm.rbcS carboxy terminus coding sequence
; OTHER INFORMATION: downstream of Zea mays rbcS intron
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1222)..(3180)
; OTHER INFORMATION: variant Cry3BB1 coding sequence encoding v11231
; NAME/KEY: terminator
; LOCATION: (3198)..(3431)
; OTHER INFORMATION: T-Ta.hsp17
US-10-232-665-36

Alignment Scores:
Pred. No.: 5,9e-13 Length: 3455
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-10-232-665-36 (1-3455)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThAlaThrArgThrAsnProAlaGln 20
Db 825 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 860

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 861 -----GCCGTGCTCCGTTCTCGGGGCTCAAGTCCACCGCAGCCTCCCGTCGCCCGC 914

QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyValGileArgCys 58
Db 915 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGGGGAAGGATCCGGTGC 965

RESULT 17
US-09-377-466B-13
; Sequence 13, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4149
; TYPE: DNA

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: cassette
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; NAME/KEY: intron
; LOCATION: (669)..(1472)
; OTHER INFORMATION: I-Zm.Hsp70
; NAME/KEY: intron
; LOCATION: (1489)..(1635)
; OTHER INFORMATION: amino terminal TS-Zm.rbcS
; NAME/KEY: intron
; LOCATION: (1636)..(1798)
; OTHER INFORMATION: I-Zm.rbcS
; NAME/KEY: intron
; LOCATION: (1799)..(1885)
; OTHER INFORMATION: carboxy terminus TS-Zm.rbcS
; NAME/KEY: CDS
; LOCATION: (1885)..(3843)
; OTHER INFORMATION: Cry3Bb1 variant v11231
; NAME/KEY: terminator
; LOCATION: (3871)..(4127)
; OTHER INFORMATION: T-AGRTu.nos 3' transcription termination and
; OTHER INFORMATION: polyadenylation sequence
US-09-377-466B-13

```

```

Alignment Scores:
Pred. No.: 7.44e-13 Length: 4149
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

```

US-10-628-525A-34 (1-58) x US-09-377-466B-13 (1-4149)

```

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGln 20
DB 1488 ATGGCGCCACCGTGATGGCTCGTCGCCACC-----1523
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 1524 -----GCCGTCGCTCGTTCTCGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 1577
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyVargileArgCys 58
DB 1578 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 1628

```

```

RESULT 18
US-10-232-665-13
; Sequence 13, Application US/10232665
; Patent No. 6943281
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/10/232,665
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4149
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; NAME/KEY: promoter

```

```

; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: intron
; LOCATION: (669)..(1472)
; OTHER INFORMATION: I-Zm.Hsp70
; NAME/KEY: intron
; LOCATION: (1489)..(1635)
; OTHER INFORMATION: amino terminal TS-Zm.rbcS
; NAME/KEY: intron
; LOCATION: (1636)..(1798)
; OTHER INFORMATION: I-Zm.rbcS
; NAME/KEY: intron
; LOCATION: (1799)..(1885)
; OTHER INFORMATION: carboxy terminus TS-Zm.rbcS
; NAME/KEY: CDS
; LOCATION: (1885)..(3843)
; OTHER INFORMATION: Cry3Bb1 variant v11231
; NAME/KEY: terminator
; LOCATION: (3871)..(4127)
; OTHER INFORMATION: T-AGRTu.nos 3' transcription termination and
; OTHER INFORMATION: polyadenylation sequence
US-10-232-665-13

```

```

Alignment Scores:
Pred. No.: 7.44e-13 Length: 4149
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 3 Gaps: 2

```

US-10-628-525A-34 (1-58) x US-10-232-665-13 (1-4149)

```

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAenProAlaGln 20
DB 1488 ATGGCGCCACCGTGATGGCTCGTCGCCACC-----1523
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 1524 -----GCCGTCGCTCGTTCTCGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 1577
QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyVargileArgCys 58
DB 1578 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 1628

```

```

RESULT 19
US-09-186-002-16
; Sequence 16, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3666)..(5573)
; OTHER INFORMATION: completely synthesized

```

US-09-186-002-16

## Alignment Scores:

Pred. No.: 1.8e-12 Length: 8349  
Score: 196.50 Matches: 46  
Percent Similarity: 79.3% Conservatives: 0  
Best Local Similarity: 79.3% Mismatches: 1  
Query Match: 69.7% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-186-002-16 (1-8349)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

Db 3269 ATGGGCGCCACCGTGATGCTCGTCCGCCACC----- 3304

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40

Db 3305 -----GCCGTGCTCCGTTCTTGGGGCTCAAGTCCACGCCAGCGCTCCCGTCCGCCGC 3358

QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

Db 3359 CGCTCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 3409

## RESULT 20

US-08-622-740-9

; Sequence 9, Application US/08622740

; Patent No. 5950390

## ; GENERAL INFORMATION:

; APPLICANT: Lundquist, Ronald C.

; APPLICANT: Walters, David A.

; APPLICANT: Kirihara, Julie A.

; TITLE OF INVENTION: Methods and Compositions for the

; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants

; TITLE OF INVENTION: and Cells Thereof

; NUMBER OF SEQUENCES: 22

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg, Woessner &amp; Kluth, P.A.

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/622,740

; FILING DATE: 27-MARCH-1996

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Woessner, Warren D.

; REGISTRATION NUMBER: 30,440

; REFERENCE/DOCKET NUMBER: 950.013US4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 195 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-622-740-9

## Alignment Scores:

Pred. No.: 1.68e-13 Length: 195  
Score: 187.50 Matches: 44  
Percent Similarity: 80.0% Conservatives: 0  
Best Local Similarity: 80.0% Mismatches: 1  
Query Match: 66.5% Indels: 11

DB:

2

Gaps:

2

US-10-628-525A-34 (1-58) x US-08-622-740-9 (1-195)

QY 4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAla 23

Db 61 ACCGTGATGATGGCTCGTCCGCCACC-----GCC 90

QY 24 ValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgSerSer 43

Db 91 GTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCCGCCGGTCTCTCC 150

QY 44 ArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

Db 151 AGAAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 192

RESULT 21

US-08-440-689-9

; Sequence 9, Application US/08440689

; Patent No. 6025545

## ; GENERAL INFORMATION:

; APPLICANT: Lundquist, Ronald C.

; APPLICANT: Walters, David A.

; APPLICANT: Kirihara, Julie A.

; TITLE OF INVENTION: Methods and Compositions for the

; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants

; TITLE OF INVENTION: and Cells Thereof

; NUMBER OF SEQUENCES: 22

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg, Woessner &amp; Kluth, P.A.

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/440,689

; FILING DATE: 15-MAY-1995

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Woessner, Warren D.

; REGISTRATION NUMBER: 30,440

; REFERENCE/DOCKET NUMBER: 950.013US2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 195 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-440-689-9

## Alignment Scores:

Pred. No.: 1.68e-13 Length: 195  
Score: 187.50 Matches: 44  
Percent Similarity: 80.0% Conservatives: 0  
Best Local Similarity: 80.0% Mismatches: 0  
Query Match: 66.5% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-08-440-689-9 (1-195)

QY 4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAla 23

Db 61 ACCGTGATGATGGCTCGTCCGCCACC-----GCC 90

QY 24 ValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArgSerSer 43  
Db 91 GTCCGTCCTCGTTCAGGGGCTCAAGTCCACCCAGGCTCCCGCGCCGCGGTCTCTCC 150

QY 44 ArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 151 AGAAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 192

RESULT 22  
US-09-122-399-9  
; Sequence 9, Application US/09122399  
; Patent No. 6329574  
; GENERAL INFORMATION:  
; APPLICANT: Lundquist, Ronald C.  
; APPLICANT: Walters, David A.  
; APPLICANT: Kirihara, Julie A.  
; TITLE OF INVENTION: Methods and Compositions for the  
; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants  
; TITLE OF INVENTION: and Cells Thereof  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.  
; STREET: 3500 IDS Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09122.399  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/112.245  
; FILING DATE: 25-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Woessner, Warren D.  
; REGISTRATION NUMBER: 30,440  
; REFERENCE/DOCKET NUMBER: 950.13US01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-339-0331  
; TELEFAX: 612-339-3061  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 195 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-122-399-9

Alignment Scores:  
Pred. No.: 1.68e-13 Length: 195  
Score: 187.50 Matches: 44  
Percent Similarity: 80.0% Conservative: 0  
Best Local Similarity: 80.0% Mismatches: 0  
Query Match: 66.5% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-122-399-9 (1-195)

QY 4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAla 23  
Db 61 ACCGTGATGATGGCTCGTCGGCCACC-----GCC 90

QY 24 ValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArgSerSer 43  
Db 91 GTCCGTCCTCGTTCAGGGGCTCAAGTCCACCCAGGCTCCCGCGCCGCGGTCTCTCC 150

QY 44 ArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

Db 151 AGAAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 192

RESULT 23  
US-08-440-646A-9  
; Sequence 9, Application US/08440646A  
; Patent No. 6777589  
; GENERAL INFORMATION:  
; APPLICANT: Lundquist, Ronald C.  
; APPLICANT: Walters, David A.  
; APPLICANT: Kirihara, Julie A.  
; TITLE OF INVENTION: Methods and Compositions for the  
; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants  
; TITLE OF INVENTION: and Cells Thereof  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.  
; STREET: 3500 IDS Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440.646A  
; FILING DATE: 15-May-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/112.245  
; FILING DATE: 25-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Woessner, Warren D.  
; REGISTRATION NUMBER: 30,440  
; REFERENCE/DOCKET NUMBER: 950.13US01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-339-0331  
; TELEFAX: 612-339-3061  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 195 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-08-440-646A-9

Alignment Scores:  
Pred. No.: 1.68e-13 Length: 195  
Score: 187.50 Matches: 44  
Percent Similarity: 80.0% Conservative: 0  
Best Local Similarity: 80.0% Mismatches: 0  
Query Match: 66.5% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-08-440-646A-9 (1-195)

QY 4 ThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAla 23  
Db 61 ACCGTGATGATGGCTCGTCGGCCACC-----GCC 90

QY 24 ValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArgSerSer 43  
Db 91 GTCCGTCCTCGTTCAGGGGCTCAAGTCCACCCAGGCTCCCGCGCCGCGGTCTCTCC 150

QY 44 ArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 151 AGAAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 192

RESULT 24

US-08-095-726-12  
; Sequence 12, Application US/08095726  
; Patent No. 5530188  
; GENERAL INFORMATION:  
; APPLICANT: Ausich, Rodney L  
; APPLICANT: Brinkhaus, Friedhelm L  
; APPLICANT: Mukharji, Indrani  
; APPLICANT: Proffitt, John H  
; APPLICANT: Yarger, James G  
; APPLICANT: Yen, Hwei-Che B  
; TITLE OF INVENTION: Beta-Carotene Biosynthesis in  
; TITLE OF INVENTION: Genetically Engineered Hosts  
; NUMBER OF SEQUENCES: 79  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
; STREET: 200 E Randolph St  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60680-0703  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/095,726  
; FILING DATE: 21-JUL-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/785,566  
; FILING DATE: 30-OCT-1991  
; NAME: Galloway, No. 5530188val B  
; ATTORNEY/AGENT INFORMATION:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3128567180  
; TELEFAX: 3128564972  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-095-726-12  
  
Alignment Scores:  
Pred. No.: 2,52e-10 Length: 177  
Score: 159.50 Matches: 32  
Percent Similarity: 79.3% Conservative: 14  
Best Local Similarity: 55.2% Mismatches: 11  
Query Match: 56.6% Indels: 1  
DB: 2 Gaps: 1  
  
US-10-628-525A-34 (1-58) x US-08-095-726-12 (1-177)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 1 ATGGCTTCTCAGTT---CTTTCCTGCGAGTGGCCACCGCAGCAATGTTGCTCAA 57  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 58 GCTAACATGGTGGCGCTTTTCACTGGCCTTAAGTCAGCTGCCTCATTCCTCTGTTCAAGG 117  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 118 AAGCAAAACCTTGGACATCATCTTCATTGCCAACAACGGGAGAGTGCATGC 171  
  
RESULT 25  
US-08-095-043-12  
; Sequence 12, Application US/08096043  
; Patent No. 5530189  
; GENERAL INFORMATION:  
; APPLICANT: Ausich, Rodney L  
; APPLICANT: Brinkhaus, Friedhelm L  
; APPLICANT: Mukharji, Indrani  
; APPLICANT: Proffitt, John H

; APPLICANT: Ausich, Rodney L  
; APPLICANT: Brinkhaus, Friedhelm L  
; APPLICANT: Mukharji, Indrani  
; APPLICANT: Proffitt, John H  
; APPLICANT: Yarger, James G  
; APPLICANT: Yen, Hwei-Che B  
; TITLE OF INVENTION: Lycopene Biosynthesis in  
; TITLE OF INVENTION: Genetically Engineered Hosts  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
; STREET: 200 E Randolph St  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60680-0703  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/096,043  
; FILING DATE: 22-JUL-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/785,568  
; FILING DATE: 30-OCT-1991  
; NAME: Galloway, No. 5530189val B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3128567180  
; TELEFAX: 3128564972  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-096-043-12  
  
Alignment Scores:  
Pred. No.: 2,52e-10 Length: 177  
Score: 159.50 Matches: 32  
Percent Similarity: 79.3% Conservative: 14  
Best Local Similarity: 55.2% Mismatches: 11  
Query Match: 56.6% Indels: 1  
DB: 2 Gaps: 1  
  
US-10-628-525A-34 (1-58) x US-08-096-043-12 (1-177)  
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 1 ATGGCTTCTCAGTT---CTTTCCTGCGAGTGGCCACCGCAGCAATGTTGCTCAA 57  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 58 GCTAACATGGTGGCGCTTTTCACTGGCCTTAAGTCAGCTGCCTCATTCCTCTGTTCAAGG 117  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 118 AAGCAAAACCTTGGACATCATCTTCATTGCCAACAACGGGAGAGTGCATGC 171  
  
RESULT 26  
US-08-093-577-8  
; Sequence 8, Application US/08093577  
; Patent No. 5545816  
; GENERAL INFORMATION:  
; APPLICANT: Ausich, Rodney L  
; APPLICANT: Brinkhaus, Friedhelm L  
; APPLICANT: Mukharji, Indrani  
; APPLICANT: Proffitt, John H



APPLICANT: Yarger, James G  
APPLICANT: Yen, Hwei-Che B  
TITLE OF INVENTION: Phytoene Biosynthesis in  
TITLE OF INVENTION: Genetically Engineered Hosts  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corp., Patents and Licensing Dept  
STREET: 200 E Randolph St  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60680-0703  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/093,577  
FILING DATE: 19-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/785,569  
FILING DATE: 30-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, No. 545816val B  
TELEPHONE: 3128567180  
TELEFAX: 3128564972  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-093-577-8

Alignment Scores:  
Pred. No.: 2,52e-10 Length: 177  
Score: 159.50 Matches: 32  
Percent Similarity: 79.3% Conservative: 14  
Best Local Similarity: 55.2% Mismatches: 11  
Query Match: 56.6% Indels: 1  
Gaps: 2

US-10-628-525A-34 (1-58) x US-08-093-577-8 (1-177)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAnProAlaGln 20  
Db 1 ATGGCTTCCTCAGTT---CTTCTCTGCAGCAGTTGCCACCGCAGCAATGTTGCTCAA 57  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 58 GCTAACATGTGGCGCTTTCATCGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGG 117

QY 41 ArgSerSerArgSerLeuGlyAnValAlaSerAnGlyGlyArgileArgCys 58  
Db 118 AAGCAAAACCTTGACATCATCTTCATTGCCAGCAACGGCGAGAGAGTGCAATGC 171

RESULT 27  
US-08-331-004A-6  
Sequence 6, Application US/08331004A  
Patent No. 5618988  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Randal  
APPLICANT: Eschenfeldt, William H  
APPLICANT: English, Jami  
APPLICANT: Brinkhaus, Friedhelm L  
TITLE OF INVENTION: Enhanced Carotenoid Accumulation  
TITLE OF INVENTION: in Storage Organs of Genetically  
TITLE OF INVENTION: Engineered Plants  
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amoco Corporation, Law Dept  
STREET: 55 Shuman Boulevard, Suite 600  
CITY: Naperville  
STATE: IL  
COUNTRY: USA  
ZIP: 60563-8437  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/331,004A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, No. 5618988val B  
TELEPHONE: 7087172447  
TELEFAX: 7087172430  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-331-004A-6

Alignment Scores:  
Pred. No.: 2,52e-10 Length: 177  
Score: 159.50 Matches: 32  
Percent Similarity: 79.3% Conservative: 14  
Best Local Similarity: 55.2% Mismatches: 11  
Query Match: 56.6% Indels: 1  
Gaps: 2

US-10-628-525A-34 (1-58) x US-08-331-004A-6 (1-177)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAnProAlaGln 20  
Db 1 ATGGCTTCCTCAGTT---CTTCTCTGCAGCAGTTGCCACCGCAGCAATGTTGCTCAA 57  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 58 GCTAACATGTGGCGCTTTCATCGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGG 117

QY 41 ArgSerSerArgSerLeuGlyAnValAlaSerAnGlyGlyArgileArgCys 58  
Db 118 AAGCAAAACCTTGACATCATCTTCATTGCCAGCAACGGCGAGAGAGTGCAATGC 171

RESULT 28  
US-08-096-623A-12  
Sequence 12, Application US/08096623A  
Patent No. 5684238  
GENERAL INFORMATION:  
APPLICANT: Ausich, Rodney L  
APPLICANT: Brinkhaus, Friedhelm L  
APPLICANT: Mukharji, Indrani  
APPLICANT: Proffitt, John H  
APPLICANT: Yarger, James G  
APPLICANT: Yen, Hwei-Che B  
TITLE OF INVENTION: Biosynthesis of Zeaxanthin and  
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Welsh & Katz, Ltd.  
STREET: 120 S. Riverside Plaza, 22nd Floor  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606



; LENGTH: 204  
 ; TYPE: DNA  
 ; ORGANISM: Nicotiana tabacum  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(204)  
 US-09-839-477-3

Alignment Scores:  
 Pred. No.: 3.01e-10 Length: 204  
 Score: 159.50 Matches: 32  
 Percent Similarity: 79.3% Conservative: 14  
 Best Local Similarity: 55.2% Mismatches: 11  
 Query Match: 56.6% Indels: 1  
 DB: 3 Gaps: 1

US-10-628-525A-34 (1-58) x US-09-839-477-3 (1-204)

QY	1	MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln	20
Db	1	ATGGCTTCCTCAGTT--CTTCTCTGCAGCAGTTGCCACCCGACGAATGTTGCTCAA	57
QY	21	AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg	40
Db	58	GCTAACATGGTTCACCTTTCACCTGCGCTTAAGTCAGCTGCCTCATTCCTGTTTCAAGG	117
QY	41	ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys	58
Db	118	AAGCAAAACCTTGACATCACTTCCTATTCAGCAGCAACGGGGAGAGTGCAATGC	171

Search completed: March 31, 2006, 23:22:58  
 Job time : 83.568 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 00:58:46 ; Search time 274.022 Seconds  
(without alignments)  
1750.313 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MATVWMASSATATRTNPAQ.....ARRSSRLGNVASNGGRIRC 58

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-Q=/abs/ABSSWEB spool/US10628525/runat\_31032006\_095135\_17190/app\_query.fasta\_1  
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-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
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-THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext  
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-USER=US10628525 @CGN 1.1 2715 @runat\_31032006\_095135\_17190 -NCPU=6 -ICPU=3  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main.\*

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- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	203.5	72.2	183	6	US-10-140-410-1			Sequence 1, Appli
2	203.5	72.2	228	3	US-09-987-899-69			Sequence 69, Appl
3	203.5	72.2	229	3	US-09-987-899-84			Sequence 84, Appl
4	203.5	72.2	230	3	US-09-987-899-264			Sequence 264, App
5	203.5	72.2	235	3	US-09-987-899-79			Sequence 79, Appl
6	203.5	72.2	236	3	US-09-987-899-70			Sequence 70, Appl
7	203.5	72.2	238	3	US-09-987-899-66			Sequence 66, Appl

249	3	US-09-987-899-71	Sequence 71, Appl
254	3	US-09-987-899-53	Sequence 53, Appl
265	3	US-09-987-899-40	Sequence 40, Appl
272	3	US-09-987-899-45	Sequence 45, Appl
276	3	US-09-987-899-26	Sequence 26, Appl
276	3	US-09-987-899-51	Sequence 51, Appl
284	3	US-09-987-899-32	Sequence 32, Appl
286	3	US-09-987-899-37	Sequence 37, Appl
291	3	US-09-987-899-47	Sequence 47, Appl
297	3	US-09-987-899-14	Sequence 14, Appl
298	3	US-09-987-899-21	Sequence 21, Appl
305	3	US-09-987-899-16	Sequence 16, Appl
307	3	US-09-987-899-29	Sequence 29, Appl
309	3	US-09-987-899-15	Sequence 15, Appl
311	3	US-09-987-899-30	Sequence 30, Appl
312	3	US-09-987-899-68	Sequence 68, Appl
315	3	US-09-987-899-11	Sequence 11, Appl
317	3	US-09-987-899-10	Sequence 10, Appl
319	3	US-09-987-899-4	Sequence 4, Appli
344	3	US-09-987-899-231	Sequence 231, App
409	3	US-09-987-899-215	Sequence 215, App
415	3	US-09-987-899-244	Sequence 244, App
438	3	US-09-987-899-210	Sequence 210, App
441	3	US-09-987-899-229	Sequence 229, App
443	3	US-09-987-899-225	Sequence 225, App
740	8	US-10-425-115-83321	Sequence 83321, A
1085	8	US-10-425-115-83320	Sequence 83320, A
1945	8	US-10-425-115-83331	Sequence 83331, A
5281	3	US-09-921-263-1	Sequence 1, Appli
5909	3	US-09-921-263-2	Sequence 2, Appli
197	3	US-09-987-899-270	Sequence 270, App
198	3	US-09-987-899-99	Sequence 99, Appl
258	3	US-09-987-899-48	Sequence 48, Appl
268	3	US-09-987-899-54	Sequence 54, Appl
269	3	US-09-987-899-62	Sequence 62, Appl
276	3	US-09-987-899-44	Sequence 44, Appl
278	3	US-09-987-899-22	Sequence 22, Appl
283	3	US-09-987-899-31	Sequence 31, Appl
286	3	US-09-987-899-41	Sequence 41, Appl
290	3	US-09-987-899-35	Sequence 35, Appl
291	3	US-09-987-899-25	Sequence 25, Appl
291	3	US-09-987-899-34	Sequence 34, Appl
291	3	US-09-987-899-49	Sequence 49, Appl
296	3	US-09-987-899-38	Sequence 38, Appl
310	3	US-09-987-899-23	Sequence 23, Appl
310	3	US-09-987-899-27	Sequence 27, Appl
316	3	US-09-987-899-9	Sequence 9, Appli
381	3	US-09-987-899-220	Sequence 220, App
411	3	US-09-987-899-221	Sequence 221, App
414	3	US-09-987-899-213	Sequence 213, App
433	3	US-09-987-899-211	Sequence 211, App
434	3	US-09-987-899-223	Sequence 223, App
434	3	US-09-987-899-224	Sequence 224, App
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226	3	US-09-987-899-97	Sequence 97, Appl
428	3	US-09-987-899-217	Sequence 217, App
453	3	US-09-987-899-230	Sequence 230, App
199	3	US-09-987-899-105	Sequence 105, App
312	3	US-09-987-899-42	Sequence 42, Appl
382	3	US-09-987-899-235	Sequence 235, App
285	3	US-09-987-899-75	Sequence 75, Appl
415	5	US-10-005-530-49	Sequence 49, Appl
415	5	US-10-213-791-13	Sequence 13, Appl
415	6	US-10-198-478-3	Sequence 3, Appli
416	5	US-10-232-665-25	Sequence 25, Appl
416	5	US-10-232-665-30	Sequence 30, Appl
3450	5	US-10-232-665-17	Sequence 17, Appl
3455	5	US-10-232-665-36	Sequence 36, Appl
4149	5	US-10-232-665-13	Sequence 13, Appl
8349	6	US-10-198-478-16	Sequence 16, Appl
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232	3	US-09-987-899-82	Sequence 82, Appl

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128 195.5 69.3 2390 8 US-10-425-115-13220  
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137 191.5 67.9 418 3 US-09-987-899-249  
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140 189.5 67.2 316 3 US-09-987-899-108  
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142 187.5 66.5 195 9 US-10-919-228-9  
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145 185.5 65.8 200 3 US-09-987-899-107  
146 184.5 64.7 384 3 US-09-987-899-265  
147 179.5 63.7 259 3 US-09-987-899-52  
148 179.5 63.7 367 3 US-09-987-899-257  
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150 178.5 63.3 314 3 US-09-987-899-73

ALIGNMENTS

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Sequence 241, Appl  
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Sequence 13220, A  
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Sequence 142195,  
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; Sequence 1, Application US/10140410  
; Publication No. US20030213013A1  
; GENERAL INFORMATION:  
; APPLICANT: Caimi, Perry G.  
; APPLICANT: Lightner, Jonathan E.  
; TITLE OF INVENTION: Fructose Polymer Synthesis in Monocot Plastids  
; FILE REFERENCE: BB1347 US NA  
; CURRENT APPLICATION NUMBER: US/10/140,410  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: PCT/US00/31788  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: 60/166,268  
; PRIOR FILING DATE: 1999-11-18  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 1  
; LENGTH: 183  
; TYPE: DNA  
; ORGANISM: Zea mays  
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Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 6 Gaps: 2  
  
US-10-628-525A-34 (1-58) x US-10-140-410-1 (1-183)  
Qy 1 MetalProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db 1 ATGGCGCCACCGTGCATGATGCGCTCGTCGGCCACC----- 36  
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerIeuProValAlaArg 40  
Db 37 -----GCCGTGCGCTCCGTTCCAGGGGCTTAAGTCCACGCCAGCGCTCCCGTCGCCGCGC 90  
Qy 41 ArgSerSerArgSerLeuGlyValAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
Db 91 CCTCTCTTAGAAGCTCGCAACGTC---AGCAACGGCGGAAGAATCCGGTGC 141  
  
RESULT 2  
US-09-987-899-69  
; Sequence 69, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 69  
; LENGTH: 228  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700042688H1  
US-09-987-899-69

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Alignment Scores:
Pred. No.: 1.41e-18 Length: 228
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-69 (1-228)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCTCGTGGCCACC-----72

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 126

Qy 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 3
US-09-987-899-84
; Sequence 84, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 84
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700198026H1
US-09-987-899-84

Alignment Scores:
Pred. No.: 1.42e-18 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-84 (1-229)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGATGCTCGTGGCCACC-----87

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 141

Qy 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 142 CGCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 4
US-09-987-899-264
; Sequence 264, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 79
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700046244H1
US-09-987-899-264

Alignment Scores:
Pred. No.: 1.42e-18 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-264 (1-230)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCTCGTGGCCACC-----72

Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 126

Qy 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 5
US-09-987-899-79
; Sequence 79, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 79
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700046244H1
US-09-987-899-79
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Alignment Scores:
Pred. No.: 1,46e-18 Length: 235
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-79 (1-235)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 47 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 82
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 93 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 136
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 137 CGCTCCTCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 187

RESULT 6
US-09-987-899-70
; Sequence 70, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 70
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700044947H1
US-09-987-899-70
Alignment Scores:
Pred. No.: 1,47e-18 Length: 236
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-70 (1-236)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 13 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 48
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 49 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 102
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 103 CGCTCCTCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 153

RESULT 7
US-09-987-899-66
; Sequence 66, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 66
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700044245H1
US-09-987-899-66
Alignment Scores:
Pred. No.: 1,48e-18 Length: 238
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-66 (1-238)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 14 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 49
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 50 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 103
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 104 CGCTCCTCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 154

RESULT 8
US-09-987-899-71
; Sequence 71, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 71
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700045847H1
```



## US-09-987-899-71

## Alignment Scores:

Pred. No.: 1.56e-18 Length: 249  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-71 (1-249)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 50 ATGGGCGCCACCGTGATGCGCTCGTGGCCACC----- 85  
 QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 86 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 139  
 QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 |||||  
 Db 140 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

## RESULT 9

US-09-987-899-53

; Sequence 53, Application US/09987899

; Publication No. US20040116682A1

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jingdong

; APPLICANT: Miller, Phillip W.

; APPLICANT: O Connell, Keith M.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

; FILE REFERENCE: 16517.258

; CURRENT APPLICATION NUMBER: US/09/987,899

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 09/262,979

; PRIOR FILING DATE: 1999-03-04

; PRIOR APPLICATION NUMBER: US 60/076,712

; PRIOR FILING DATE: 1998-03-06

; NUMBER OF SEQ ID NOS: 7341

; SEQ ID NO 53

; LENGTH: 264

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700044292H1

US-09-987-899-53

## Alignment Scores:

Pred. No.: 1.68e-18 Length: 264  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-53 (1-264)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 46 ATGGGCGCCACCGTGATGCGCTCGTGGCCACC----- 81  
 QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 82 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 135  
 QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 |||||  
 Db 136 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186

## RESULT 10

US-09-987-899-40

; Sequence 40, Application US/09987899

; Publication No. US20040116682A1

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jingdong

; APPLICANT: Miller, Phillip W.

; APPLICANT: O Connell, Keith M.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

; FILE REFERENCE: 16517.258

; CURRENT APPLICATION NUMBER: US/09/987,899

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 09/262,979

; PRIOR FILING DATE: 1999-03-04

; PRIOR APPLICATION NUMBER: US 60/076,712

; PRIOR FILING DATE: 1998-03-06

; NUMBER OF SEQ ID NOS: 7341

; SEQ ID NO 40

; LENGTH: 265

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700025653H1

US-09-987-899-40

## Alignment Scores:

Pred. No.: 1.69e-18 Length: 265  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-40 (1-265)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 |||||  
 Db 21 ATGGGCGCCACCGTGATGCGCTCGTGGCCACC----- 56  
 QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 |||||  
 Db 57 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 110  
 QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 |||||  
 Db 111 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 161

## RESULT 11

US-09-987-899-45

; Sequence 45, Application US/09987899

; Publication No. US20040116682A1

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jingdong

; APPLICANT: Miller, Phillip W.

; APPLICANT: O Connell, Keith M.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

; FILE REFERENCE: 16517.258

; CURRENT APPLICATION NUMBER: US/09/987,899

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 09/262,979

; PRIOR FILING DATE: 1999-03-04

; PRIOR APPLICATION NUMBER: US 60/076,712

; PRIOR FILING DATE: 1998-03-06

; NUMBER OF SEQ ID NOS: 7341

; SEQ ID NO 45

; LENGTH: 272

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700042186H1  
US-09-987-899-45

Alignment Scores:  
Pred. No.: 1.74e-18 Length: 272  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-45 (1-272)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
Db 43 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 78  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
|||||  
Db 79 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 132  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
|||||  
Db 133 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 183

RESULT 12

US-09-987-899-26

; Sequence 26, Application US/09987899  
; Publication No. US20040116682A1

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jingdong

; APPLICANT: Miller, Phillip W.

; APPLICANT: O Connell, Keith M.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

; FILE OF INVENTION: With the Carbon Assimilation Pathway

; FILE REFERENCE: 16517.258

; CURRENT APPLICATION NUMBER: US/09/987,899

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 09/262,979

; PRIOR FILING DATE: 1999-03-04

; PRIOR APPLICATION NUMBER: US 60/076,712

; NUMBER OF SEQ ID NOS: 7341

; SEQ ID NO 26

; LENGTH: 276

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700045728H1

US-09-987-899-26

Alignment Scores:

Pred. No.: 1.77e-18 Length: 276  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-26 (1-276)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
Db 41 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 76  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
|||||  
Db 77 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 130  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
|||||  
Db 131 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 181

RESULT 13

US-09-987-899-51

; Sequence 51, Application US/09987899

; Publication No. US20040116682A1

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jingdong

; APPLICANT: Miller, Phillip W.

; APPLICANT: O Connell, Keith M.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

; FILE OF INVENTION: With the Carbon Assimilation Pathway

; FILE REFERENCE: 16517.258

; CURRENT APPLICATION NUMBER: US/09/987,899

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 09/262,979

; PRIOR FILING DATE: 1999-03-04

; PRIOR APPLICATION NUMBER: US 60/076,712

; PRIOR FILING DATE: 1998-03-06

; NUMBER OF SEQ ID NOS: 7341

; SEQ ID NO 51

; LENGTH: 276

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700433801H1

US-09-987-899-51

Alignment Scores:

Pred. No.: 1.77e-18 Length: 276  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-51 (1-276)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
Db 46 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 81  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
|||||  
Db 82 -----GCCGTGCGTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 135  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
|||||  
Db 136 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 186

RESULT 14

US-09-987-899-32

; Sequence 32, Application US/09987899

; Publication No. US20040116682A1

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jingdong

; APPLICANT: Miller, Phillip W.

; APPLICANT: O Connell, Keith M.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated

; FILE OF INVENTION: With the Carbon Assimilation Pathway

; FILE REFERENCE: 16517.258

; CURRENT APPLICATION NUMBER: US/09/987,899

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: US 09/262,979

; PRIOR FILING DATE: 1999-03-04

; PRIOR APPLICATION NUMBER: US 60/076,712

; PRIOR FILING DATE: 1998-03-06

; NUMBER OF SEQ ID NOS: 7341

; SEQ ID NO 32

; LENGTH: 284

; TYPE: DNA

; ORGANISM: Zea mays

```
;
; FEATURE:
; OTHER INFORMATION: Clone ID: 700100637H1
US-09-987-899-32

Alignment Scores:
Pred. No.: 1.83e-18 Length: 284
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-32 (1-284)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 50 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC-----85
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 86 -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 139
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 140 CGCTCTCCAGAACCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

RESULT 15
US-09-987-899-37
; Sequence 37, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 37
; LENGTH: 286
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700212658H1
US-09-987-899-37

Alignment Scores:
Pred. No.: 1.85e-18 Length: 286
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-37 (1-286)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC-----83
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 137
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 140 CGCTCTCCAGAACCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

;
; FEATURE:
; OTHER INFORMATION: Clone ID: 700100637H1
US-09-987-899-32

Alignment Scores:
Pred. No.: 1.83e-18 Length: 284
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-32 (1-284)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 50 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC-----85
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 86 -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 139
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 140 CGCTCTCCAGAACCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

RESULT 16
US-09-987-899-47
; Sequence 47, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 47
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700097886H1
US-09-987-899-47

Alignment Scores:
Pred. No.: 1.88e-18 Length: 291
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-47 (1-291)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 57 ATGGCGCCACCGTGATGATGGCTCGTCGCCACC-----92
QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 93 -----GCCGTGCTCGTTCAGGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 146
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 147 CGCTCTCCAGAACCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 197

RESULT 17
US-09-987-899-14
; Sequence 14, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 14
; LENGTH: 297
; TYPE: DNA
```

```
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700101196H1
US-09-987-899-14

Alignment Scores:
Pred. No.: 1.93e-18 Length: 297
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-14 (1-297)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 12 ATGGGCGCCACCGTGTATGCGCTCGTCGGCCACC----- 47
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 48 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGCTCGCCGC 101
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 102 CGCTCTCCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 152

RESULT 18
US-09-987-899-21
; Sequence 21, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 21
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700099783H1
US-09-987-899-21

Alignment Scores:
Pred. No.: 1.94e-18 Length: 298
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-21 (1-298)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGGCGCCACCGTGTATGCGCTCGTCGGCCACC----- 83
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGCTCGCCGC 137
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58

; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700101196H1
US-09-987-899-14

Alignment Scores:
Pred. No.: 1.93e-18 Length: 297
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-14 (1-297)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 12 ATGGGCGCCACCGTGTATGCGCTCGTCGGCCACC----- 47
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 48 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGCTCGCCGC 101
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 102 CGCTCTCCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 152

RESULT 19
US-09-987-899-16
; Sequence 16, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 16
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700100270H1
US-09-987-899-16

Alignment Scores:
Pred. No.: 1.99e-18 Length: 305
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-16 (1-305)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 42 ATGGGCGCCACCGTGTATGCGCTCGTCGGCCACC----- 77
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 78 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGCTCGCCGC 131
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 132 CGCTCTCCAGAAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 182

RESULT 20
US-09-987-899-29
; Sequence 29, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 29
; LENGTH: 307
```

```
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700211770H1
US-09-987-899-29

Alignment Scores:
Pred. No.: 2,01e-18 Length: 307
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-29 (1-307)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 50 ATGGGCGCCACCGTGATGGCTCGTCGGCCACC-----85
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLyseSerThrAlaSerLeuProValAlaArg 40
Db 86 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 139
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 140 CGCTCTCTCCAGAACGCTCGGCAACGTC---AGCAACGCGGGAAGGATCCGGTGC 190

RESULT 21
US-09-987-899-15
; Sequence 15, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 15
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700097309H1
US-09-987-899-15

Alignment Scores:
Pred. No.: 2,02e-18 Length: 309
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-15 (1-309)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGGCGCCACCGTGATGGCTCGTCGGCCACC-----83
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLyseSerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 137
```

```
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 138 CGCTCTCTCCAGAACGCTCGGCAACGTC---AGCAACGCGGGAAGGATCCGGTGC 198

RESULT 22
US-09-987-899-30
; Sequence 30, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 30
; LENGTH: 311
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700095614H1
US-09-987-899-30

Alignment Scores:
Pred. No.: 2,04e-18 Length: 311
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-30 (1-311)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 42 ATGGGCGCCACCGTGATGGCTCGTCGGCCACC-----77
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLyseSerThrAlaSerLeuProValAlaArg 40
Db 78 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 131
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 132 CGCTCTCTCCAGAACGCTCGGCAACGTC---AGCAACGCGGGAAGGATCCGGTGC 182

RESULT 23
US-09-987-899-68
; Sequence 68, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 68
```

```
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(312)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 700215027H1
US-09-987-899-68

Alignment Scores:
Pred. No.: 2,05e-18 Length: 312
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-68 (1-312)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 43 ATGGCGCCACCGTGATGAGCTCGTCGGCCACC----- 78
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 79 -----GCCGTCCGTCCTCCAGGGGCTCAAGTCCACGCCGAGCTCCCGTCGCCCGC 132
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 133 CGCTCTCTCCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 183

RESULT 24
US-09-987-899-11
; Sequence 11, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 11
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700098235H1
US-09-987-899-11

Alignment Scores:
Pred. No.: 2,07e-18 Length: 315
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-11 (1-315)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGCGCCACCGTGATGAGCTCGTCGGCCACC----- 83
```

```
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTCCGTCCTCCAGGGGCTCAAGTCCACGCCGAGGCTCCCGTCGCCCGC 137
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 138 CGCTCTCTCCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 188

RESULT 25
US-09-987-899-10
; Sequence 10, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 10
; LENGTH: 317
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700099925H1
US-09-987-899-10

Alignment Scores:
Pred. No.: 2,09e-18 Length: 317
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-10 (1-317)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 50 ATGGCGCCACCGTGATGAGCTCGTCGGCCACC----- 85
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 86 -----GCCGTCCGTCCTCCAGGGGCTCAAGTCCACGCCGAGGCTCCCGTCGCCCGC 139
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 140 CGCTCTCTCCAGAAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 190

RESULT 26
US-09-987-899-4
; Sequence 4, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
```

```
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 4
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 70098783H1
US-09-987-899-4

Alignment Scores:
Pred. No.: 2.1e-18 Length: 319
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-4 (1-319)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 41 ATGGCGCCACCGTGATGCTCGTGGCCACC----- 76

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 77 -----GCCGTGCTCGGTTCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 130

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 131 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 181

RESULT 27
US-09-987-899-231
; Sequence 231, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 231
; LENGTH: 344
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3062-047-Q1-K1-B2
US-09-987-899-231

Alignment Scores:
Pred. No.: 2.3e-18 Length: 344
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-231 (1-344)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 46 ATGGCGCCACCGTGATGCTCGTGGCCACC----- 81
```

```
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 82 -----GCCGTGCTCGGTTCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 135

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 136 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186

RESULT 28
US-09-987-899-215
; Sequence 215, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 215
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-002-Q1-K1-B12
US-09-987-899-215

Alignment Scores:
Pred. No.: 2.82e-18 Length: 409
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-215 (1-409)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 50 ATGGCGCCACCGTGATGCTCGTGGCCACC----- 85

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 86 -----GCCGTGCTCGGTTCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCCGC 139

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 140 CGCTCTCCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

RESULT 29
US-09-987-899-244
; Sequence 244, Application US/09987899
; Publication No. US20040116682A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
```

;  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 244  
; LENGTH: 415  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB84-027-Q1-E1-H12  
US-09-987-899-244

Alignment Scores:  
Pred. No.: 2,87e-18 Length: 415  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-244 (1-415)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAsnProAlaGln 20  
DB 99 ATGGGCGCCACCGTGATGCTCGTGGCCACC----- 134  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
DB 135 -----GCCGTGCTCCGTTCCAGGGGCTCAAAGTCCACCGCAGCTCCCGTGGCCGC 188  
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
DB 189 CGCTCTCTCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 239

## RESULT 30

US-09-987-899-210  
; Sequence 210, Application US/09987899  
; Publication No. US20040116682A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 210  
; LENGTH: 438  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3078-018-Q1-K1-H8  
US-09-987-899-210

Alignment Scores:  
Pred. No.: 3,06e-18 Length: 438  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 3 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-210 (1-438)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThrAsnProAlaGln 20  
|||||

DB 41 ATGGGCGCCACCGTGATGCTCGTGGCCACC----- 76  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40  
|||||  
DB 77 -----GCCGTGCTCCGTTCCAGGGGCTCAAAGTCCACCGCAGCTCCCGTGGCCGC 130  
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
|||||  
DB 131 CGCTCTCTCAGAGCCTCGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 181

Search completed: April 2, 2006, 02:11:05  
Job time : 276.022 secs



GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 01:09:48 ; Search time 181.109 Seconds  
(without alignments)  
1278.753 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MATVMMASATATRTNPAQ.....ARRSRSLGNVAGGRIRC 58

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abs/ABSWEB\_spool/US10628525/runat\_31032006\_095139\_17270/app\_query.fasta.1  
-DB=Published Applications NA New -QWFI=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62  
-TRANS=human40 cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abes05h  
-USER=US10628525 @CGN 1.1 2249 @runat\_31032006\_095139\_17270 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

1: /SID55/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
2: /SID55/ptodata/2/pubpna/US06\_NEW\_PUB.seq:  
3: /SID55/ptodata/2/pubpna/US07\_NEW\_PUB.seq:  
4: /SID55/ptodata/2/pubpna/PTC\_NEW\_PUB.seq:  
5: /SID55/ptodata/2/pubpna/US09\_NEW\_PUB.seq:  
6: /SID55/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
7: /SID55/ptodata/2/pubpna/US11\_NEW\_PUB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	196.5	69.7	416	14	US-11-192-801-30

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Sequence 36, Appl  
Sequence 13, Appl  
Sequence 19, Appl  
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Sequence 29, Appl  
Sequence 5, Appl  
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Sequence 22, Appl  
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Sequence 2328, A  
Sequence 539532,  
Sequence 353, App  
Sequence 1, Appl  
Sequence 5026, Ap  
Sequence 811437,  
Sequence 3445, Ap  
Sequence 18507, A  
Sequence 121813,  
Sequence 220043,  
Sequence 833452,  
Sequence 12875, A  
Sequence 23191, A  
Sequence 1418, App  
Sequence 542, App  
Sequence 91751, A  
Sequence 705160,  
Sequence 197, App  
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Sequence 84, Appl  
Sequence 1093, Ap  
Sequence 173, App  
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Sequence 42914, A

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ALIGNMENTS

RESULT 1
US-11-192-801-25
; Sequence 25, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/10/232.665
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377.466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 25
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; OTHER INFORMATION: occurring nucleotide sequence encoding Zea mays
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; OTHER INFORMATION: targeting peptide
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US-11-192-801-25
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Score: 196.50 Matches: 46
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Query Match: 69.7% Indels: 11
DB: 14 Gaps: 2

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; Sequence 30, Application US/11192801
; Publication No. US20050273882A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
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; CURRENT APPLICATION NUMBER: US/11/192,801  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: US/10/232,665  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
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US-11-192-801-30

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Percent Similarity: 79.3% Conservative: 0  
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DB: 14 Gaps: 2

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; Sequence 17, Application US/11/192801  
; Publication No. US20050273882A1  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/11/192,801  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: US/10/232,665  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
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US-11-192-801-17

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DB: 14 Gaps: 2

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Db 915 CGCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 965

## RESULT 4

US-11-192-801-36  
; Sequence 36, Application US/11/192801  
; Publication No. US20050273882A1  
; GENERAL INFORMATION:  
; APPLICANT: Romano, Charles P.  
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants  
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn  
; CURRENT APPLICATION NUMBER: US/11/192,801  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: US/10/232,665  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US/09/377,466  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 43  
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; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: expression  
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; OTHER INFORMATION: P-CaMV.AS4  
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/ FEATURE:
/ NAME/KEY: transit_peptide
/ LOCATION: (1135)..(1221)
/ OTHER INFORMATION: TS-Zm.rbcs carboxy terminus coding sequence
/ OTHER INFORMATION: downstream of Zea mays rbcs intron
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1222)..(3180)
/ OTHER INFORMATION: variant Cry3BB1 coding sequence encoding v11231
/ FEATURE:
/ NAME/KEY: terminator
/ LOCATION: (3198)..(3431)
/ OTHER INFORMATION: T-Ta.hsp17
US-11-192-801-36

Alignment Scores:
Pred. No.: 7.34e-13 Length: 3455
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 14 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-192-801-36 (1-3455)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThraAsnProAlaGln 20
Db 825 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 860

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 861 -----GCCGTCGCTCCGTTCTTGGGGCTCAAGTCCACCGCAGCCTCCCGTCGCCGC 914

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 915 CGCTCTCCAGAGGCTCGGCACGTC---AGCAACGGCGGAGGATCGGTGC 965

RESULT 5
US-11-192-801-13
/ Sequence 13, Application US/11192801
/ Publication No. US20050273882A1
/ GENERAL INFORMATION:
/ APPLICANT: Romano, Charles P.
/ TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
/ FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
/ CURRENT APPLICATION NUMBER: US/11/192,801
/ CURRENT FILING DATE: 2005-07-29
/ PRIOR APPLICATION NUMBER: US/10/232,665
/ PRIOR FILING DATE: 2002-08-29
/ PRIOR APPLICATION NUMBER: US/09/377,466
/ PRIOR FILING DATE: 1999-08-19
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 13
/ LENGTH: 4149
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: expression
/ OTHER INFORMATION: cassette
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (25)..(640)
/ OTHER INFORMATION: P-CaMv.35S
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (669)..(1472)
/ OTHER INFORMATION: I-Zm.Hsp70
/ FEATURE:
/ NAME/KEY: transit_peptide
/ LOCATION: (1489)..(1635)
/ OTHER INFORMATION: amino terminal TS-Zm.rbcs
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (1636)..(1798)
/ OTHER INFORMATION: I-Zm.rbcs
/ FEATURE:
/ NAME/KEY: transit_peptide
/ LOCATION: (1799)..(1885)
/ OTHER INFORMATION: carboxy terminus TS-Zm.rbcs
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1885)..(3843)
/ OTHER INFORMATION: Cry3Bb1 variant v11231
/ FEATURE:
/ NAME/KEY: terminator
/ LOCATION: (3871)..(4127)
/ OTHER INFORMATION: T-AGRTcu.nos 3' transcription termination and
/ OTHER INFORMATION: polyadenylation sequence
US-11-192-801-13

Alignment Scores:
Pred. No.: 8.78e-13 Length: 4149
Score: 196.50 Matches: 46
Percent Similarity: 79.3% Conservative: 0
Best Local Similarity: 79.3% Mismatches: 1
Query Match: 69.7% Indels: 11
DB: 14 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-192-801-13 (1-4149)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThraAsnProAlaGln 20
Db 1488 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 1523

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 1524 -----GCCGTCGCTCCGTTCTTGGGGCTCAAGTCCACCGCAGCCTCCCGTCGCCGC 1577

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgIleArgCys 58
Db 1578 CGCTCTCCAGAGGCTCGGCACGTC---AGCAACGGCGGAGGATCGGTGC 1628

RESULT 6
US-10-840-688-19
/ Sequence 19, Application US/10840688
/ Publication No. US2005028968A1
/ GENERAL INFORMATION:
/ APPLICANT: Weaver, Lisa M
/ APPLICANT: Mitsky, Timothy A
/ APPLICANT: Rapp, William D
/ APPLICANT: Gruys, Kenneth J
/ APPLICANT: Liang, Jihong
/ TITLE OF INVENTION: Plants with Increased Levels of One or More Amino Acids
/ FILE REFERENCE: REN-00-095
/ CURRENT APPLICATION NUMBER: US/10/840,688
/ CURRENT FILING DATE: 2004-05-06
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 19
```

```
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-840-688-19

Alignment Scores:
Pred. No.: 7.22e-07 Length: 264
Score: 135.50 Matches: 26
Percent Similarity: 71.2% Conservative: 11
Best Local Similarity: 50.0% Mismatches: 14
Query Match: 48.0% Indels: 1
DB: 8 Gaps: 1

US-10-628-525A-34 (1-58) x US-10-840-688-19 (1-264)
QY 7 MetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAlaValAlaPro 26
Db 13 ATGCTCTCTTCGCTACTATGTT---GCCTCTCGGCTCAGGCCACTATGTCGCTCCT 69
QY 27 PheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgSerSerArgSerLeu 46
Db 70 TTCACGGACTTAAGTCTCTCGCTTCCTCCAGCCACCAGGCTTACACAGCATT 129
QY 47 GlyAsnValAlaSerAenGlyGlyArgIleArgCys 58
Db 130 ACTTCATCATCAAGCAACGGCGGAAGATTAACTGC 165

RESULT 7
US-11-096-568A-21808
; Sequence 21808, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 5471
; SEQ ID NO 21808
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1193)
; OTHER INFORMATION: Ceres Seq. ID no. 12406389
US-11-096-568A-21808

Alignment Scores:
Pred. No.: 66.4 Length: 1193
Score: 72.50 Matches: 20
Percent Similarity: 64.6% Conservative: 11
Best Local Similarity: 41.7% Mismatches: 14
Query Match: 25.7% Indels: 3
DB: 11 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-096-568A-21808 (1-1193)
QY 9 SerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSerAlaValAlaPropheGln 28
Db 214 ACCGGGCATCGGCCACGGCTCGCCCGCCCTGCGCCGACGACGCGCTCACCGGTGTC 273
QY 29 GlyLeuLysSerThrAlaSerLeu-----ProValAlaArgSerSerArgSerLeu 46
Db 274 TCACCGCGGGAGCGGAGCGGGAGCGCGCGCGCTCTCTCGCGCGG--- 330
QY 47 GlyAsnValAlaSerAenGlyGly 54
Db 331 GGCTCGCAGTCGTCTTCGCGAGGC 354

RESULT 8
US-11-087-100-29
```

```
; Sequence 29, Application US/11087100
; Publication No. US20050266440A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Platt, James
; APPLICANT: Kuner, Jerry
```

```
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
; FILE OF INVENTION: System and Uses Thereof
```

```
; FILE REFERENCE: 2997-29
```

```
; CURRENT APPLICATION NUMBER: US/11/087,100
```

```
; CURRENT FILING DATE: 2005-03-21
```

```
; PRIOR APPLICATION NUMBER: 09/231,899
```

```
; PRIOR FILING DATE: 1999-01-14
```

```
; PRIOR APPLICATION NUMBER: 60/284,066
```

```
; PRIOR FILING DATE: 2001-04-16
```

```
; PRIOR APPLICATION NUMBER: 60/298,796
```

```
; PRIOR FILING DATE: 2001-06-15
```

```
; PRIOR APPLICATION NUMBER: 60/323,269
```

```
; PRIOR FILING DATE: 2001-09-18
```

```
; NUMBER OF SEQ ID NOS: 37
```

```
; SOFTWARE: PatentIn version 3.3
```

```
; SEQ ID NO 29
```

```
; LENGTH: 1500
```

```
; TYPE: DNA
```

```
; ORGANISM: Schizochytrium sp.
```

```
; FEATURE:
```

```
; NAME/KEY: CDS
```

```
; LOCATION: (1)..(1500)
```

```
; US-11-087-100-29
```

```
Alignment Scores:
```

```
Pred. No.: 162 Length: 1500
```

```
Score: 70.00 Matches: 19
```

```
Percent Similarity: 56.9% Conservative: 14
```

```
Best Local Similarity: 32.8% Mismatches: 23
```

```
Query Match: 24.8% Indels: 2
```

```
DB: 14 Gaps: 1
```

```
US-10-628-525A-34 (1-58) x US-11-087-100-29 (1-1500)
```

```
QY 2 AlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAla 21
```

```
Db 1022 TCGCCAAACCCCGCCAGCGCGCCAGCTCAACCGCGCCAGCCAGCCAGGCGCAGTACCTCG 1081
```

```
QY 22 -----SerAlaValAlaPropheGlnGlyLeuLysSerThrAlaSerLeuProValAla 39
```

```
Db 1082 ACGCGCTCGACATTGTCTCCGCGCGGCAAGAGAGCTCGGCTACGCCCGCGGTCCA 1141
```

```
QY 40 ArgArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArg 57
```

```
Db 1142 AGACGGTCAACCGCAACGACTGGTCTTCTTCGTCGCCACTTTGTTGACTCGG 1195
```

```
RESULT 9
```

```
US-11-087-084-29
```

```
; Sequence 29, Application US/11087084
```

```
; Publication No. US20050273883A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Metz, James
```

```
; APPLICANT: Barclay, William
```

```
; APPLICANT: Platt, James
```

```
; APPLICANT: Kuner, Jerry
```

```
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
```

```
; FILE OF INVENTION: System and Uses Thereof
```

```
; FILE REFERENCE: 2997-29
```

```
; CURRENT APPLICATION NUMBER: US/11/087,084
```

```
; CURRENT FILING DATE: 2005-03-21
```

```
; PRIOR APPLICATION NUMBER: 09/231,899
```

```
; PRIOR FILING DATE: 1999-01-14
```

```
; PRIOR APPLICATION NUMBER: 60/284,066
```

```
; PRIOR FILING DATE: 2001-04-16
```

```
; PRIOR APPLICATION NUMBER: 60/298,796
```

```
; PRIOR FILING DATE: 2001-06-15
```

;  
; PRIOR APPLICATION NUMBER: 60/323,269  
; PRIOR FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 29

;  
; LENGTH: 1500  
; TYPE: DNA  
; ORGANISM: Schizochytrium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1500)  
US-11-087-084-29

Alignment Scores:  
Pred. No.: 162 Length: 1500  
Score: 70.00 Matches: 19  
Percent Similarity: 56.9% Conservatives: 14  
Best Local Similarity: 32.8% Mismatches: 23  
Query Match: 24.8% Indels: 2  
DB: 14 Gaps: 1

US-10-628-525A-34 (1-58) x US-11-087-084-29 (1-1500)

QY 2 AlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAla 21  
:::||||| ||| |||:::||||| |||::: |||  
Db 1022 TCGCCAAACGCCCGCCAGCCAGCTCAACCGCGCAGCGACCGAGCCAGGCGCCAGTACCTCG 1081  
QY 22 -----SerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAla 39  
|||:::||||| |||:::||||| |||::: |||  
Db 1082 ACGCGTGCACATTGCTCCGCGCAGCGGCAAGAGAGCGCTCGGCTACGCCACGGTTCCA 1141  
QY 40 ArgArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgileArg 57  
|||||:::||||| |||:::||||| |||::: |||  
Db 1142 AGACGGTCAACCGCAAGAGAGCTGTTCTTCTCGTGCCACTTTTGGTTGACTCGG 1195

RESULT 10  
US-11-087-085-29  
; Sequence 29, Application US/11087085  
; Publication No. US20050273884A1  
; GENERAL INFORMATION:  
; APPLICANT: Metz, James  
; APPLICANT: Barclay, William  
; APPLICANT: Platt, James  
; APPLICANT: Kuner, Jerry  
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase  
; FILE REFERENCE: 2997-29  
; CURRENT APPLICATION NUMBER: US/11/087,085  
; PRIOR FILING DATE: 2005-03-21  
; PRIOR APPLICATION NUMBER: 60/284,066  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/298,796  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/323,269  
; PRIOR FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 29

Alignment Scores:  
Pred. No.: 162 Length: 1500  
Score: 70.00 Matches: 19  
Percent Similarity: 56.9% Conservatives: 14  
Best Local Similarity: 32.8% Mismatches: 23  
Query Match: 24.8% Indels: 2  
DB: 14 Gaps: 1

US-11-087-085-29  
; LENGTH: 1500  
; TYPE: DNA  
; ORGANISM: Schizochytrium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1500)  
US-11-087-085-29

Alignment Scores:  
Pred. No.: 162 Length: 1500  
Score: 70.00 Matches: 19  
Percent Similarity: 56.9% Conservatives: 14  
Best Local Similarity: 32.8% Mismatches: 23  
Query Match: 24.8% Indels: 2  
DB: 14 Gaps: 1

Query Match: 24.8% Indels: 2  
DB: 14 Gaps: 1

US-10-628-525A-34 (1-58) x US-11-087-085-29 (1-1500)

QY 2 AlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAla 21  
:::||||| ||| |||:::||||| |||::: |||  
Db 1022 TCGCCAAACGCCCGCCAGCCAGCTCAACCGCGCAGCGACCGAGCCAGGCGCCAGTACCTCG 1081  
QY 22 -----SerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAla 39  
|||:::||||| |||:::||||| |||::: |||  
Db 1082 ACGCGTGCACATTGCTCCGCGCAGCGGCAAGAGAGCGCTCGGCTACGCCACGGTTCCA 1141  
QY 40 ArgArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgileArg 57  
|||||:::||||| |||:::||||| |||::: |||  
Db 1142 AGACGGTCAACCGCAAGAGAGCTGTTCTTCTCGTGCCACTTTTGGTTGACTCGG 1195

RESULT 11  
US-11-087-100-5  
; Sequence 5, Application US/11087100  
; Publication No. US2005026640A1  
; GENERAL INFORMATION:  
; APPLICANT: Metz, James  
; APPLICANT: Barclay, William  
; APPLICANT: Platt, James  
; APPLICANT: Kuner, Jerry  
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase  
; FILE REFERENCE: 2997-29  
; CURRENT APPLICATION NUMBER: US/11/087,100  
; PRIOR FILING DATE: 2005-03-21  
; PRIOR APPLICATION NUMBER: 60/231,899  
; PRIOR FILING DATE: 1999-01-14  
; PRIOR APPLICATION NUMBER: 60/284,066  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/298,796  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/323,269  
; PRIOR FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5

Alignment Scores:  
Pred. No.: 478 Length: 4509  
Score: 70.00 Matches: 19  
Percent Similarity: 56.9% Conservatives: 14  
Best Local Similarity: 32.8% Mismatches: 23  
Query Match: 24.8% Indels: 2  
DB: 14 Gaps: 1

US-11-087-100-5  
; LENGTH: 4509  
; TYPE: DNA  
; ORGANISM: Schizochytrium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(4509)  
US-11-087-100-5

Alignment Scores:  
Pred. No.: 478 Length: 4509  
Score: 70.00 Matches: 19  
Percent Similarity: 56.9% Conservatives: 14  
Best Local Similarity: 32.8% Mismatches: 23  
Query Match: 24.8% Indels: 2  
DB: 14 Gaps: 1

US-10-628-525A-34 (1-58) x US-11-087-100-5 (1-4509)

QY 2 AlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAla 21  
:::||||| ||| |||:::||||| |||::: |||  
Db 2372 TCGCCAAACGCCCGCCAGCCAGCTCAACCGCGCAGCGACCGAGCCAGGCGCCAGTACCTCG 2431  
QY 22 -----SerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAla 39  
|||:::||||| |||:::||||| |||::: |||  
Db 2432 ACGCGTGCACATTGCTCCGCGCAGCGGCAAGAGAGCGCTCGGCTACGCCACGGTTCCA 2491  
QY 40 ArgArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgileArg 57  
|||||:::||||| |||:::||||| |||::: |||  
Db 2492 AGACGGTCAACCGCAAGAGAGCTGTTCTTCTCGTGCCACTTTTGGTTGACTCGG 2545

Alignment Scores:  
Pred. No.: 478 Length: 4509  
Score: 70.00 Matches: 19  
Percent Similarity: 56.9% Conservatives: 14  
Best Local Similarity: 32.8% Mismatches: 23  
Query Match: 24.8% Indels: 2  
DB: 14 Gaps: 1

US-11-087-100-5  
; LENGTH: 4509  
; TYPE: DNA  
; ORGANISM: Schizochytrium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(4509)  
US-11-087-100-5

Alignment Scores:  
Pred. No.: 478 Length: 4509  
Score: 70.00 Matches: 19  
Percent Similarity: 56.9% Conservatives: 14  
Best Local Similarity: 32.8% Mismatches: 23  
Query Match: 24.8% Indels: 2  
DB: 14 Gaps: 1

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; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/323,269
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 4509
; TYPE: DNA
; ORGANISM: Schizochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4509)
US-11-087-085-5

Alignment Scores:
Pred. No.: 478 Length: 4509
Score: 70.00 Matches: 19
Percent Similarity: 56.9% Conservatve: 14
Best Local Similarity: 32.8% Mismatches: 23
Query Match: 24.8% Indels: 2
DB: 14 Gaps: 1

US-10-628-525A-34 (1-58) x US-11-087-085-5 (1-4509)

Qy 2 AlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAla 21
Db 2372 TCGCCAACGCCGCCACGCCGCCAGCTCAACGCCGCCACGCCGCCAGTACCTCG 2431
Qy 22 -----SerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAla 39
Db 2432 ACGCCGTCGACATGTCTCCGGCAGCGGCAGAGAGAGCCTCGGCTACGCCACGGTTCCA 2491
Qy 40 ArgArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArg 57
Db 2492 AGACGGGTCAACCGACGACTGCTTCTCTCGTGCCACTTTTGGTTGACTCGG 2545

RESULT 14
US-11-096-568A-13282
; Sequence 13282, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Poly
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 13282
; LENGTH: 746
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(746)
; OTHER INFORMATION: Ceres Seq. ID no. 15174052
US-11-096-568A-13282

Alignment Scores:
Pred. No.: 107 Length: 746
Score: 69.00 Matches: 16
Percent Similarity: 50.9% Conservatve: 11
Best Local Similarity: 30.2% Mismatches: 26
Query Match: 24.5% Indels: 0
DB: 11 Gaps: 0

US-10-628-525A-34 (1-58) x US-11-096-568A-13282 (1-746)

Qy 3 ProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSer 22
Db 130 CCTCTCCGGCGCGGTGCGCTGTCAGTCGCCACGCCACCACTACCACTCGGGCGGCT 189
Qy 23 AlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgArgSer 42

```







```

; ORGANISM: Streptomyces sp.
US-11-143-980-12

Alignment Scores:
Pred. No.: 325 Length: 1341
Score: 67.00 Matches: 16
Percent Similarity: 50.0% Conservative: 6
Best Local Similarity: 36.4% Mismatches: 22
Query Match: 23.8% Indels: 0
DB: 14 Gaps: 0

US-10-628-525A-34 (1-58) x US-11-143-980-12 (1-1341)
QY 2 AlaProThrValMetMetAlaSerAlaThrAlaThrArgThrAsnProAlaGlnAla 21
Db 422 TCGCCATGACCTGCCCTACCGGAGCGCGGAGAGCGGTACTCCACCGATGCCAAC 481

QY 22 SerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArgArg 41
Db 482 TCTGGGGGCCACCCACGAGGCAAGTCTCGAGCACCTCGACACCGGTATCGAGATCG 541

QY 42 SerSerArgSer 45
Db 542 TCCAGCCGATCA 553

RESULT 21
US-11-143-980-1/c
; Sequence 1, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
; APPLICANT: He, Min
; APPLICANT: Hucul, John
; APPLICANT: Hallli, Bradley A.
; APPLICANT: Wagenaar, Melissa M.
; APPLICANT: Graziani, Edmund
; APPLICANT: Summers, Mia
; APPLICANT: Kulowski, Kerry
; APPLICANT: Pong, Kevin
; TITLE OF INVENTION: Biotynthetic Gene Cluster for the Production of a Complex
; FILE REFERENCE: AM-101426US
; CURRENT APPLICATION NUMBER: US/11/143,980
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/664,483
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US 60/576,895
; PRIOR FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 116856
; TYPE: DNA
; ORGANISM: Streptomyces sp.
US-11-143-980-1

Alignment Scores:
Pred. No.: 2,6e+04 Length: 116856
Score: 67.00 Matches: 16
Percent Similarity: 50.0% Conservative: 6
Best Local Similarity: 36.4% Mismatches: 22
Query Match: 23.8% Indels: 0
DB: 14 Gaps: 0

US-10-628-525A-34 (1-58) x US-11-143-980-1 (1-116856)
QY 2 AlaProThrValMetMetAlaSerAlaThrAlaThrArgThrAsnProAlaGlnAla 21
Db 11956 TCGCCATGACCTGCCCTACCGGAGCGCGGAGAGCGGTACTCCACCGATGCCAAC 11897

QY 22 SerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArgArg 41
Db 11896 TCTGGGGGCCACCCACGAGGCAAGTCTCGAGCACCTCGACACCGGTATCGAGATCG 11837

; ORGANISM: Streptomyces sp.
US-11-143-980-12

Alignment Scores:
Pred. No.: 325 Length: 1341
Score: 67.00 Matches: 16
Percent Similarity: 50.0% Conservative: 6
Best Local Similarity: 36.4% Mismatches: 22
Query Match: 23.8% Indels: 0
DB: 14 Gaps: 0

US-10-628-525A-34 (1-58) x US-11-143-980-12 (1-1341)
QY 2 AlaProThrValMetMetAlaSerAlaThrAlaThrArgThrAsnProAlaGlnAla 21
Db 422 TCGCCATGACCTGCCCTACCGGAGCGCGGAGAGCGGTACTCCACCGATGCCAAC 481

QY 22 SerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArgArg 41
Db 482 TCTGGGGGCCACCCACGAGGCAAGTCTCGAGCACCTCGACACCGGTATCGAGATCG 541

QY 42 SerSerArgSer 45
Db 542 TCCAGCCGATCA 553

RESULT 21
US-11-143-980-1/c
; Sequence 1, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
; APPLICANT: He, Min
; APPLICANT: Hucul, John
; APPLICANT: Hallli, Bradley A.
; APPLICANT: Wagenaar, Melissa M.
; APPLICANT: Graziani, Edmund
; APPLICANT: Summers, Mia
; APPLICANT: Kulowski, Kerry
; APPLICANT: Pong, Kevin
; TITLE OF INVENTION: Biotynthetic Gene Cluster for the Production of a Complex
; FILE REFERENCE: AM-101426US
; CURRENT APPLICATION NUMBER: US/11/143,980
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/664,483
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US 60/576,895
; PRIOR FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 116856
; TYPE: DNA
; ORGANISM: Streptomyces sp.
US-11-143-980-1

Alignment Scores:
Pred. No.: 2,6e+04 Length: 116856
Score: 67.00 Matches: 16
Percent Similarity: 50.0% Conservative: 6
Best Local Similarity: 36.4% Mismatches: 22
Query Match: 23.8% Indels: 0
DB: 14 Gaps: 0

US-10-628-525A-34 (1-58) x US-11-143-980-1 (1-116856)
QY 2 AlaProThrValMetMetAlaSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSer 22
Db 5459 CGTCCGCGAGTCGGGGCGGCGAGCGGACCCGAGGAGCGGAATCCCTCGAGGGAGGGA 5528

QY 23 AlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArgArgSer 42
Db 5529 AGGGCGCGCCCTCGCGAGCGGCTCGAGCCCGCCACCTCGGTCTATCCCGGCTCGCGGA 5588

QY 43 SerArgSerLeuGlyAsnValAlaSerAsnGlyGly---ArgIleArgCys 58
Db 5589 GGCTCAGGCGCCCGGAGATGCGGGCGGAGGGGCGGCGGACCCCTGC 5639

RESULT 23
US-09-925-065A-811437/c
; Sequence 811437, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
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; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 811437
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-811437

Alignment Scores:
Pred. No.: 145          Length: 450
Score: 66.00           Matches: 16
Percent Similarity: 63.9% Conservative: 7
Best Local Similarity: 44.4% Mismatches: 13
Query Match: 23.4%      Indels: 0
DB: 6                  Gaps: 0

US-10-628-525A-34 (1-58) x US-09-925-065A-811437 (1-450)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 379 ATGGCTCCGTCAGCTCATTCGCAACCTCTGCCTCTGGGTTCGTGATTCCTCGCTCA 320

QY 21 AlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeu 36
Db 319 GCCTCCCAAGTAGTAGGATTACAGGTGCCCGCCACCATGCTGGCTG 272

RESULT 24
US-11-136-527-3446/c
; Sequence 3446, Application US/11136527
; Publication No. US2005028750A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3446
; LENGTH: 6000
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3446

Alignment Scores:
Pred. No.: 2,11e+03      Length: 6000
Score: 65.50            Matches: 27
Percent Similarity: 56.2% Conservative: 9
Best Local Similarity: 42.2% Mismatches: 14
Query Match: 23.2%      Indels: 14
DB: 14                  Gaps: 2

US-10-628-525A-34 (1-58) x US-11-136-527-3446 (1-6000)

QY 4 ThrValMetMetAlaSerSerAlaThrAla-ThrArgThrAsnProAlaGlnAlaSerAl 23
Db 242 AGCATGGTGACACCGACGAGTCGACAGTGGACACCGCAACCGCCAGCAGCCTCTTG 183

QY 23 aVal-----AlaProPhe--GlnGlyLeuLysSerThrAlaSer----- 35
Db 182 TGCACTCGATGTGGGCTCCGTGGTGGGGTCTCACTCCACCGAGTCAGCCACGGG 123

QY 36 -----LeuProValAlaArgSerSerArgSerSerLeuGlyAsnValAlaSer 51
Db 122 TCCGAGAGCCCCCTGGCGCTTGCCTGGAGCGCGCGTGTCTTCTCCCATGGTGGCGCA 63

QY 52 AsnGly 53
Db 62 AACGGT 57
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## RESULT 25

```
US-11-096-568A-18507/c
; Sequence 18507, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18507
; LENGTH: 1517
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1517)
; OTHER INFORMATION: Ceres Seq. ID no. 12365500
US-11-096-568A-18507
```

## Alignment Scores:

```
Pred. No.: 625          Length: 1517
Score: 65.00           Matches: 23
Percent Similarity: 54.2% Conservative: 9
Best Local Similarity: 39.0% Mismatches: 24
Query Match: 23.0%      Indels: 3
DB: 11                  Gaps: 1
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US-10-628-525A-34 (1-58) x US-11-096-568A-18507 (1-1517)

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QY 2 AlaProThr-----ValMetMetAlaSerSerAlaThrAla-ThrArgThrAsnProAl 19
Db 768 GCGCCCACTCGCGCTTGTGTCATGACGACGATCGCTCGGTAGTCGACGCGGCTCC 709

QY 19 aGlnAlaSerAlaValaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAl 39
Db 708 ACAGGCTCGGCTCGGGCTTGTTACTCGGGTGTGTCGTACAGCACCAGCGCGGCGCG 649

QY 39 aArgArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgLeuArg 57
Db 648 GCGGCGAGCAGCGCGTAGTTCGAAGCACGCGTGGCACAGAGCGTTCGCGCGCGGG 594
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## RESULT 26

```
US-09-925-065A-121813/c
; Sequence 121813, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121813
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-121813
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Db 1219 CCGTCGGCGGTGCACCTCTCGGGGCTACGACATCCCGGCCAGACCGCGTCTTCATCA 1278
QY 23 AlavalalaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgArgSer 42
Db 1279 ACACCTTCGCCATGGCGCGG-----ACCCGAGATCT 1311
QY 43 SerArgSerLeuGlyAanValAlaSerAasnGlyClyArg 55
Db 1312 GGGAGGAGCGCTGGAGTACTCGCCGAGCGGTTCGAGG 1350

RESULT 30
US-11-096-568A-23191
; Sequence 23191, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23191
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1347)
; OTHER INFORMATION: Ceres Seq. ID no. 12411590
US-11-096-568A-23191

Alignment Scores:
Pred. No.: 727 Length: 1347
Score: 64.00 Matches: 19
Percent Similarity: 51.2% Conservative: 3
Best Local Similarity: 44.2% Mismatches: 13
Query Match: 22.7% Indels: 8
DB: 11 Gaps: 1

US-10-628-525A-34 (1-58) x US-11-096-568A-23191 (1-1347)
QY 3 ProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGlnAlaSer 22
Db 493 CCCGCGACGCGCGCAGCGTCTCAGACGCGCCACGTCCTCCACTTCGCGTCCCGCGCGCC 552
QY 23 AlavalalaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArgArgSer 42
Db 553 GCC-----TGACGGCTTCGTCTCCAGGCGGAGGCGCC 588
QY 43 SerArgSer 45
Db 589 AGGCGGAGC 597

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

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Perfect score: 282

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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	203.5	72.2	183	42	US-10-140-410-1
2	203.5	72.2	183	75	US-60-166-268-1
3	203.5	72.2	185	11	US-08-113-561A-14
4	203.5	72.2	188	30	US-09-696-664A-651
5	203.5	72.2	228	22	US-09-262-979-69
6	203.5	72.2	228	23	US-09-304-517A-3880
7	203.5	72.2	228	23	US-09-371-146A-3880

Sequence 1, Appl  
Sequence 1, Appl  
Sequence 14, Appl  
Sequence 651, Appl  
Sequence 69, Appl  
Sequence 3880, Ap





```

RESULT 1
US-10-140-410-1
: Sequence 1 Application US/10140410
: GENERAL INFORMATION:
: APPLICANT: Ceimi Perry G.
: APPLICANT: Lightner, Jonathan E.
: TITLE OF INVENTION: Fructose Polymer Synthesis in Monocot Plastids
: FILE REFERENCE: BBI347 US,NA

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Alignment Scores:		
Pred. No.:	1.13e-19	183
Score:	203.50	47
Percent Similarity:	81.0%	Conservative: 0
Best Local Similarity:	81.0%	Mismatches: 0
Query Match:	72.2%	Indels: 11
DB:	42	Gaps: 2

US-10-628-525A-34 (1-58) x US-10-140-410-1 (1-183)

[illegible]

RESULT 2  
US-60-166-268-1  
; Sequence 1, Application US/60166268  
; GENERAL INFORMATION:  
; APPLICANT: Calmi, Perry G.  
; APPLICANT: Lightner, Joanthan E.  
; TITLE OF INVENTION: Fructose Polymer Synthesis in Monocot Plastids  
; FILE REFERENCE: BB1347 US PV  
; CURRENT APPLICATION NUMBER: US/60/166,268  
; CURRENT FILING DATE: 1999-11-18  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 1

Alignment Scores:		
Pred. No.:	1.13e-19	Length:
Score:	203.50	Matches:
Percent Similarity:	81.0%	Conservative:
Best Local Similarity:	81.0%	Mismatches:
Query Match:	72.2%	Indels:
DB:	75	Gaps:
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		47
		0
		11
		2

US-10-628-525A-34 (1-58) x US-60-166-268-1 (1-183)

Qy	1	MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln	20
Db	1	ATGGCGCCACCGTGATGGCTCGTGGCCACC-----	36
Qy	21	AlaSerAlaValAlaIleProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg	40
Db	37	-----GCCGTGCTCGCTTCAGAGGGGCTTAAGTCCACGGCCAGCCTCCCGTCGCCCGC	90
Qy	41	ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys	58
Db	91	CGTCTCTTAGAGCTTCGGCAACGTC-----AGCACGGCGGAGAGATCGGGTC	141

### RESULT 3

```

US-08-113-561A-14
; Sequence 14, Application US/08113561A
; GENERAL INFORMATION:
; APPLICANT: Adams, Thomas R. et al.
; TITLE OF INVENTION: Methods and Compositions for the
; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants
; TITLE OF INVENTION: and Cells Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/113,561A
; FILING DATE: 25-AUG-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/565,844
; FILING DATE: 09-AUG-1990
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: DEKM-055/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 713/789-2679
; TELEX: 79-0924

```

Alignment Scores:		
Pred. No.:	1.16e-19	Length:
Score:	203.50	Matches:
Percent Similarity:	81.0%	Conservative:
Best Local Similarity:	81.0%	Mismatches:
Query Match:	72.2%	Indels:
DB:	11	Gaps:
		185
		47
		0
		0
		11
		2

US-10-628-525A-34 (1-58) x US-08-113-561A-14 (1-185)

**Oy**

1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
|||||  
  
42 ATGGCGGCCACCTGCATCATTCCTTCCCTCCCAGC-----77

Qy 21 AlaSerAlaValAlaProPheGlnClyLeuIlysserThrAlaSerLeuProValAlaArg 40

```
Db 78 -----GCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCGC 131
QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgGlyCys 58
Db 132 CGGTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 182

RESULT 4
US-09-696-664A-651
; Sequence 651, Application US/0969664A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patrice
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51721)B
; CURRENT APPLICATION NUMBER: US/09/696,664A
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/161,619
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 17472
; SEQ ID NO 651
; LENGTH: 188
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3179-028-P1-K6-H7
US-09-696-664A-651

Alignment Scores:
Pred. No.: 1,19e-19 Length: 188
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 30 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-696-664A-651 (1-188)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCGCTCGTCCGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgGlyCys 58
Db 127 CGCTCTCCAGAGCCTTGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 5
US-09-262-979-69
; Sequence 69, Application US/09262979
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; TITLE OF INVENTION: Carbon Assimilation Pathway
; FILE REFERENCE: 38-21(15091)B
; CURRENT APPLICATION NUMBER: US/09/262,979
; CURRENT FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: US 60/076,912
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 69
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Zea mays

Db 78 -----GCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCGC 131
QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgGlyCys 58
Db 132 CGGTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 182

RESULT 4
US-09-696-664A-651
; Sequence 651, Application US/0969664A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patrice
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51721)B
; CURRENT APPLICATION NUMBER: US/09/696,664A
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/161,619
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 17472
; SEQ ID NO 651
; LENGTH: 188
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3179-028-P1-K6-H7
US-09-696-664A-651

Alignment Scores:
Pred. No.: 1,19e-19 Length: 188
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 30 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-696-664A-651 (1-188)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCGCTCGTCCGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgGlyCys 58
Db 127 CGCTCTCCAGAGCCTTGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 5
US-09-262-979-69
; Sequence 69, Application US/09262979
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; TITLE OF INVENTION: Carbon Assimilation Pathway
; FILE REFERENCE: 38-21(15091)B
; CURRENT APPLICATION NUMBER: US/09/262,979
; CURRENT FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: US 60/076,912
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 69
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Zea mays

Db 78 -----GCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCGC 131
QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgGlyCys 58
Db 132 CGGTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 182

RESULT 4
US-10-628-525A-34 (1-58) x US-09-262-979-69 (1-228)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGATGCGCTCGTCCGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCGTCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAlaValAlaSerAsnGlyGlyArgGlyCys 58
Db 127 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 7
US-09-371-146A-3880
; Sequence 380, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
```

; CURRENT APPLICATION NUMBER: US/09/371,146A  
; CURRENT FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 294310  
; SEQ ID NO 3880  
; LENGTH: 228  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-371-146A-3880

Alignment Scores:  
Pred. No.: 1.63e-19 Length: 228  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-371-146A-3880 (1-228)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 72  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40  
Db -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 126  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgCys 58  
Db 127 CGCTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

## RESULT 8

US-09-985-678-3880  
; Sequence 3880, Application US/09985678  
; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 16517.255/38-21(15097)P  
; CURRENT APPLICATION NUMBER: US/09/985,678  
; CURRENT FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 295529  
; SEQ ID NO 3880  
; LENGTH: 228  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-985-678-3880

Alignment Scores:  
Pred. No.: 1.63e-19 Length: 228  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-985-678-3880 (1-228)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 72  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40  
Db -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 126  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgCys 58  
Db 127 CGCTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

## RESULT 9

US-09-987-899-69  
; Sequence 69, Application US/09987899  
; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 69  
; LENGTH: 228  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700042688H1  
US-09-987-899-69

Alignment Scores:  
Pred. No.: 1.63e-19 Length: 228  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-69 (1-228)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
Db ATGGCGCCACCGTGATGGCTCGTCGCCACC----- 72  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuIysSerThrAlaSerLeuProValAlaArg 40  
Db -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 126  
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgCys 58  
Db 127 CGCTCTCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

## RESULT 10

US-09-262-979-84  
; Sequence 84, Application US/09262979  
; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With The  
; FILE REFERENCE: Carbon Assimilation Pathway  
; CURRENT APPLICATION NUMBER: US/09/262,979  
; CURRENT FILING DATE: 1999-03-04  
; EARLIER APPLICATION NUMBER: US 60/076,912  
; EARLIER FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 84  
; LENGTH: 229  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700198026H1  
US-09-262-979-84

```
Alignment Scores:
Pred. No.: 1.64e-19 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 22 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-262-979-84 (1-229)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 87
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCAGCCGAGCTCCCGTCGCCCGC 141
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 142 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 11
US-09-304-517A-28585
; Sequence 28585, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 28585
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
US-09-304-517A-28585

Alignment Scores:
Pred. No.: 1.64e-19 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-304-517A-28585 (1-229)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 87
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCAGCCGAGCTCCCGTCGCCCGC 141
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 142 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 12
US-09-371-146A-28585
; Sequence 28585, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
```

```
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 28585
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-146A-28585

Alignment Scores:
Pred. No.: 1.64e-19 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-371-146A-28585 (1-229)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 87
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCAGCCGAGCTCCCGTCGCCCGC 141
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 142 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 13
US-09-985-678-28585
; Sequence 28585, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 28585
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
US-09-985-678-28585

Alignment Scores:
Pred. No.: 1.64e-19 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-985-678-28585 (1-229)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC----- 87
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCAGCCGAGCTCCCGTCGCCCGC 141
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 142 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 14
US-09-987-899-84
; Sequence 84, Application US/09987899
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; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 1517.258
; CURRENT APPLICATION NUMBER: US/09/987,899
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 84
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700198026H1
; US-09-987-899-84

Alignment Scores:
Pred. No.: 1.64e-19 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-84 (1-229)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGGCCCCACCGTGATGCGCTCGTCCGCCACC----- 87
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 141
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgileArgCys 58
Db 142 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 15
US-09-262-979-264
; Sequence 264, Application US/09262979
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With The
; FILE REFERENCE: 38-21(15091)B
; CURRENT APPLICATION NUMBER: US/09/262,979
; CURRENT FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: US 60/076,912
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 264
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-F6
; US-09-262-979-264

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0

Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-84 (1-229)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGGCCCCACCGTGATGCGCTCGTCCGCCACC----- 87
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 88 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 141
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgileArgCys 58
Db 142 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 192

RESULT 16
US-09-304-517A-97485
; Sequence 97485, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 97485
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-304-517A-97485

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-304-517A-97485 (1-230)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGGCCCCACCGTGATGCGCTCGTCCGCCACC----- 72
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 126
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgileArgCys 58
Db 127 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 17
US-09-394-745-33403
; Sequence 33403, Application US/09394745
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalagudi, Raghunath V.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15454)B
; CURRENT APPLICATION NUMBER: US/09/394,745
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 57264
; SEQ ID NO 33403
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
```

```

Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 22 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-262-979-264 (1-230)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGGCCCCACCGTGATGCGCTCGTCCGCCACC----- 72
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 126
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgileArgCys 58
Db 127 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177
```

```

RESULT 16
US-09-304-517A-97485
; Sequence 97485, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 97485
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-304-517A-97485

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-304-517A-97485 (1-230)

Qy 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGGCCCCACCGTGATGCGCTCGTCCGCCACC----- 72
Qy 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTCGCTCGTTCCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 126
Qy 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgileArgCys 58
Db 127 CGCTCTCTCCAGAACCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177
```

```

RESULT 17
US-09-394-745-33403
; Sequence 33403, Application US/09394745
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalagudi, Raghunath V.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15454)B
; CURRENT APPLICATION NUMBER: US/09/394,745
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 57264
; SEQ ID NO 33403
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
```

```
/ OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-P6
US-09-394-745-33403

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-394-745-33403 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 37 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 73 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCGAGCTCCCGTCGCCCGC 126

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 127 CGCTCCTCCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 18
US-09-565-306-53165
; Sequence 53165, Application US/09565306
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalugudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15459)C
; CURRENT APPLICATION NUMBER: US/09/565,306
; CURRENT FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 53165
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-P6

US-09-565-306-53165

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 27 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-565-306-53165 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 37 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 73 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCGAGCTCCCGTCGCCCGC 126

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 127 CGCTCCTCCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 19
US-09-654-617-326566
; Sequence 326566, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
```

```
/ TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 326566
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
US-09-654-617-326566

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 29 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-654-617-326566 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 37 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 73 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCGAGCTCCCGTCGCCCGC 126

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 127 CGCTCCTCCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 20
US-09-684-016-326566
; Sequence 326566, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 326566
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
US-09-684-016-326566

Alignment Scores:
Pred. No.: 1.66e-19 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 29 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-684-016-326566 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 37 ATGGCGCCACCGTGATGATGGCTCGTCGGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
DB 73 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCGAGCTCCCGTCGCCCGC 126

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 127 CGCTCCTCCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177
```



; NUMBER OF SEQ ID NOS: 295529  
; SEQ ID NO 5011  
; LENGTH: 235  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-304-517A-5011

Alignment Scores:  
Pred. No.: 1.72e-19 Length: 235  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservatives: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-304-517A-5011 (1-235)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThraAsnProAlaGln 20  
Db 47 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 82  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 83 -----GCCGTCCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCCGCCGC 136  
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
Db 137 CGCTCTCCAGAGCTCGGCAACGTC---ACGACGGCGGAAGGATCCGGTGC 187

## RESULT 25

US-09-371-146A-5011  
; Sequence 5011, Application US/09371146A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: ANNOTATED PLANT GENES  
; FILE REFERENCE: 38-21(15097)C  
; CURRENT APPLICATION NUMBER: US/09/371,146A  
; CURRENT FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 294310  
; SEQ ID NO 5011  
; LENGTH: 235  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-371-146A-5011

Alignment Scores:  
Pred. No.: 1.72e-19 Length: 235  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservatives: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-371-146A-5011 (1-235)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThraAsnProAlaGln 20  
Db 47 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 82  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 83 -----GCCGTCCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCCGCCGC 136  
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
Db 137 CGCTCTCCAGAGCTCGGCAACGTC---ACGACGGCGGAAGGATCCGGTGC 187

## RESULT 26

US-09-985-678-5011  
; Sequence 5011, Application US/09985678

; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Annotated Plant Genes  
; FILE REFERENCE: 16517.255/38-21(15097)F  
; CURRENT APPLICATION NUMBER: US/09/985,678  
; CURRENT FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: US 09/304,517  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 295529  
; SEQ ID NO 5011  
; LENGTH: 235  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-985-678-5011

Alignment Scores:  
Pred. No.: 1.72e-19 Length: 235  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservatives: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-985-678-5011 (1-235)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThraArgThraAsnProAlaGln 20  
Db 47 ATGGCGCCACCGTGATGATGGCTCGTGGCCACC----- 82  
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 83 -----GCCGTCCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCCGCCGC 136  
QY 41 ArgSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgGlyArgCys 58  
Db 137 CGCTCTCCAGAGCTCGGCAACGTC---ACGACGGCGGAAGGATCCGGTGC 187

## RESULT 27

US-09-987-899-79  
; Sequence 79, Application US/09987899  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.258  
; CURRENT APPLICATION NUMBER: US/09/987,899  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 79  
; LENGTH: 235  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700046244H1  
US-09-987-899-79

Alignment Scores:  
Pred. No.: 1.72e-19 Length: 235  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservatives: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 39 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-987-899-79 (1-235)



```
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 47 ATGGCGCCACCGTGATGGCTCGTCGGCCACC-----82
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 83 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 136
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 137 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 187

RESULT 28
US-09-262-979-70
; Sequence 70, Application US/09262979
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; FILE OF INVENTION: Carbon Assimilation Pathway
; FILE REFERENCE: 38-21(15091)B
; CURRENT APPLICATION NUMBER: US/09/262,979
; CURRENT FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: US 60/076,912
; EARLIER FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 70
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700044947H1
US-09-262-979-70

Alignment Scores:
Pred. No.: 1,73e-19 Length: 236
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 22 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-262-979-70 (1-236)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 13 ATGGCGCCACCGTGATGGCTCGTCGGCCACC-----48
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 49 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 102
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 103 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 153

RESULT 29
US-09-304-517A-4574
; Sequence 4574, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Annotated Plant Genes
; TITLE OF INVENTION: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 4574
; LENGTH: 236
; TYPE: DNA
```

```
; ORGANISM: Zea mays
US-09-304-517A-4574

Alignment Scores:
Pred. No.: 1,73e-19 Length: 236
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-304-517A-4574 (1-236)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 13 ATGGCGCCACCGTGATGGCTCGTCGGCCACC-----48
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 49 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 102
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 103 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 153

RESULT 30
US-09-371-146A-4574
; Sequence 4574, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 4574
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-146A-4574

Alignment Scores:
Pred. No.: 1,73e-19 Length: 236
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 23 Gaps: 2

US-10-628-525A-34 (1-58) x US-09-371-146A-4574 (1-236)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 13 ATGGCGCCACCGTGATGGCTCGTCGGCCACC-----48
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 49 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCTCCCGTCGCCCGC 102
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 103 CGCTCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 153
```

Search completed: April 2, 2006, 03:27:39  
Job time : 1588.5 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 21:21:57 ; Search time 108.468 Seconds  
(without alignments)  
1603.719 Million cell updates/sec

Title: US-10-628-525A-34

Perfect score: 282

Sequence: 1 MAPTVMASSATATRNPAQ.....ARRSSRLGNVASNGGRIRC 58

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 6698573 seqs, 1499593917 residues

Total number of hits satisfying chosen parameters: 13397146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+p2n.model -DRV=xlh  
-Q=/abs/ABSWEB spool/US10628525/runat\_31032006\_095132\_17106/app query.fasta\_1  
-DB=Pending Patents.NA.New -QFMT=fastap -SUFFIX=p2n.rpn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=150 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=ab806h  
-USER=US10628525 @CGN 1.1.1552 @runat\_31032006\_095132\_17106 -NCPU=6 -ICPU=3  
-NO WMAP -NEG SCORES=0 -WAIT -DSRBLCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending Patents.NA.New:\*  
1: /SID55/ptodata/2/pna/US06\_NEW\_COMB.seq:\*  
2: /SID55/ptodata/2/pna/US07\_NEW\_COMB.seq:\*  
3: /SID55/ptodata/2/pna/US08\_NEW\_COMB.seq:\*  
4: /SID55/ptodata/2/pna/US09\_NEW\_COMB.seq:\*  
5: /SID55/ptodata/2/pna/US10\_NEW\_COMB.seq:\*  
6: /SID55/ptodata/2/pna/US11\_NEW\_COMB.seq:\*  
7: /SID55/ptodata/2/pna/US12\_NEW\_COMB.seq:\*  
8: /SID55/ptodata/2/pna/US13\_NEW\_COMB.seq:\*  
9: /SID55/ptodata/2/pna/US14\_NEW\_COMB.seq:\*  
10: /SID55/ptodata/2/pna/US15\_NEW\_COMB.seq:\*  
11: /SID55/ptodata/2/pna/US16\_NEW\_COMB.seq:\*  
12: /SID55/ptodata/2/pna/US17\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	203.5	72.2	188	8	US-11-330-364-651 Sequence 651, App
2	203.5	72.2	228	8	US-11-244-330A-69 Sequence 69, App
3	203.5	72.2	229	8	US-11-244-330A-84 Sequence 84, App
4	203.5	72.2	230	8	US-11-244-330A-264 Sequence 264, App
5	203.5	72.2	230	8	US-11-353-150-53165 Sequence 53165, A

6	203.5	72.2	235	8	US-11-244-330A-79	Sequence 79, App
7	203.5	72.2	236	8	US-11-244-330A-70	Sequence 70, App
8	203.5	72.2	238	8	US-11-244-330A-66	Sequence 66, App
9	203.5	72.2	249	8	US-11-244-330A-71	Sequence 71, App
10	203.5	72.2	264	8	US-11-244-330A-53	Sequence 53, App
11	203.5	72.2	265	8	US-11-244-330A-40	Sequence 40, App
12	203.5	72.2	272	8	US-11-244-330A-45	Sequence 45, App
13	203.5	72.2	276	8	US-11-244-330A-26	Sequence 26, App
14	203.5	72.2	276	8	US-11-244-330A-51	Sequence 51, App
15	203.5	72.2	284	8	US-11-244-330A-32	Sequence 32, App
16	203.5	72.2	286	8	US-11-244-330A-37	Sequence 37, App
17	203.5	72.2	291	8	US-11-244-330A-47	Sequence 47, App
18	203.5	72.2	297	8	US-11-244-330A-14	Sequence 14, App
19	203.5	72.2	298	8	US-11-244-330A-16	Sequence 16, App
20	203.5	72.2	305	8	US-11-244-330A-29	Sequence 29, App
21	203.5	72.2	307	8	US-11-244-330A-15	Sequence 15, App
22	203.5	72.2	309	8	US-11-244-330A-30	Sequence 30, App
23	203.5	72.2	311	8	US-11-244-330A-68	Sequence 68, App
24	203.5	72.2	312	8	US-11-244-330A-11	Sequence 11, App
25	203.5	72.2	315	8	US-11-244-330A-10	Sequence 10, App
26	203.5	72.2	317	8	US-11-244-330A-4	Sequence 4, App
27	203.5	72.2	319	8	US-11-244-330A-231	Sequence 231, App
28	203.5	72.2	344	8	US-11-353-150-43160	Sequence 43160, A
29	203.5	72.2	349	8	US-11-329-388-18378	Sequence 18378, A
30	203.5	72.2	357	8	US-11-329-388-16426	Sequence 16426, A
31	203.5	72.2	364	8	US-11-329-388-16940	Sequence 16940, A
32	203.5	72.2	375	8	US-11-329-388-16940	Sequence 16940, A
33	203.5	72.2	409	8	US-11-244-330A-215	Sequence 215, App
34	203.5	72.2	409	8	US-11-329-388-14858	Sequence 14858, A
35	203.5	72.2	409	8	US-11-353-150-43494	Sequence 43494, A
36	203.5	72.2	415	8	US-11-244-330A-244	Sequence 244, App
37	203.5	72.2	438	8	US-11-244-330A-210	Sequence 210, App
38	203.5	72.2	438	8	US-11-353-150-68984	Sequence 68984, A
39	203.5	72.2	441	8	US-11-244-330A-229	Sequence 229, App
40	203.5	72.2	443	8	US-11-244-330A-225	Sequence 225, App
41	203.5	72.2	617	8	US-11-330-364-12143	Sequence 12143, A
42	203.5	72.2	1242	1	PCT-US05-45517-219	Sequence 219, App
43	203.5	72.2	1242	10	US-11-303-745-219	Sequence 219, App
44	202.5	71.8	197	8	US-11-244-330A-270	Sequence 270, App
45	202.5	71.8	197	8	US-11-329-388-13647	Sequence 13647, A
46	202.5	71.8	198	8	US-11-244-330A-99	Sequence 99, App
47	202.5	71.8	258	8	US-11-244-330A-48	Sequence 48, App
48	202.5	71.8	268	8	US-11-244-330A-54	Sequence 54, App
49	202.5	71.8	269	8	US-11-244-330A-62	Sequence 62, App
50	202.5	71.8	276	8	US-11-244-330A-44	Sequence 44, App
51	202.5	71.8	278	8	US-11-244-330A-22	Sequence 22, App
52	202.5	71.8	283	8	US-11-244-330A-31	Sequence 31, App
53	202.5	71.8	286	8	US-11-244-330A-41	Sequence 41, App
54	202.5	71.8	290	8	US-11-244-330A-35	Sequence 35, App
55	202.5	71.8	291	8	US-11-244-330A-25	Sequence 25, App
56	202.5	71.8	291	8	US-11-244-330A-34	Sequence 34, App
57	202.5	71.8	291	8	US-11-244-330A-49	Sequence 49, App
58	202.5	71.8	296	8	US-11-244-330A-38	Sequence 38, App
59	202.5	71.8	310	8	US-11-244-330A-23	Sequence 23, App
60	202.5	71.8	316	8	US-11-244-330A-9	Sequence 9, App
61	202.5	71.8	381	8	US-11-244-330A-220	Sequence 220, App
62	202.5	71.8	384	10	US-11-227-183A-553	Sequence 553, App
63	202.5	71.8	386	8	US-11-329-388-15097	Sequence 15097, A
64	202.5	71.8	411	8	US-11-244-330A-221	Sequence 221, App
65	202.5	71.8	414	8	US-11-244-330A-213	Sequence 213, App
66	202.5	71.8	414	8	US-11-329-388-15586	Sequence 15586, A
67	202.5	71.8	433	8	US-11-244-330A-211	Sequence 211, App
68	202.5	71.8	434	8	US-11-244-330A-223	Sequence 223, App
69	202.5	71.8	434	8	US-11-244-330A-224	Sequence 224, App
70	202.5	71.8	434	8	US-11-329-388-13655	Sequence 13655, A
71	202.5	71.8	434	8	US-11-329-388-15585	Sequence 15585, A
72	202.5	71.8	435	8	US-11-329-388-15375	Sequence 15375, A
73	202.5	71.8	446	10	US-11-227-183A-2995	Sequence 2995, App
74	202.5	71.8	450	8	US-11-329-388-15092	Sequence 15092, A
75	202.5	71.8	478	8	US-11-353-150-19891	Sequence 19891, A
76	202.5	71.8	283	8	US-11-244-330A-39	Sequence 39, App
77	199.5	70.7	226	8	US-11-244-330A-97	Sequence 97, App
78	198.5	70.4				



```
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700042688H1
US-11-244-330A-69

Alignment Scores:
Pred. No.: 7,07e-17 Length: 228
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservatives: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-69 (1-228)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGGCTCGTCGCCACC-----72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCTCCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 3
US-11-244-330A-84
; Sequence 84, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Philip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 84
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700198026H1
US-11-244-330A-84

Alignment Scores:
Pred. No.: 7,11e-17 Length: 229
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservatives: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-84 (1-229)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 52 ATGGCGCCACCGTGATGGCTCGTCGCCACC-----87
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 127 CGCTCTCCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 4
US-11-244-330A-264
; Sequence 264, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Philip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 264
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-F6
US-11-244-330A-264

Alignment Scores:
Pred. No.: 7,16e-17 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservatives: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-264 (1-230)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 37 ATGGCGCCACCGTGATGGCTCGTCGCCACC-----72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 73 -----GCCGTGCTCGTTCCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 126
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 127 CGCTCTCCAGAAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 5
US-11-353-150-53165
; Sequence 53165, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
```

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; SEQ ID NO 53165
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3068-029-Q1-K1-F6
US-11-353-150-53165

Alignment Scores:
Pred. No.: 7,16e-17 Length: 230
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-353-150-53165 (1-230)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 37 ATGGCGCCACCGTGTATGCTCGTCGGCCACC----- 72
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
DB 73 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCGCTCCCGTCGCGCGC 126
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 127 CGCTCCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 177

RESULT 6
US-11-244-330A-79
; Sequence 79, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 79
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700044947H1
US-11-244-330A-70

Alignment Scores:
Pred. No.: 7,41e-17 Length: 236
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-70 (1-236)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 13 ATGGCGCCACCGTGTATGCTCGTCGGCCACC----- 48
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
DB 49 -----GCCGTCGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCGCTCCCGTCGCGCGC 102
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
DB 103 CGCTCCTCCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 153

RESULT 8
US-11-244-330A-66
; Sequence 66, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
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; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 66
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700044245H1
US-11-244-330A-66

Alignment Scores:
Pred. No.: 7.5e-17 Length: 238
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-66 (1-238)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 14 ATGGCGCCACCGTGATGGCTCGTCCGCCACC----- 49
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 50 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 103
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 104 CGCTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 154

RESULT 9
US-11-244-330A-71
; Sequence 71, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; PRIOR FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 71
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700045847H1
US-11-244-330A-71

Alignment Scores:
Pred. No.: 7.98e-17 Length: 249
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-71 (1-249)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20

; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 66
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700044245H1
US-11-244-330A-66

Alignment Scores:
Pred. No.: 7.5e-17 Length: 238
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-66 (1-238)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 14 ATGGCGCCACCGTGATGGCTCGTCCGCCACC----- 49
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 50 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 103
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 104 CGCTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 154

RESULT 9
US-11-244-330A-71
; Sequence 71, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; PRIOR FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 1999-03-04
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 71
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700045847H1
US-11-244-330A-71

Alignment Scores:
Pred. No.: 7.98e-17 Length: 249
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-71 (1-249)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 46 ATGGCGCCACCGTGATGGCTCGTCCGCCACC----- 81
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 82 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 135
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 136 CGCTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186

RESULT 11
US-11-244-330A-40
; Sequence 40, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
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; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 40
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700025653H1
US-11-244-330A-40

Alignment Scores:
Pred. No.: 8,69e-17 Length: 265
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-40 (1-265)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 21 ATGGGCCCCACCGTGATGATGGCTCGTGGCCACC----- 56
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 57 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 110
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 111 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 161

RESULT 12
US-11-244-330A-45
; Sequence 45, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 45
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700042186H1
US-11-244-330A-45

Alignment Scores:
Pred. No.: 9e-17 Length: 272
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2
```

```
US-10-628-525A-34 (1-58) x US-11-244-330A-45 (1-272)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 43 ATGGGCCCCACCGTGATGATGGCTCGTGGCCACC----- 78
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 79 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 132
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 133 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 183

RESULT 13
US-11-244-330A-26
; Sequence 26, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 26
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700045728H1
US-11-244-330A-26

Alignment Scores:
Pred. No.: 9,18e-17 Length: 276
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-26 (1-276)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 41 ATGGGCCCCACCGTGATGATGGCTCGTGGCCACC----- 76
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
Db 77 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTGGCCGC 130
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 131 CGCTCTCTCAGAAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 181

RESULT 14
US-11-244-330A-51
; Sequence 51, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
```



; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)  
; CURRENT APPLICATION NUMBER: US/11/244,330A  
; CURRENT FILING DATE: 2005-10-06  
; PRIOR APPLICATION NUMBER: US 09/987,899  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 51  
; LENGTH: 276  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700433801H1  
US-11-244-330A-51

Alignment Scores:  
Pred. No.: 9,18e-17 Length: 276  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-51 (1-276)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThrArgThrAsnProAlaGln 20  
Db 46 ATGGCGCCACCGTGATGCGCTCGTCGGCCACC----- 81

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 82 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 135

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgileArgCys 58  
Db 136 CGCTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186

RESULT 15  
US-11-244-330A-32  
; Sequence 32, Application US/11244330A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)  
; CURRENT APPLICATION NUMBER: US/11/244,330A  
; CURRENT FILING DATE: 2005-10-06  
; PRIOR APPLICATION NUMBER: US 09/987,899  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 32  
; LENGTH: 284  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700100637H1  
US-11-244-330A-32

Alignment Scores:  
Pred. No.: 9,55e-17 Length: 284  
Score: 203.50 Matches: 47

Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-32 (1-284)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThrArgThrAsnProAlaGln 20  
Db 50 ATGGCGCCACCGTGATGCGCTCGTCGGCCACC----- 85

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 86 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 139

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgileArgCys 58  
Db 140 CGCTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 190

RESULT 16  
US-11-244-330A-37  
; Sequence 37, Application US/11244330A  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Miller, Phillip W.  
; APPLICANT: O Connell, Keith M.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
; TITLE OF INVENTION: With the Carbon Assimilation Pathway  
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)  
; CURRENT APPLICATION NUMBER: US/11/244,330A  
; CURRENT FILING DATE: 2005-10-06  
; PRIOR APPLICATION NUMBER: US 09/987,899  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 09/262,979  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: US 60/076,712  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 7341  
; SEQ ID NO 37  
; LENGTH: 286  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700212658H1  
US-11-244-330A-37

Alignment Scores:  
Pred. No.: 9,64e-17 Length: 286  
Score: 203.50 Matches: 47  
Percent Similarity: 81.0% Conservative: 0  
Best Local Similarity: 81.0% Mismatches: 0  
Query Match: 72.2% Indels: 11  
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-37 (1-286)

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThraThrArgThrAsnProAlaGln 20  
Db 48 ATGGCGCCACCGTGATGCGCTCGTCGGCCACC----- 83

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
Db 84 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCTCCCGTCGCCCGC 137

QY 41 ArgSerSerArgSerLeuGlyAenValAlaSerAenGlyGlyArgileArgCys 58  
Db 138 CGCTCTCTCAGAACGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 188

RESULT 17  
US-11-244-330A-47  
; Sequence 47, Application US/11244330A  
; GENERAL INFORMATION:

```
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 47
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700097886H1
US-11-244-330A-47

Alignment Scores:
Pred. No.:          9.87e-17          Length:          291
Score:              203.50           Matches:          47
Percent Similarity: 81.0%             Conservative:    0
Best Local Similarity: 81.0%          Mismatches:      0
Query Match:        72.2%             Indels:          11
DB:                  8                Gaps:            2

US-10-628-525A-34 (1-58) x US-11-244-330A-47 (1-291)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 57 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC-----92
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 93 -----GCCGTCCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCGCCCGC 146
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 147 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 197

RESULT 18
US-11-244-330A-14
; Sequence 14, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 14
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700101196H1
US-11-244-330A-14
```

```
Alignment Scores:
Pred. No.:          1.02e-16          Length:          297
Score:              203.50           Matches:          47
Percent Similarity: 81.0%             Conservative:    0
Best Local Similarity: 81.0%          Mismatches:      0
Query Match:        72.2%             Indels:          11
DB:                  8                Gaps:            2

US-10-628-525A-34 (1-58) x US-11-244-330A-14 (1-297)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 12 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC-----47
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 48 -----GCCGTCCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCGCCCGC 101
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 102 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 152

RESULT 19
US-11-244-330A-21
; Sequence 21, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 21
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 70009783H1
US-11-244-330A-21

Alignment Scores:
Pred. No.:          1.02e-16          Length:          298
Score:              203.50           Matches:          47
Percent Similarity: 81.0%             Conservative:    0
Best Local Similarity: 81.0%          Mismatches:      0
Query Match:        72.2%             Indels:          11
DB:                  8                Gaps:            2

US-10-628-525A-34 (1-58) x US-11-244-330A-21 (1-298)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGCGCCACCGTGATGATGCGCTCGTCGGCCACC-----83
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuYsSerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTCCGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCGCCCGC 137
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 138 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAAGGATCGGTGC 188

US-11-244-330A-14
```

```
RESULT 20
US-11-244-330A-16
; Sequence 16, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 16
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700100270H1
US-11-244-330A-16

Alignment Scores:
Pred. No.: 1.05e-16 Length: 305
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-16 (1-305)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 42 ATGGCGCCACCGTGATGGCTCGTGGCCACC-----77
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 78 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCGC 131
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 132 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 182

RESULT 21
US-11-244-330A-29
; Sequence 29, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 29
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700211770H1
US-11-244-330A-29

Alignment Scores:
Pred. No.: 1.06e-16 Length: 307
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-29 (1-307)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 50 ATGGCGCCACCGTGATGGCTCGTGGCCACC-----85
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 86 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCGC 139
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58
Db 140 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 190

RESULT 22
US-11-244-330A-15
; Sequence 15, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 15
; LENGTH: 309
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700097309H1
US-11-244-330A-15

Alignment Scores:
Pred. No.: 1.07e-16 Length: 309
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-15 (1-309)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
Db 48 ATGGCGCCACCGTGATGGCTCGTGGCCACC-----83
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLySerThrAlaSerLeuProValAlaArg 40
Db 84 -----GCCGTGCTCGTTCAGGGGCTCAAGTCCACCGCCAGCCTCCCGTCGCCGC 137
```

```
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyValArgIleArgCys 58
    |||
Db 138 CGCTCTCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 188

RESULT 23
US-11-244-330A-30
; Sequence 30, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; PRIOR FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 30
; LENGTH: 311
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700095614H1
US-11-244-330A-30

Alignment Scores:
Pred. No.: 1,08e-16 Length: 311
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservatives: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-30 (1-311)
QY 1 MetaLapProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
    |||
Db 42 ATGGGCGCCACCGTGTATGCTCGTCCGCCACC----- 77

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
    |||
Db 78 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCCGCCGC 131

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyValArgIleArgCys 58
    |||
Db 132 CGCTCTCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 182

RESULT 24
US-11-244-330A-68
; Sequence 68, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; PRIOR FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
```

```
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 68
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)---(312)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: 700215027H1
US-11-244-330A-68

Alignment Scores:
Pred. No.: 1,09e-16 Length: 312
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservatives: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-68 (1-312)
QY 1 MetaLapProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
    |||
Db 43 ATGGGCGCCACCGTGTATGCTCGTCCGCCACC----- 78

QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40
    |||
Db 79 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACGCCAGCGCTCCCGTCCGCCGC 132

QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyValArgIleArgCys 58
    |||
Db 133 CGCTCTCTCCAGAGCTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 183

RESULT 25
US-11-244-330A-11
; Sequence 11, Application US/11244330A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; PRIOR FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 11
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700098235H1
US-11-244-330A-11

Alignment Scores:
Pred. No.: 1,1e-16 Length: 315
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservatives: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-11 (1-315)
```

QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 48 ATGGCGCCACCGATGATGGCTCGTCGGCCACC----- 83  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 84 -----GCCGTCGCTCGTTCACAGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 137  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 Db 138 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 188

RESULT 26  
 US-11-244-330A-10  
 ; Sequence 10, Application US/11244330A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheikh, Nordine  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Miller, Phillip W.  
 ; APPLICANT: O Connell, Keith M.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
 ; FILE REFERENCE: 16517.339 (38-21(15091)D/US)  
 ; CURRENT APPLICATION NUMBER: US/11/244,330A  
 ; CURRENT FILING DATE: 2005-10-06  
 ; PRIOR APPLICATION NUMBER: US 09/987,899  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: US 09/262,979  
 ; PRIOR FILING DATE: 1999-03-04  
 ; PRIOR APPLICATION NUMBER: US 60/076,712  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 7341  
 ; SEQ ID NO 10  
 ; LENGTH: 317  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700099925H1  
 US-11-244-330A-10

Alignment Scores:  
 Pred. No.: 1,11e-16 Length: 317  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-10 (1-317)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 50 ATGGCGCCACCGATGATGGCTCGTCGGCCACC----- 85  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 86 -----GCCGTCGCTCGTTCACAGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 139  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 Db 140 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 190

RESULT 27  
 US-11-244-330A-4  
 ; Sequence 4, Application US/11244330A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheikh, Nordine  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Miller, Phillip W.  
 ; APPLICANT: O Connell, Keith M.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
 ; FILE REFERENCE: 16517.339 (38-21(15091)D/US)

; CURRENT APPLICATION NUMBER: US/11/244,330A  
 ; CURRENT FILING DATE: 2005-10-06  
 ; PRIOR APPLICATION NUMBER: US 09/987,899  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: US 09/262,979  
 ; PRIOR FILING DATE: 1999-03-04  
 ; PRIOR APPLICATION NUMBER: US 60/076,712  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 7341  
 ; SEQ ID NO 4  
 ; LENGTH: 319  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700098783H1  
 US-11-244-330A-4

Alignment Scores:  
 Pred. No.: 1,12e-16 Length: 319  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11  
 DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-244-330A-4 (1-319)  
 QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20  
 Db 41 ATGGCGCCACCGATGATGGCTCGTCGGCCACC----- 76  
 QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLysSerThrAlaSerLeuProValAlaArg 40  
 Db 77 -----GCCGTCGCTCGTTCACAGGGCTCAAGTCCACGCCAGCCTCCCGTCGCCCGC 130  
 QY 41 ArgSerSerArgSerLeuGlyAsnValAlaSerAsnGlyGlyArgIleArgCys 58  
 Db 131 CGCTCTCCAGAGCCTCGGCAACGTC---AGCAACGGCGGAGGATCCGGTGC 181

RESULT 28  
 US-11-244-330A-231  
 ; Sequence 231, Application US/11244330A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheikh, Nordine  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Miller, Phillip W.  
 ; APPLICANT: O Connell, Keith M.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated  
 ; FILE REFERENCE: 16517.339 (38-21(15091)D/US)  
 ; CURRENT APPLICATION NUMBER: US/11/244,330A  
 ; CURRENT FILING DATE: 2005-10-06  
 ; PRIOR APPLICATION NUMBER: US 09/987,899  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: US 09/262,979  
 ; PRIOR FILING DATE: 1999-03-04  
 ; PRIOR APPLICATION NUMBER: US 60/076,712  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 7341  
 ; SEQ ID NO 231  
 ; LENGTH: 344  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3062-047-Q1-K1-B2  
 US-11-244-330A-231

Alignment Scores:  
 Pred. No.: 1,24e-16 Length: 344  
 Score: 203.50 Matches: 47  
 Percent Similarity: 81.0% Conservative: 0  
 Best Local Similarity: 81.0% Mismatches: 0  
 Query Match: 72.2% Indels: 11

```
DB: 8 Gaps: 2
US-10-628-525A-34 (1-58) x US-11-244-330A-231 (1-344)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 46 ATGGCGCCACCGCTGATGGCTCGTCGGCCACC----- 81
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
DB 82 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCCGTGCGCCGC 135
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaAlaSerAsnGlyGlyVargileArgCys 58
DB 136 CGCTCCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 186

RESULT 29
US-11-353-150-43160
; Sequence 43160, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Comer, Timothy W.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 43160
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3062-047-Q1-K1-B2
US-11-353-150-43160

Alignment Scores:
Pred. No.: 1,27e-16 Length: 349
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-353-150-43160 (1-349)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 51 ATGGCGCCACCGCTGATGGCTCGTCGGCCACC----- 86
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
DB 87 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCCGTGCGCCGC 140
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaAlaSerAsnGlyGlyVargileArgCys 58
DB 141 CGCTCCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 191

RESULT 30
US-11-329-388-18378
; Sequence 18378, Application US/11329388
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US
; CURRENT APPLICATION NUMBER: US/11/329,388
```

```
; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: 09/553,094
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 18831
; SEQ ID NO 18378
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB84-027-Q1-E1-H12
US-11-329-388-18378

Alignment Scores:
Pred. No.: 1,31e-16 Length: 357
Score: 203.50 Matches: 47
Percent Similarity: 81.0% Conservative: 0
Best Local Similarity: 81.0% Mismatches: 0
Query Match: 72.2% Indels: 11
DB: 8 Gaps: 2

US-10-628-525A-34 (1-58) x US-11-329-388-18378 (1-357)
QY 1 MetAlaProThrValMetMetAlaSerSerAlaThrAlaThrArgThrAsnProAlaGln 20
DB 41 ATGGCGCCACCGCTGATGGCTCGTCGGCCACC----- 76
QY 21 AlaSerAlaValAlaProPheGlnGlyLeuLeuSerThrAlaSerLeuProValAlaArg 40
DB 77 -----GCCGTGCTCCGTTCCAGGGGCTCAAGTCCACCGCAGCCTCCCCGTGCGCCGC 130
QY 41 ArgSerSerArgSerLeuGlyAsnValAlaAlaSerAsnGlyGlyVargileArgCys 58
DB 131 CGCTCCTCCAGAGCTTCGGCAACGTC---AGCAACGGCGGAAGGATCCGGTGC 181

Search completed: April 2, 2006, 04:09:37
Job time : 110.468 secs
```

GenCore version 5.1.7  
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OM protein - nucleic search, using frame plus p2n model

Run on: April 1, 2006, 04:29:01 ; Search time 1155.21 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525A-35  
Perfect score: 297  
Sequence: 1 MAQILAPSTQWQRIITKSP.....KKVAHSAKFRVMAVNSGNT 58

Scoring table:

BLOSUM62 Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abs/ABSSWEB.spool/US10628525/runat\_31032006\_095113\_16622/app\_query.fasta\_1  
-DB=GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOCALLIGN=200 -THR\_SCORE=pcp -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h  
-USER=US10628525 @CGN\_1.1.4375 @runat\_31032006\_095113\_16622 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	297	100.0	1540	15	PEACHGS2A
2	265	89.2	1489	15	PSU22971
3	240	80.8	1577	15	AF031082

4	223	75.1	1552	15	AY225150
5	223	75.1	131577	14	AC148968
6	222	74.7	1595	15	AF124244
7	217	73.1	564	15	AY62529
8	217	73.1	1293	15	AY187005
9	217	73.1	1293	15	AY187006
10	217	73.1	1436	15	AY187004
11	217	73.1	1696	15	AF459587
12	201	70.7	1541	15	AF353620
13	210	67.7	1632	15	BT013265
14	199	67.0	1523	15	AY426758
15	195.5	65.8	1510	15	PVGSCH
16	180	60.8	1666	15	AF169795
17	179	60.3	1590	15	NSGS2AA
18	174	58.6	1640	15	AY162465
19	174	58.6	1665	15	AF162466
20	172	57.9	1537	15	AF019561
21	126	42.4	5232	15	AF019561
22	124	41.8	1575	15	BNA271909
23	124	41.8	1597	15	BNGSL2
24	117	39.4	1579	15	AF145480
25	115	38.7	1324	15	AF122977
26	115	38.7	1473	15	AF428461
27	115	38.7	1519	15	AY081252
28	115	38.7	1548	15	S69727
29	115	38.7	1570	15	AF428319
30	115	38.7	1580	15	AY091114
31	115	38.7	1598	15	AY088222
32	115	38.7	7498	15	AB015045
33	115	38.7	63989	15	AB013393
34	107.5	36.2	1651	15	AOGLNS
35	96.5	32.5	1296	15	AY026353
36	83	27.9	110000	1	CR931997
37	75	25.3	158560	8	AC024614
38	74	24.9	311321	1	NMA322491
39	73	24.6	1721	1	AF246375
40	73	24.6	1543	6	AX430070
41	73	24.6	2418	6	AX430071
42	73	24.6	2445	6	AX430069
43	72.5	24.4	642	5	AF006007
44	72.5	24.4	2770	5	AF210640
45	72.5	24.4	110000	1	AB017340
46	72.5	24.4	111124	5	CR383684
47	72.5	24.4	211489	5	BX323451
48	72.5	24.4	285929	14	BX571956
49	72	24.2	163375	9	AC146896
50	72	24.2	173841	9	AL732391
51	72	24.2	189211	9	AC093447
52	71.5	24.1	636	5	AY035309
53	71.5	24.1	1879	5	AY120894
54	71	23.9	2177	5	AB062114
55	71	23.9	3415	5	AF286875
56	71	23.9	3494	5	OMESP70
57	71	23.9	110000	1	AB006470
58	71	23.9	110000	1	AY305378
59	70.5	23.7	2320	9	BC089846
60	70.5	23.7	2375	5	BC056709
61	70.5	23.7	73423	14	AC135749
62	70.5	23.7	149256	8	AC110603
63	70.5	23.7	171843	5	BX511232
64	70.5	23.7	171843	5	BX511232
65	70.5	23.7	242530	5	AC145948
66	70.5	23.7	245603	14	AC132997
67	70.5	23.7	276713	14	AC097881
68	70	23.6	465	5	AY929160
69	70	23.6	752	5	DQ013309
70	70	23.6	110000	1	AE016822
71	70	23.6	139958	14	AC141936
72	70	23.6	223959	9	AC122922
73	69.5	23.4	1062	6	BD163619
74	69.5	23.4	1062	6	AX121502
75	69.5	23.4	1192	6	AX773599
76	69.5	23.4	1539	6	AR616032

AY225150	Medicago
AC148968	Medicago
AF124244	Medicago
AY62529	Lotus cor
AY187005	Lotus cor
AY187006	Lotus cor
AY187004	Lotus cor
AF459587	Lotus jap
AF353620	Glycine m
BT013265	Lycopersi
AY426758	Nicotiana
X12738	French Bean
AF169795	Juglans n
X66940	N. sylvestri
AY162465	Crataegus
AF162466	Spiraea n
AF019561	Daucus ca
AF21909	Brassica
X72751	B. napus mRN
Y12458	Brassica na
AF145480	Mesembrya
AF122977	Arabidops
AF428461	Arabidops
AY081252	Arabidops
S69727	light-regul
AF428319	Arabidops
AY091114	Arabidops
AY088222	Arabidops
AB015045	Arabidops
AB013393	Arabidops
X71361	A. officinal
AY026353	Beta vulg
Continuation (22 o	
AC024614	Homo sapi
AL162754	Neisseria
AF246375	Acidithio
AX430070	Sequence
AX430069	Sequence
AF006007	Danio rer
AF210640	Danio rer
Continuation (25 o	
CR383684	Zebrafish
BX323451	Zebrafish
BX571956	Danio rer
AC146896	Mus muscu
AL732391	Mouse DNA
AC093447	Mus muscu
AY035309	Cyprinus
AY120894	Cyprinus
AB062114	Xiphophor
AF286875	Oryzias l
AJ001312	Oreochrom
Continuation (13 o	
Continuation (3 of	
BC089846	Rattus no
BC056709	Danio rer
AC135749	Rattus no
AC110603	Homo sapi
EX511232	Zebrafish
EX511232	Zebrafish
AC145948	Gallus ga
AC132997	Rattus no
AC097881	Rattus no
AY929160	Acanthopa
DQ013309	Oligocott
Continuation (20 o	
AC141936	Rattus no
AC122922	Mus muscu
BD163619	Novel pol
AX121502	Sequence
AX773599	Sequence
AR616032	Sequence

77	69.5	23.4	1539	6	AR616033	AR616033 Sequence
78	69.5	23.4	1539	6	AX065785	AX065785 Sequence
79	69.5	23.4	1539	6	AX065787	AX065787 Sequence
80	69.5	23.4	110000	1	BA000036_13	Continuation (14 of
81	69.5	23.4	152732	14	AC074204	AC074204 Mus muscu
82	69.5	23.4	163710	9	AC140404	AC140404 Mus muscu
83	69.5	23.4	182898	9	AC133198	AC133198 Mus muscu
84	69.5	23.4	187260	9	AC087802	AC087802 Mus muscu
85	69.5	23.4	193694	14	AC120728	AC120728 Rattus no
86	69.5	23.4	228349	9	AC079044	AC079044 Mus muscu
87	69.5	23.4	248439	14	AC098173	AC098173 Rattus no
88	69.5	23.4	349459	1	BX927151	BX927151 Corynebac
89	69.5	23.4	349980	6	AX127147	AX127147 Sequence
90	69	23.2	656	5	AY971578	AY971578 Rachycent
91	69	23.2	698	5	AF187726	AF187726 Platycteth
92	69	23.2	933	5	AF1875174	AF1875174 Bos tauru
93	69	23.2	1374	2	DQ004584	DQ004584 Sesamia n
94	69	23.2	1422	4	BTAS34372	BTAS34372 Bos tauru
95	69	23.2	1433	4	BTAS19787	BTAS19787 Bos tauru
96	69	23.2	2064	5	AB062113	AB062113 Xiphophor
97	69	23.2	2073	5	AY423555	AY423555 Dicotylar
98	69	23.2	2332	5	AY589091S4	AY589091S4 Bos tauru
99	69	23.2	2971	5	FRHSPT702	FRHSPT702 F.rubripes
100	69	23.2	4791	15	OHSC70A	X67711 O.sativa hs
101	69	23.2	5352	5	FRHSP704	Y08581 F.rubripes
102	69	23.2	7784	11	AB078779	AB078779 Cloning v
103	69	23.2	110000	1	BA000013_1	Continuation (2 of
104	69	23.2	139522	15	AC145061	AC145061 Medicago
105	69	23.2	196404	14	AC150221	AC150221 Callithri
106	69	23.2	209102	14	AC162401	AC162401 Bos tauru
107	69	23.2	230210	9	AC164267	AC164267 Bos tauru
108	69	23.2	250519	9	AC140288	AC140288 Mus muscu
109	69	23.2	278550	14	AC152220	AC152220 Bos tauru
110	68.5	23.1	1830	2	AY274366	AY274366 Drosophill
111	68.5	23.1	54929	8	AL731868	AL731868 Human DNA
112	68.5	23.1	110000	14	AL732359_08	Continuation (9 of
113	68.5	23.1	113124	14	AC150076	AC150076 Gallus ga
114	68.5	23.1	163974	8	AB011399	AB011399 Homo sapi
115	68.5	23.1	177364	14	AC150041	AC150041 Gallus ga
116	68.5	23.1	207790	14	AC150166	AC150166 Gallus ga
117	68.5	23.1	331211	8	AB016897	AB016897 Homo sapi
118	68	22.9	601	6	AR660144	AR660144 Sequence
119	68	22.9	601	6	AR660145	AR660145 Sequence
120	68	22.9	601	6	AR660146	AR660146 Sequence
121	68	22.9	601	6	AR668767	AR668767 Sequence
122	68	22.9	601	6	AR668768	AR668768 Sequence
123	68	22.9	601	6	AR668769	AR668769 Sequence
124	68	22.9	1934	8	AB169323	AB169323 Macaca fa
125	68	22.9	2681	4	BOVHSP111	L10428 Bos taurus
126	68	22.9	34589	6	AR659795	AR659795 Sequence
127	68	22.9	35645	8	AC133914	AC133914 Homo sapi
128	68	22.9	41651	2	AY190962	AY190962 Drosophill
129	68	22.9	55673	8	AC117944	AC117944 Homo sapi
130	68	22.9	59258	6	AR659540	AR659540 Sequence
131	68	22.9	103610	14	AC015780	AC015780 Homo sapi
132	68	22.9	110000	1	AE006470_03	Continuation (4 of
133	68	22.9	110000	1	AE006470_04	Continuation (5 of
134	68	22.9	110000	15	AR008212_165	Continuation (166
135	68	22.9	140106	8	AC096713	AC096713 Homo sapi
136	68	22.9	142215	8	AC133065	AC133065 Homo sapi
137	68	22.9	148984	8	HS105016	AL031311 Human DNA
138	68	22.9	152449	15	AP004728	AP004728 Oryza sat
139	68	22.9	188015	8	AC126538	AC126538 Homo sapi
140	68	22.9	188076	14	AC166614	AC166614 Oryctolag
141	68	22.9	209060	14	AC019005	AC019005 Homo sapi
142	68	22.9	257621	14	AC094703	AC094703 Rattus no
143	68	22.9	273875	14	AC107003	AC107003 Rattus no
144	68	22.9	299903	14	AC152609	AC152609 Bos tauru
145	67.5	22.7	1338	6	BD211491	BD211491 Human cal
146	67.5	22.7	1578	6	CQ719025	CQ719025 Sequence
147	67.5	22.7	1932	15	MDJSP3	MDJSP3
148	67.5	22.7	2103	6	BD156167	BD156167 Primer fo
149	67.5	22.7	2103	6	AX876511	AX876511 Sequence
RESULT 1						RESULT 2
PEACHGS2A						PEACHGS2A
LOCUS						LOCUS
DEFINITION						DEFINITION
1540 bp mRNA linear PLN 27-APR-1993						1540 bp mRNA linear PLN 27-APR-1993
Pisum sativum glutamine synthetase (chloroplast GS2) mRNA, complete						Pisum sativum glutamine synthetase (chloroplast GS2) mRNA, complete
cds.						cds.
ACCESSION						ACCESSION
M20664 J03878						M20664 J03878
VERSION						VERSION
M20664.1 GI:169058						M20664.1 GI:169058
KEYWORDS						KEYWORDS
glutamine synthetase (chloroplast GS2).						glutamine synthetase (chloroplast GS2).
SOURCE						SOURCE
Pisum sativum (pea)						Pisum sativum (pea)
ORGANISM						ORGANISM
Pisum sativum						Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.						Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
1 (bases 1 to 1540)						1 (bases 1 to 1540)
REFERENCE						REFERENCE
Tingey,S.V., Tsai,F.Y., Edwards,J.W., Walker,E.L. and Coruzzi,G.M.						Tingey,S.V., Tsai,F.Y., Edwards,J.W., Walker,E.L. and Coruzzi,G.M.
Chloroplast and cytosolic glutamine synthetase are encoded by homologous nuclear genes which are differentially expressed in vivo						Chloroplast and cytosolic glutamine synthetase are encoded by homologous nuclear genes which are differentially expressed in vivo
J. Biol. Chem. 263 (20), 9651-9657 (1988)						J. Biol. Chem. 263 (20), 9651-9657 (1988)
JOURNAL						JOURNAL
PUBMED						PUBMED
2898472						2898472
COMMENT						COMMENT
Original source text: P.sativum (strain sparkle) 21 day old plant root, cDNA to mRNA, clone PGS185.						Original source text: P.sativum (strain sparkle) 21 day old plant root, cDNA to mRNA, clone PGS185.
Draft entry and computer-readable sequence [1] kindly submitted by G. Coruzzi, 14-SEP-1988.						Draft entry and computer-readable sequence [1] kindly submitted by G. Coruzzi, 14-SEP-1988.
FEATURES						FEATURES
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/db_xref="GI:169059"						/db_xref="GI:169059"
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ORIGIN						ORIGIN
Unreported.						Unreported.
Alignment Scores:						Alignment Scores:
Pred. No.: 2,348-25 Length: 1540						Pred. No.: 2,348-25 Length: 1540
Score: 297.00 Matches: 58						Score: 297.00 Matches: 58
Percent Similarity: 100.0% Conservative: 0						Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0						Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0						Query Match: 100.0% Indels: 0
DB: 15 Gaps: 0						DB: 15 Gaps: 0
US-10-628-525A-35 (1-58) x PEACHGS2A (1-1540)						US-10-628-525A-35 (1-58) x PEACHGS2A (1-1540)
QY						QY
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68 ATGGCGCAGATTTTGGCACCCTTCGACGCAATGGCAGATGAGATCAGAAAACCTCTCT 127						68 ATGGCGCAGATTTTGGCACCCTTCGACGCAATGGCAGATGAGATCAGAAAACCTCTCT 127
QY						QY
21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 40						21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 40
128 TGTGCAACTCCCAATCACATCAAGATGTGGAGTCTTCTTGTGTTATGAAAACAACTAAGAAA 187						128 TGTGCAACTCCCAATCACATCAAGATGTGGAGTCTTCTTGTGTTATGAAAACAACTAAGAAA 187
QY						QY
41 ValAlaHisSerAlaIysPheArgValMetAlaValAsnSerGluAsnGlyThr 58						41 ValAlaHisSerAlaIysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
DB						DB
188 GTTGGCATCTTCGTAAATTTAGATTATGGCAGTCAACTCTGAAATATGGCACC 241						188 GTTGGCATCTTCGTAAATTTAGATTATGGCAGTCAACTCTGAAATATGGCACC 241



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PSU22971      1889 bp      DNA      linear      PLN 31-OCT-1995
LOCUS
DEFINITION    Pisum sativum glutamine synthetase (GS2) gene, nuclear gene
               encoding chloroplast protein, partial cds.
ACCESSION     U22971
VERSION       U22971.1 GI:1045309
KEYWORDS      Pisum sativum (pea)
SOURCE        Pisum sativum
ORGANISM      Pisum sativum
               Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
               Pisum.
REFERENCE     1 (bases 1 to 1889)
AUTHORS       Tjaden, G., Edwards, J.W. and Coruzzi, G.M.
TITLE         Cis elements and trans-acting factors affecting regulation of a
               nonphotosynthetic light-regulated gene for chloroplast glutamine
               synthetase
JOURNAL       Plant Physiol. 108 (3), 1109-1117 (1995)
PUBMED       7630938
REFERENCE     2 (bases 1 to 1889)
AUTHORS       Tjaden, G.
TITLE         Direct Submission
JOURNAL       Submitted (17-MAR-1995) Gabrielle Tjaden, Biology Department, New
               York University, 1009 Main Building, New York, NY 10003, USA
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               /db_xref="taxon:3888"
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               /genes="GS2"
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               /genes="GS2"
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## ORIGIN

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Alignment Scores:
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Score:          265.00      Matches:      52
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:     89.2%      Indels:      0
DB:              15      Gaps:      0

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US-10-628-525A-35 (1-58) x PSU22971 (1-1489)

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QY      1 MetAlaGlnIleuAlaProSerThrGlnTTPGlnMetArgIleThrLysThrSerPro 20
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QY      21 CysAlaThrProIleThrSerLysMetTTPSerSerLeuValMetLysGlnThrLysLys 40
DB      1394 TTGCAACTCCCATCATCATCAAGATGTGGAGTTCTTTGTTATGAAACAACATAAGAAA 1453

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QY      41 ValAlaHisSerAlaLysPheArgValMetAlaVal 52
DB      1454 GTTGGCGCATTTCTGTAATAATTAGATTATGCGAGTC 1489
RESULT 3
AP031082
LOCUS
DEFINITION    Canavalia lineata glutamine synthetase (gln) mRNA, nuclear gene
               encoding chloroplast protein, complete cds.
ACCESSION     AP031082
VERSION       AP031082.1 GI:6578119
KEYWORDS      Canavalia lineata
SOURCE        Canavalia lineata
ORGANISM      Canavalia lineata
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
               Canavalia.
REFERENCE     1 (bases 1 to 1577)
AUTHORS       Choi, Y.A., Kim, S.G. and Kwon, Y.M.
TITLE         The plastidic glutamine synthetase activity is directly modulated
               by means of redox change at two unique cysteine residues
JOURNAL       Plant Sci. 149 (2), 175-182 (1999)
REFERENCE     2 (bases 1 to 1577)
AUTHORS       Choi, Y.A. and Kwon, Y.M.
TITLE         Direct Submission
JOURNAL       Submitted (23-OCT-1997) Biology, Seoul National University, Seoul
               151-742, Korea
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               PTKKRRARAI FSNPKVQARVPWYIGIEQETITLLQTNVNPWLPGLVGGYFGPGQPPYCS
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               YLIERITEGQGVLSLDPKPIQDWNAGCHTNYSTKSMREGEFVIKKAILNLSLR
               HSDHRAVGEGERLRTGKHETADINTPSGVNARGCSIRVGRDTEKNGKGYLEDRRP
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ORIGIN
Alignment Scores:
Pred. No.:      1.34e-18      Length:      1577
Score:          240.00      Matches:      46
Percent Similarity: 87.9%      Conservative: 5
Best Local Similarity: 79.3%      Mismatches: 7
Query Match:     80.8%      Indels:      0
DB:              15      Gaps:      0
US-10-628-525A-35 (1-58) x AP031082 (1-1577)
QY      1 MetAlaGlnIleuAlaProSerThrGlnTTPGlnMetArgIleThrLysThrSerPro 20
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QY      21 CysAlaThrProIleThrSerLysMetTTPSerSerLeuValMetLysGlnThrLysLys 40
DB      151 AATGCAAGTCCCGTCACATCAACATGTGGAGTTCTTTGTTATGAAACAATAAGAAA 210
QY      41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGlnuGlyThr 58

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Db	211	GCTACAAGTTCGCTAAATTAGAGTCTGCTGCAATCAAGTCTGAAATGGCACC	264
RESULT 4			
LOCUS	AY225150	1552 bp mRNA linear	PLN 15-MAY-2003
DEFINITION	Medicago truncatula glutamine synthetase (GS2) mRNA, complete cds;		
ACCESSION	AY225150		
VERSION	AY225150.1	GI:28629469	
KEYWORDS			
SOURCE	Medicago truncatula (barrel medic)		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.		
REFERENCE	1 (bases 1 to 1552)		
AUTHORS	Melo, P.M., Lima, L.M., Santos, I.M., Carvalho, H.G. and Cullimore, J.V.		
TITLE	Expression of the Plastid-Located Glutamine Synthetase of Medicago truncatula. Accumulation of the Precursor in Root Nodules Reveals an in Vivo Control at the Level of Protein Import into Plastids		
JOURNAL	Plant Physiol. 132 (1), 390-399 (2003)		
PUBMED	12746544		
REFERENCE	2 (bases 1 to 1552)		
AUTHORS	Melo, P., Lima, L., Carvalho, H. and Cullimore, J.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-JAN-2003) Institute for Molecular and Cellular Biology, Rua do Campo Alegre, 823, Porto 4150, Portugal		
FEATURES	source		
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ORIGIN			
Alignment Scores:			
Pred. No.:	1.36e-16	Length:	1552
Score:	223.00	Matches:	47
Percent Similarity:	88.9%	Conservative:	1
Best Local Similarity:	87.0%	Mismatches:	6
Query Match:	75.1%	Indels:	0
DB:	15	Gaps:	0
US-10-628-525A-35 (1-58) x AY225150 (1-1552)			
Qy	1	MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro	20
Db	41	ATGGCACAGATTTTGCTCTCTCTACAAATGTCACGAAGTACACAAAATCTCTCCC	100
Qy	21	CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys	40
Db	101	GTTCGAATCCCAATTCATCAAGATGTGGAGTTCTTTGGTTATGAAACAAACAGAAA	160
Qy	41	ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer	54



SKFRVLAIKSDGSTINRLLEGLNLDVTPYTDKFAIEYIWIIGTGVDRSKRTISKPV  
SH"

ORIGIN

Alignment Scores:

Pred. No.:	2,61e-16	Length:	564
Score:	217.00	Matches:	42
Percent Similarity:	84.5%	Conservative:	7
Best Local Similarity:	72.4%	Mismatches:	9
Query Match:	73.1%	Indels:	0
DB:	15	Gaps:	0

US-10-628-525A-35 (1-58) x AH014864S1 (1-564)

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QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
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Db 61 AATGCAAGTCCCATACATCAACATGTGGAGTCTCTTTATTGTGGAACAAACAAAGAAA 120  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58  
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Db 121 GTTGACGTGCTTCTAAGTTAGAGTACTGGCAATCAAGTCTGTAGTGCACACC 174

RESULT 8

AY187005

LOCUS

DEFINITION

AY187005

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lotus corniculatus var. japonicus (Lotus japonicus)

Lotus corniculatus var. japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

Submitted (26-NOV-2002) Bioquímica Vegetal y Biología Molecular, Facultad de Química, Apartado 553, Sevilla 41080, Spain

Location/Qualifiers

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CDS

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SH"

ORIGIN

Alignment Scores:

Pred. No.:	5,86e-16	Length:	1293
Score:	217.00	Matches:	42
Percent Similarity:	84.5%	Conservative:	7
Best Local Similarity:	72.4%	Mismatches:	9
Query Match:	73.1%	Indels:	0
DB:	15	Gaps:	0

US-10-628-525A-35 (1-58) x AY187005 (1-1293)

QY 1 MetAlaGInLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
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QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
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Db 61 AATGCAAGTCCCATACATCAACATGTGGAGTCTCTTTATTGTGGAACAAACAAAGAAA 120  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58  
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Db 121 GTTGACGTGCTTCTAAGTTAGAGTACTGGCAATCAAGTCTGTAGTGCACACC 174

RESULT 9

AY187006

LOCUS

DEFINITION

AY187006

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lotus corniculatus var. japonicus (Lotus japonicus)

Lotus corniculatus var. japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

Submitted (26-NOV-2002) Bioquímica Vegetal y Biología Molecular, Facultad de Química, Apartado 553, Sevilla 41080, Spain

Location/Qualifiers

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/tissue\_type="leaves"

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SH"

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## ORIGIN

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Alignment Scores:
Pred. No.: 5.86e-16 Length: 1293
Score: 217.00 Matches: 42
Percent Similarity: 84.5% Conservative: 7
Best Local Similarity: 72.4% Mismatches: 9
Query Match: 73.1% Indels: 0
DB: 15 Gaps: 0

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US-10-628-525A-35 (1-58) x AY187006 (1-1293)

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Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 1 ATGGCACAGATTGGCACCTCGACGCAATGGCAGCAGAGATCACCAAAACCTCTCCC 60

Qy 21 CysAlaThrProIleThrSerLysMetTyrSerSerLysValMetLysGlnThrLys 40
Db 61 AATGCAAGTCCCAATACATCAACATGTGGAGTCTTTATTGTGGAACAAACAGAAA 120

Qy 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 121 GTTGACGCTCTTAAGTTAGTACTGCGCAATCAAGTCTGATGGTAGCACC 174

```

## RESULT 10

```

AY187004
LOCUS
DEFINITION
Lotus corniculatus var. japonicus glutamine synthetase mRNA,
complete cds.

```

```

ACCESSION
VERSION
SOURCE
KEYWORDS
ORGANISM

```

Lotus corniculatus var. japonicus (Lotus japonicus)

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

```

```

REFERENCE
1 (bases 1 to 1436)
Arcondeguy,T., Betti,M. and Marquez,A.J.
Lotus japonicus plastidic glutamine synthetase
Unpublished

```

```

REFERENCE
2 (bases 1 to 1436)
Arcondeguy,T., Betti,M. and Marquez,A.J.
Direct Submission
Submitted (26-NOV-2002) Biochimica Vegetal y Biologia Molecular,
University of Seville, Avenida Prof. Garcia Gonzales s/n, Seville
41080, Spain

```

```

REFERENCE
3 (bases 1 to 1436)
Arcondeguy,T., Betti,M. and Marquez,A.J.
Direct Submission
Submitted (14-MAR-2005) Biochimica Vegetal y Biologia Molecular,
University of Seville, Avenida Prof. Garcia Gonzales s/n, Seville
41080, Spain

```

```

REMARK
COMMENT
Sequence update by submitter
On Mar 14, 2005 this sequence version replaced gi:26892200.
FEATURES
Location/Qualifiers
source
1..1436
/organism="Lotus corniculatus var. japonicus"
/mol_type="mRNA"
/variety="japonicus"
/db_xref="taxon:34305"
/tissue_type="leaves"
1..1293
/BC_number="6.3.1.2"

```

## CDS

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SKFRVLAIKSDGSTINRLEGLNLDVTPYTDKFAIYIWIWGGTGDVRSKRTISKPV

```

```

/codon_start=1
/product="glutamine synthetase"
/protein_id="AA084563.1"
/db_xref="GI:26892201"

```

```

/translation="MAQILAPSTQWQTRITKSPNASPITSNMSSLLWKQKVKARA
SKFRVLAIKSDGSTINRLEGLNLDVTPYTDKFAIYIWIWGGTGDVRSKRTISKPV
SHPELKPKNYDSSSTQAFDDSEVILYPOAIFRDPFRGNNILVICDAYTPQGEPI
PTNKRRAAEIFSNPKVAEIPWYIEQETLLQTDVKWPLGVPGVPGQPGPYCA
AGADKSPGRDISAHYKACLYAGINISGTNGEVMQWBYQVGSVIGIAGDHIWASR
YHLIRTEQAGVVLTLDPKPIEGDWNAGAHNTYSTKMEEGGFEVVKAILNLSLR
HODHIRAYGEGNERLLTGKHETADINTFSGVANRGCSIRVGRDTEKEGKYLEDRRP
ASNMDPVVVTALLAETLLWEPTLEAALAAQKIQLVK"

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 6.49e-16 Length: 1436
Score: 217.00 Matches: 42
Percent Similarity: 84.5% Conservative: 7
Best Local Similarity: 72.4% Mismatches: 9
Query Match: 73.1% Indels: 0
DB: 15 Gaps: 0

```

US-10-628-525A-35 (1-58) x AY187004 (1-1436)

```

Qy 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 1 ATGGCACAGATTGGCACCTCGACGCAATGGCAGCAGAGATCACCAAAACCTCTCCC 60

```

```

Qy 21 CysAlaThrProIleThrSerLysMetTyrSerSerLysValMetLysGlnThrLys 40
Db 61 AATGCAAGTCCCAATACATCAACATGTGGAGTCTTTATTGTGGAACAAACAGAAA 120

```

```

Qy 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 121 GTTGACGCTCTTAAGTTAGTACTGCGCAATCAAGTCTGATGGTAGCACC 174

```

## RESULT 11

```

AF459587
LOCUS
DEFINITION
Lotus japonicus glutamine synthetase precursor, mRNA, complete cds;
nuclear gene for chloroplast product.

```

```

ACCESSION
VERSION
SOURCE
KEYWORDS
ORGANISM

```

Lotus corniculatus var. japonicus (Lotus japonicus)

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

```

```

REFERENCE
1 (bases 1 to 1696)
Simon-Rosin,U., Colebatch,G. and Udvardi,M.
CDNA encoding plastidic glutamine synthetase
Unpublished

```

```

REFERENCE
2 (bases 1 to 1696)
Simon-Rosin,U., Colebatch,G. and Udvardi,M.
Direct Submission
Submitted (16-DEC-2001) AG-Udvardi, Max-Planck-Institute for Plant
Molecular Physiology, Am Mühlenberg 1, Golm D-14476, Germany

```

```

FEATURES
Location/Qualifiers
source
1..1696
/organism="Lotus corniculatus var. japonicus"
/mol_type="mRNA"
/variety="japonicus"
/db_xref="taxon:34305"
/tissue_type="nitrogen-fixing nodules"
147..1439
/codon_start=1
/product="glutamine synthetase precursor"
/protein_id="AA167439.1"
/db_xref="GI:18266053"

```

## CDS

```

SKFRVLAIKSDGSTINRLEGLNLDVTPYTDKFAIYIWIWGGTGDVRSKRTISKPV

```

SHPSLPKWNYSSTGQAPDDSEVILYPOAI FRDPFRGNNILVICDAYTPQGEPI  
 PTKRHRAAEI FSNPKVQAEI PMYGI EOEYTLLOTDVKWPLCPVGVGPQGPYCA  
 AGADKSFGRDISDAHYKACLIAGINISGTEVMQGWYQVGPVIGIAGDHIAWAS  
 YLLERITQAGVVLIDPKPIGDWNGAGANTYSTKSMREGGSEVVIKAILNLSL  
 HQDHIRAYGEGNERLTGKHETASINTFSWGVANRGCSIRVGRDTEKKGYLEDRR  
 ASNMDFYVVVTTALLAETLLWEPTLEAALAAQIKLV"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,63e-16 Length: 1696  
 Score: 217.00 Matches: 42  
 Percent Similarity: 84.5% Conservative: 7  
 Best Local Similarity: 72.4% Mismatches: 9  
 Query Match: 73.1% Indels: 0  
 DB: 15 Gaps: 0

US-10-628-525A-35 (1-58) x AF459587 (1-1696)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 |||||  
 Db 147 ATGGCACAGATTTTGGCACCCTCGAGCAATGGCAGCAGATCATCAAAACCTCTCCC 206  
 |||||  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 207 AATGCAAGTCCCATACATCAACATGTGGAGTCTCTTTATTGTGGAAACAAACAGAAA 266  
 |||||  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58  
 |||||  
 Db 267 GTTGCAAGTCTTCTTAAGTTTAGTACTGGCAATCAAGTCTGNTGGTAGCACC 320  
 |||||

## RESULT 12

AF353620 1541 bp mRNA linear PLN 15-NOV-2001  
 LOCUS  
 DEFINITION Glycine max glutamine synthetase precursor, mRNA, complete cds;  
 nuclear gene for chloroplast product.

ACCESSION AF353620

VERSION AF353620.1 GI:13877510

KEYWORDS Glycine max (soybean)

SOURCE Glycine max

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

REFERENCE 1 (bases 1 to 1541)

AUTHORS Bemis,K.L.

TITLE Characterization of chloroplast glutamine synthetase in soybean

JOURNAL (Glycine max)

REFERENCE 2 (bases 1 to 1541)

AUTHORS Bemis,K.L., Kahle,A., Moguel-Espanda,S., Ortega,J.L. and

Sengupta-Gopalan,C.

Direct Submission

Submitted (26-FEB-2001) Agronomy and Horticulture, New Mexico State  
 University, Skeen Hall Rm W329. Espina St. and College Dr., Las  
 Cruces, NM 88003, USA

## FEATURES

source Location/Qualifiers

1..1541

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Resnik"

/db\_xref="taxon:3847"

/clone="pGmglndelta1"

30..1328

/EC\_number="6.3.1.2"

/note="GS-2"

/codon\_start=1

/product="glutamine synthetase precursor"

/protein\_id="AAK43833.1"

/db\_xref="GI:13877511"

/translation="MAQILAPSTQWMSKSPNASPTSNMSSLLWKNQKVSPT  
 SSAPRVMAIKSDNSINRLGLMLDITPFDKIIARYIWIIGTGIDVRSKSRISK  
 VPEHPSELPKWNYSSTGQAPDDSEVILYPOAIFKDPFRGNNILVICDSYTPQGE

PIPTNKRHRAAEI FSNPKVQAEVPMYGI EOEYTLLOTDVKWPLCPVGVGPQGPY  
 CSAGADKSFGRDISDAHYKACLIAGINISGTEVMQGWYQVGPVIGIAGDHIAW  
 SRYLLERITQAGVVLIDPKPIGDWNGAGCHTNYSTKSMREDDGGSEVVIKAILNLS  
 LRHKDHI SAYEGNERLTGKHETASINTFSWGVANRGCSIRVGRDTEKKGYLEDR  
 RPTSNMDFYVVATSLAETLLWEPTLEAALAAQIKLV"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4,69e-15 Length: 1541  
 Score: 210.00 Matches: 43  
 Percent Similarity: 86.2% Conservative: 7  
 Best Local Similarity: 74.1% Mismatches: 6  
 Query Match: 70.7% Indels: 2  
 DB: 15 Gaps: 1

US-10-628-525A-35 (1-58) x AF353620 (1-1541)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 |||||  
 Db 30 ATGGCACAGATTTTGGCTCCCTCTACGCNATGGCAGATGAGATCTCAAAATCCTCTCCC 89  
 |||||  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 90 AATGCAAGTCCCATACATCAACATGTGGAGTCTCTTTATTGTGGAAACAAATAAGAAA 149  
 |||||  
 QY 41 ValAlaA-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56  
 |||||  
 Db 150 GTTCCACCACCAAGTCTGTCTAAATTTAGAGTATGGCAATTAAGTCTGACAAT 203  
 |||||

## RESULT 13

BT013265

LOCUS BT013265

DEFINITION Lycopersicon esculentum clone 134810R, mRNA sequence.

ACCESSION BT013265

VERSION BT013265.1 GI:47104680

KEYWORDS FLI CDNA.

SOURCE Lycopersicon esculentum (Solanum lycopersicum)

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 1632)

AUTHORS Kirkness,E.F., Wang,W. and Vazeille,A.

TITLE Direct Submission

JOURNAL Submitted (11-MAY-2004) The Institute for Genomic Research, 9712

Medical Center Drive, Rockville, MD 20850, USA

Location/Qualifiers

source

1..1632

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/db\_xref="taxon:4081"

/clone="134810R"

/tissue type="callus tissue"

/note="TCACH68"

## ORIGIN

Alignment Scores:  
 Pred. No.: 5,77e-14 Length: 1632  
 Score: 201.00 Matches: 41  
 Percent Similarity: 83.3% Conservative: 9  
 Best Local Similarity: 68.3% Mismatches: 8  
 Query Match: 67.7% Indels: 2  
 DB: 15 Gaps: 1

US-10-628-525A-35 (1-58) x BT013265 (1-1632)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 |||||  
 Db 70 ATGGCTCAGATCTCGCTCCGCTCCATGCGCAGATGAGATGATCAAGAGCTCAACC 129  
 |||||  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 130 GATGCTAGTCCCTTGACTTCAAAGATGTGGAGTCTGTGGTGTCTGAAGCAGAACAAAGA 189  
 |||||

```

QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAenSerGluAenGlyThr 58
Db 190 CACGCTCTTAAAGCTCTGCCAAATTAGAGTTTTCCTCCTACAGTCTGACAAATGGCACC 249

RESULT 14
AY426758 1523 bp mRNA linear PLN 02-AUG-2004
LOCUS Nicotiana attenuata glutamine synthetase GS58 mRNA, complete cds;
DEFINITION nuclear gene for plastid product.
ACCESSION AY426758
VERSION AY426758.1 GI:40457327
SOURCE Nicotiana attenuata
ORGANISM Nicotiana attenuata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 1523)
AUTHORS Bubner,B., Gase,K. and Baldwin,I.T.
TITLE Two-fold differences are the detection limit for determining
transgene copy numbers in plants by real-time PCR
JOURNAL (er) BMC Biotechnol. 4 (1), 14 (2004)
PUBMED 15251044
REFERENCE 2 (bases 1 to 1523)
AUTHORS Schittko,U. and Baldwin,I.T.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-2003) Molecular Ecology, Max Planck Institute for
Chemical Ecology, Hans-Knoell-Strasse 8, Jena D-07745, Germany
FEATURES
source
1..1523
/organism="Nicotiana attenuata"
/mol_type="mRNA"
/db_xref="taxon:49451"
51..1349
/notes="plastidic isoform"
/codon_start=1
/product="Glutamine synthetase GS58"
/protein_id="AAR86719.1"
/db_xref="GI:40457328"
/translation="MAQILAPSAQWOMRTKSTSDANPLTSKMWSSVVLKONKRLAVK
SSAKPRVPALQSDSGTVNVEOLLNDVPTDYDKLAEVWIGGSDGDMRSKRTISK
PVKHAELPKWNYDSSGTSQAGDESEVILYQALFPDPRGNILVICDAYTPAGE
PIPTNRHKAQI FDSKVSSEVPWFIEQYTLIQNVKPLGVPVGPQPGPY
CAGADKSGRDISAHYKACLYAGINISGTNGVMPQWBFQVGPVSGIEAGDHWC
ARYILLERIQAGVVLSDPKPIEGDNGAGCHTNYSTLSMRBEGGFVKKAILNLS
LRKHHSAYGEGNERLLTGKHETASIDKFSKGVANRGASIRVRDTEKQKGYLEDR
RPASNMDPVVVTGLLAETTLWEPTLEAEALAAQKALNV"
ORIGIN
Alignment Scores:
Pred. No.: 9.3e-14 Length: 1523
Score: 199.00 Matches: 40
Percent Similarity: 83.3% Conservative: 10
Best Local Similarity: 66.7% Mismatches: 8
Query Match: 67.0% Indels: 2
DB: 15 Gaps: 1

US-10-628-525A-35 (1-58) x AY426758 (1-1523)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 51 ATGGCTCAGATTTGGCTCCATCTGCACAAATGGCAGATGAGATGACAAAGAGCTCAACA 110

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 111 GATGCTAATCCCTTGACTTCAAGATGTCGAGTGTCTGTGTATTGAGCAGAAATAAGA 170

QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAenSerGluAenGlyThr 58
Db 171 CTTCGTGTTTAAAGCTCTGCCAAATTAGAGTTTTCCTCCTCAATCTGATAGTGGCACT 230

RESULT 15

```

```

PVGSCH 1510 bp mRNA linear PLN 18-APR-2005
LOCUS French Bean mRNA for plastid-located glutamine synthetase (EC
DEFINITION 6.3.1.2).
ACCESSION X12738
VERSION X12738.1 GI:21004
KEYWORDS glutamate-ammonia ligase.
SOURCE Phaseolus vulgaris
ORGANISM Phaseolus vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
REFERENCE 1 (bases 1 to 1510)
AUTHORS Lightfoot,D.A., Green,N.K. and Cullimore,J.V.
TITLE The chloroplast-located glutamine synthetase of Phaseolus vulgaris
L.: nucleotide sequence, expression in different organs and uptake
into isolated chloroplasts
JOURNAL Plant Mol. Biol. 11, 191-202 (1988)
REFERENCE 2
AUTHORS Bennet,M.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-1989)
COMMENT Data kindly reviewed (12/5/89) by Cullimore J.
FEATURES
source
1..1510
/organism="Phaseolus vulgaris"
/mol_type="mRNA"
/cultivar="Tendergreen"
/db_xref="taxon:3885"
/clone="pcGS-delta1"
/clone_lib="leaf cDNA in pUC19"
<1..>1510
/product="GS mRNA"
64..1353
/notes="unnamed protein product; GS precursor protein"
/codon_start=1
/protein_id="CAA31234.1"
/db_xref="GI:21005"
/db_xref="GOA:P15102"
/db_xref="InterPro:IPR008146"
/db_xref="InterPro:IPR008147"
/db_xref="UniProt/Swiss-Prot:P15102"
/translation="MAQILAPSTQWQMRFTKSSRHASPTTSWSSLLMKONKQTSSA
KPRVLAVSDGSTINRLSGLNDLITPTDKLAEVWIGGSDGDMRSKRTISKPE
HPSLPKWNYSSTGQAPGDESEVILYQALFPDPRGNILVICDAYTPAGRP
TKRRAAEVSNPRVIAEVPWFIEQYTLIQNVNPLGVPVGPQPGPYCSA
GADSFGRDISAHYKACLFAGINISGTNGVMPQWBFQVGPVSGIEAGDHWC
ILERITEQAGVVLSDPKPIEGDNGAGCHTNYSTKMRDGGFVKKAILNLSLRH
KEHISAYGEGNERLLTGKHETASINTFSGVANRGCSIRVRDTEKNGKGYLED
SNMDPVVVTSLAESTLLWEPTLEAEALAAQKALKV"
transit_peptide 64..234
mat_peptide /note="transit peptide (AA -57 to -1)"
235..1350
/product="mat. GS (AA 1 - 372)"
ORIGIN
Alignment Scores:
Pred. No.: 2.39e-13 Length: 1510
Score: 195.50 Matches: 41
Percent Similarity: 81.0% Conservative: 6
Best Local Similarity: 70.7% Mismatches: 10
Query Match: 65.8% Indels: 1
DB: 15 Gaps: 1

US-10-628-525A-35 (1-58) x PVGSCH (1-1510)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 64 ATGGCAGATTTTGGCTCCCTCTACACAAATGGCAGATGAGATTCACAAATCTCTCGC 123

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40

```

```
Db 124 CATGCAAGTCCATTACATCAACACGTCGGAGTCTCTTTATTGATGAAACAAATAAGAAA 183
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 184 ACCAGT---TCGTAAATTTAGTGTCTGGCAGTTAGTCTGATGGTAGCACC 234

RESULT 16
AF169795
LOCUS AF169795 1666 bp mRNA linear PLN 23-SEP-1999
DEFINITION Juglans nigra glutamine synthetase precursor (pIGS) mRNA, complete
ACCESSION AF169795
VERSION AF169795.1 GI:5733729
KEYWORDS Juglans nigra (black walnut)
SOURCE Juglans nigra
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fagales; Juglandaceae; Juglans.
REFERENCE 1 (bases 1 to 1666)
AUTHORS Simonson,L. and Twigg,P.
TITLE Cloning and Sequencing of a Glutamine Synthetase cDNA (Accession
No. AF169795) from Juglans nigra. (PGR99-144)
JOURNAL Plant Physiol. 121 (1), 313 (1999)
REFERENCE 2 (bases 1 to 1666)
AUTHORS Simonson,R.L. and Twigg,P.G.
TITLE Direct Submision
JOURNAL Submitted (16-JUL-1999) Biology, University of Nebraska-Kearney,
905 W. 25th Street, Kearney, NE 68849, USA
FEATURES
source
1..1666
/organism="Juglans nigra"
/mol_type="mRNA"
/db_xref="taxon:16719"
gene
1..1666
/gene="pIGS"
CDS
96..1394
/gene="pIGS"
/function="assimilation of ammonia into glutamine via
glutamate"
/EC_number="6.3.1.2"
/translation="MAHILPTTRWQMRITKNSANASPMWAKMWSLLLLKQNKKGSSK
SSAKPRVPATKSNSVNRIRKLLNLDLTPYTDKIIAEYIWIIGSGIDLRKSRTISK
FVEHPSELKWNYSSTQAPGDSVILYPOAIFKDPFRGNNILVICDATTYPAGE
PIPTNKRHRAAEIFTNKKVADVPMWYIEQVETLLQONVKNPLGWPVGVPGPGQPY
CGAGADKSGFDISDAHYKACLYAGINISGTNGVMPQWQVQVGPSPVIGAGDHMC
SRYLIRTEQAGVVLSDPDKPIEGDRNGACHTNYSYKSMREGGFEVVKAILNLS
LRKHNDISAYGEGNRRUTGKHETASINTFSWGVANRGCSIRVGRETEKQKGYLEDR
RPASNMDPYVITSLAETITLWEPTNEALAAQKALNV"
transit_peptide 96..266
/gene="pIGS"
/evidence=not_experimental
mat_peptide 267..1391
/gene="pIGS"
polya_signal 1507..1512
/product="glutamine synthetase"
/gene="pIGS"

ORIGIN
Alignment Scores: 1.8e-11 Length: 1666
Pred. No.: 180.00 Matches: 37
Percent Similarity: 75.0% Conservative: 8
Best Local Similarity: 61.7% Mismatches: 13
Query Match: 60.6% Indels: 2
DB: 15 Gaps: 1

US-10-628-525A-35 (1-58) x AF169795 (1-1666)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
|||||
96 ATGGCACAATATCTTGCACACCCACATACGCGATGCGAGATGAGAAATCACAAAGAAATTTCTGCA 155
|||||
21 CybAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
|||||
156 AATGGAGTCTATGACAGCAAGATGTGGGGTCTCTCTGTTGTAACAAACAAACAGAAA 215
|||||
41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
|||||
216 GGTCTATCTAAGAGCTCAGCTAAGTTTCGGGTTTTCACACGAGTCGAGAACAGCACT 275
|||||

RESULT 17
NSGS2AA 1590 bp mRNA linear PLN 03-AUG-1999
LOCUS N.sylvestris GS-2 mRNA encoding glutamine synthetase.
DEFINITION X66940
ACCESSION X66940
VERSION X66940.1 GI:119744
KEYWORDS glutamate-ammonia ligase; glutamine synthetase.
SOURCE Nicotiana sylvestris (wood tobacco)
ORGANISM Nicotiana sylvestris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 1590)
AUTHORS Becker,T.W., Caboche,M., Carrayol,E. and Hirel,B.
TITLE Nucleotide sequence of a tobacco cDNA encoding plastidic glutamine
synthetase and light inducibility, organ specificity and diurnal
rhythmicity in the expression of the corresponding genes of tobacco
and tomato
JOURNAL Plant Mol. Biol. 19 (3), 367-379 (1992)
FEATURES
source
1..1590
/organism="Nicotiana sylvestris"
/mol_type="mRNA"
/db_xref="taxon:4096"
/tissue_type="leaf"
gene
1..1590
/gene="GS-2"
CDS
67..1365
/gene="GS-2"
/EC_number="6.3.1.2"
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PVKHASLPKWNYSSTQAPGDSVILYPOAIFKDPFRGNNILVICDATTYPAGE
PIPSNKRHAAQIEFDSKVSVEVPWFIEQVETLLQONVKNPLGWPVGVPGTQGPY
LCAGADKSGFDISDAHYKACLYAGINISGTNGVMPQWQVQVGPSPVIGAGDHMC
ARYILRITQAGVVLSDPDKPIEGDRNGACHTNYSYKSMREGGFEVVKAILNLS
LRKHINAYGEGILEKUTGNHTASIDKFSWGVAFRGSIRVGDTEKQKGYLEDR
RPASNMDPYVVVTGLLAETITLWEPTNEALAAQKALKV"
ORIGIN
Alignment Scores: 2.26e-11 Length: 1590
Pred. No.: 179.00 Matches: 37
Percent Similarity: 80.0% Conservative: 11
Best Local Similarity: 61.7% Mismatches: 10
Query Match: 60.3% Indels: 2
DB: 15 Gaps: 1

US-10-628-525A-35 (1-58) x NSGS2AA (1-1590)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
|||||
96 ATGGCACAATATCTTGCACACCCACATACGCGATGCGAGATGAGAAATCACAAAGAAATTTCTGCA 155
|||||
21 CybAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
|||||
156 AATGGAGTCTATGACAGCAAGATGTGGGGTCTCTCTGTTGTAACAAACAAACAGAAA 215
|||||
41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
|||||
216 GGTCTATCTAAGAGCTCAGCTAAGTTTCGGGTTTTCACACGAGTCGAGAACAGCACT 275
|||||

RESULT 18
NSGS2AA 1590 bp mRNA linear PLN 03-AUG-1999
LOCUS N.sylvestris GS-2 mRNA encoding glutamine synthetase.
DEFINITION X66940
ACCESSION X66940
VERSION X66940.1 GI:119744
KEYWORDS glutamate-ammonia ligase; glutamine synthetase.
SOURCE Nicotiana sylvestris (wood tobacco)
ORGANISM Nicotiana sylvestris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 1590)
AUTHORS Becker,T.W., Caboche,M., Carrayol,E. and Hirel,B.
TITLE Nucleotide sequence of a tobacco cDNA encoding plastidic glutamine
synthetase and light inducibility, organ specificity and diurnal
rhythmicity in the expression of the corresponding genes of tobacco
and tomato
JOURNAL Plant Mol. Biol. 19 (3), 367-379 (1992)
FEATURES
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/mol_type="mRNA"
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CDS
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PIPSNKRHAAQIEFDSKVSVEVPWFIEQVETLLQONVKNPLGWPVGVPGTQGPY
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ORIGIN
Alignment Scores: 2.26e-11 Length: 1590
Pred. No.: 179.00 Matches: 37
Percent Similarity: 80.0% Conservative: 11
Best Local Similarity: 61.7% Mismatches: 10
Query Match: 60.3% Indels: 2
DB: 15 Gaps: 1

US-10-628-525A-35 (1-58) x NSGS2AA (1-1590)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
|||||
96 ATGGCACAATATCTTGCACACCCACATACGCGATGCGAGATGAGAAATCACAAAGAAATTTCTGCA 155
|||||
21 CybAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
|||||
156 AATGGAGTCTATGACAGCAAGATGTGGGGTCTCTCTGTTGTAACAAACAAACAGAAA 215
|||||
41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
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216 GGTCTATCTAAGAGCTCAGCTAAGTTTCGGGTTTTCACACGAGTCGAGAACAGCACT 275
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US-10-628-525A-35 (1-58) x AV162466 (1-1665)	
QY	1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIlySerPro 20
Db	86 ATGGGCACATATTTGGCACCCTACTACAAATGGCAGACGAGATTACAAAGAACGCAC 145
QY	21 CysAlaThrProIleThrSerIlyMetTtpSerSerLeuValMetIlyGlnThrIlySer 40
Db	146 ATGCGAAGTCCTATGACGACCAAGATGGGGTCTCTCTGTTGTAACAGACGACAGAA 205
QY	41 -----ValAlaHisSerAlaIlyPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db	206 GGACCAACTAAGACCTCTACTAAATTTAGATGTTGGCCGTCGCAAGTCTGGAAGTTTATACC 265
RESULT 20	
AF019561	1537 bp mRNA linear PLN 01-OCT-1997
LOCUS	Daucus carota clone CGS201 glutamine synthetase (GS2) mRNA, nuclear
DEFINITION	gene encoding chloroplast protein, complete cds.
ACCESSION	AF019561
KEYWORDS	AF019561.1 GI:2454632
SOURCE	Daucus carota (carrot)
ORGANISM	Daucus carota
REFERENCE	1 (bases 1 to 1537)
AUTHORS	Higashi,K. and Kamada,H.
TITLE	A cDNA sequence of carrot glutamine synthetase
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1537)
AUTHORS	Higashi,K. and Kamada,H.
TITLE	Direct Submission
JOURNAL	Submitted (15-AUG-1997) Institute of Biological Sciences, University of Teukuba, Ten-nohdai, 1-1-1, Teukuba, Ibaraki 305, Japan
FEATURES	source
gene	1..1537 /organism="Daucus carota" /mol_type="mRNA" /cultivar="US-Harumakigousun" /db_xref="taxon:4039" /clone="CGS201" /tissue_type="leaf"
CDS	1..1537 /gene="GS2" 17..1315 /gene="GS2" /EC_number="6.3.1.2" /codon_start=1 /product="glutamine synthetase" /protein_id="BAB71693.1" /db_xref="GI:2454633"
ORIGIN	translation="MAQILAPSVOMQMEFTKNSTEVSSMTSKMWSLFLKONKKAPAR SSTKRALAVKSEDTINMEDLLNDVPTDYLKIAYIWIIGTGIDVRSKRTISK FVEHPSELPNWYDGSSTQAPDDSEVILYPQALFKDPFRGNNILVICTYTPQGE PIPTNKRKAQIFSDAKVLGEVPMFGEIETLMOQDVNPLGNVGVGYPGQPY CAAGADKSGFRIDISAHYKACLYAGINISGTNGEVMPCQWBFQVPSVIGIAGDHWC ARYLLERITEQAGVVLTPDKPIDGWNAGCHTNYSTKSMREGGPREVIKKAILNLS LRKHEHISAYGEGNERLTGKHETASIDFSFGVADRGCSI RVGRDTEKEGKGYLEDR RPASNMDPVVTGLLAETLLWEPTLEALAAQLSLNV"
Alignment Scores:	
Pred. No.:	1,48e-10 Length: 1537
Score:	172.00 Matches: 36
Percent Similarity:	70.0% Conservative: 6
Best Local Similarity:	60.0% Mismatches: 16
Query Match:	57.9% Indels: 2
DB:	15 Gaps: 1

US-10-628-525A-35 (1-58) x AF019561 (1-1537)	
QY	1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIlySerPro 20
Db	17 ATGGCTCAGATCTTAGCTCCGTCAGTGAATGGCAATGAGATTACAAAAAATTTCTACC 76
QY	21 CysAlaThrProIleThrSerIlyMetTtpSerSerLeuValMetIlyGlnThrIlySer 40
Db	77 GAAGTAAGTTCAATGACATCAAGATGTGGGTTCTCTATTCTTGAACAAACAGAA 136
QY	41 -----ValAlaHisSerAlaIlyPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db	137 GCACCAGCTAGAAGTTCTACCAATATAGACATTAGCAGTGAAGTCTGAGGATGGCACC 196
RESULT 21	
BNA271909	5232 bp DNA linear PLN 15-APR-2005
LOCUS	Brassica napus gln gene for plastid glutamine synthetase, exons
DEFINITION	1-12.
ACCESSION	AJ271909
VERSION	AJ271909.1 GI:6966929
KEYWORDS	gln gene; glutamine synthetase.
SOURCE	Brassica napus (rape)
ORGANISM	Brassica napus
REFERENCE	1
AUTHORS	Wojtyna,S., Ochs,G. and Wild,A.
TITLE	Cloning and Sequencing of genomic fragments coding for glutamine synthetase of Brassica napus
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 5232)
AUTHORS	Wojtyna,S.
TITLE	Direct Submission
JOURNAL	Submitted (04-FEB-2000) Wojtyna S., Allgemeine Botanik, Johannes Gutenberg-Universitaet, Muellierweg 6, 55099 Mainz, GERMANY
FEATURES	Location/Qualifiers
gene	1..5232 /organism="Brassica napus" /mol_type="genomic DNA" /cultivar="Drakkar (spring rape)" /db_xref="taxon:3708" /clone="Lambda L'2/1" /tissue_type="leaf" /clone_lib="Lambda FIX II" 1..4421 /gene="gln"
promoter	1..1470 /gene="gln"
mRNA	join(1471..1556,2022..2276,2392..2426,2515..2618, 2711..2759,2847..2953,3040..3127,3222..3350,3469..3543, 3630..3881,3961..4021,4107..4421) /gene="gln"
exon	1471..1556 /gene="gln"
intron	/number=1 1557..2021 /gene="gln"
exon	/number=1 2022..2276 /gene="gln"
CDS	join(2030..2276,2392..2426,2515..2618,2711..2759, 2847..2953,3040..3127,3222..3350,3469..3543,3630..3881, 3961..4021,4107..4246) /gene="gln" /EC_number="6.3.1.2" /function="ammonium assimilation" /codon_start=1 /product="glutamine synthetase" /protein_id="CAB72423.1"

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NKEARAAEIPFSNKKVNEEIPWFGIEQEYTLLOPNVNPWPLGNPVGAPGGPYCGVG
AEKSGWRDSDAHYKACLAGINISGTNGEVMPCQWFEQVGPSPVRIEAGDHVWCARYL
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2847..2953,3040..3127,3222..3350,3469..3543,3630..3881,
3961..4021,4107..4243)
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/EC number="6.3.1.2"
2277..2391
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2392..2426
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Best Local Similarity: 49.2% Mismatches: 14
Query Match: 42.4% Indels: 4
DB: 15 Gaps: 2

US-10-628-525A-35 (1-58) x BNA271909 (1-5232)

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QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 2090 ATTGCA-----TCGTCAAAGTATGGAATCGGTTGTGTGAACAGAAACAG 2140
QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr 58
DB 2141 AGCAGCGCAAGTCAGAGCTTCAAGTGTGGCTTCAATCTGTATACAGCACA 2197

RESULT 22
ENGLUS
LOCUS B.napus mRNA for plastidic glutamine synthetase isoform (BnGSRL-1)
DEFINITION related to the A-genome type of Brassica campestris.
ACCESSION X72751.1 GI:296222
VERSION X72751.1
KEYWORDS glutamine synthetase.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 1575)
AUTHORS Ochs,G., Schock,G. and Wild,A.
TITLE Chloroplastic glutamine synthetase from Brassica napus
JOURNAL Plant Physiol. 103 (1), 303-304 (1993)
PUBMED 7911583
REFERENCE 2
AUTHORS Ochs,G., Schock,G., Trischler,M., Kosemund,K. and Wild,A.
TITLE Complexity and expression of the glutamine synthetase multi-gene
family in the amphidiploid crop Brassica napus
JOURNAL Plant Mol. Biol. 39 (3), 395-405 (1999)
PUBMED 10092169
REFERENCE 3 (bases 1 to 1575)
AUTHORS Ochs,G.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-1993) G. Ochs, Inst fuer Allgemeine Botanik, Abt
Prof Dr A Wild, Johannes Gutenberg - Universitaet Mainz, Saarstr
21, 6500 Mainz, FRG
FEATURES
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Pred. No.: 7,3e-05 Length: 1575
Score: 124.00 Matches: 29
Percent Similarity: 69.5% Conservative: 12
Best Local Similarity: 49.2% Mismatches: 14
Query Match: 41.8% Indels: 4
DB: 15 Gaps: 2
US-10-628-525A-35 (1-58) x BNGLSL2 (1-1575)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 95 ATGGCGCAGATCTTGGCAGCTTCTCCAAATGTCAAATGAGATTGACTAAACCCAGCTCC 154
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 155 ATTGCA-----TCGTCAAGTATGGAACCTGGTGTGTGTAACAGAGAAACAG 205
QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 206 AGCAGCAGCAAGTCAGAGCTTCAAGATGATGGCTCTCCAAATCTGATAACAGCACA 262
RESULT 23
BNGSL2
LOCUS
DEFINITION
Brassica napus mRNA for plastidic glutamine synthetase isoform
(BNGSL2).
ACCESSION
Y12458
VERSION
Y12458.1 GI:1934753
KEYWORDS
gln gene; glutamine synthetase; plastidic isoform.
SOURCE
Brassica napus
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1
Ocho,G., Schock,G., Trischler,M., Kosemund,K. and Wild,A.
AUTHORS
TITLE
Complexity and expression of the glutamine synthetase multigene
family in the amphidiploid crop Brassica napus
Plant Mol. Biol. 39 (3), 395-405 (1999)
10092169
JOURNAL
PUBMED
2 (bases 1 to 1597)
REFERENCE
Ocho,G.
Direct Submission
TITLE
Submitted (08-APR-1997) G. Ocho, Institut fuer Allgemeine Botanik,
Abteilung Prof. Dr. H. Paulsen, Johannes Gutenberg - Universitaet
Mainz, D-55099 Mainz, FRG
JOURNAL
FEATURES
Location/Qualifiers
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/lab_host="E.coli"
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1. .1597
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97. .1383
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244. .1380
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/product="plastidic glutamine synthetase"
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polyA_site
/gene="gln"
ORIGIN
Alignment Scores:
Pred. No.: 7,4e-05 Length: 1597
Score: 124.00 Matches: 30
Percent Similarity: 70.5% Conservative: 13
Best Local Similarity: 49.2% Mismatches: 10
Query Match: 41.8% Indels: 8
DB: 15 Gaps: 3
US-10-628-525A-35 (1-58) x BNGSL2 (1-1597)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 97 ATGGCGCAATCTTGGCAGCTTCTCCAAATGTCAAATGAAATGACTAAACCCAGCCCC 156
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 157 ATTGCA-----TCTTCAAGTATGGAAGCTTTAAAGCATGGCTCTCCAAATCTGATAACAG 207
QY 41 ValAlaHisSerAlaLys-----PheArgValMetAlaValAsnSerGluAsnGly 57
Db 208 -----AACAGCAGCAAACTCAGAGCTTTAAAGCATGGCTCTCCAAATCTGATAACAGT 261
QY 58 Thr 58
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3'UTR

ORIGIN

Alignment Scores:  
Pred. No.: 0.000717 Length: 1324  
Score: 115.00 Matches: 28  
Percent Similarity: 66.1% Conservative: 11  
Best Local Similarity: 47.5% Mismatches: 18  
Query Match: 38.7% Indels: 2  
DB: 15 Gaps: 2

US-10-628-525A-35 (1-58) x AY122977 (1-1324)

Qy 1 MetAlaGlnIleLeuAlaProSerThrGlnTTPGlnMetArgIleThrLysThrSerPro 20  
|||||  
Db 1 ATGGCTCAGATCTTAGCAGCTTCTCCACATGTCAGATGAGTGCTTAACACTCATCA 60  
|||||  
Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
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Db 61 GTCATTGTCATCA---TCATCCCAAGTTATGAGCTCTGTGTGTTGAAACAGAGAGCAG 117  
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Qy 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluHsnGlyThr 58  
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Db 118 AGCAACACAAAGTCAGAGGCTTAGAGTCTTGCTCTCAATCTGATAACAGTACT 174  
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RESULT 26  
AF428461 1473 bp mRNA linear PLN 18-OCT-2001  
LOCUS  
Arabidopsis thaliana AT5g35630/MJE4\_9 mRNA, complete cds.  
DEFINITION  
AF428461.1 GI:16226676  
VERSION  
FLI CDNA.  
KEYWORDS  
Arabidopsis thaliana (thale cress)  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 1473)  
Cheuk,R., Chen,H., Kim,C.J., Koesema,B., Meyers,M.C., Banh,J.,  
Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,  
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,  
Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,  
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,  
Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,  
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,  
Davis,R.W., Theologis,A. and Ecker,J.R.  
Arabidopsis cDNA clones  
Unpublished

2 (bases 1 to 1473)  
Cheuk,R., Chen,H., Kim,C.J., Koesema,B., Meyers,M.C., Banh,J.,  
Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,  
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,  
Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,  
Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,  
Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,  
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,  
Davis,R.W., Theologis,A. and Ecker,J.R.  
Direct Submission

Submitted (05-OCT-2001) Salk Institute Genomic Analysis Laboratory  
(SIGNAL), Plant Biology Laboratory, The Salk Institute for  
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,  
USA

RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN  
Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,  
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
Hayashizaki,Y. and Shinozaki,K.

COMMENT

The Salk, Stanford, PGC (SSP) Consortium members carried out the  
sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H.,  
Kim,C.J., Koesema,B., Meyers,M.C., Shinn,P., Bath,J., Bowser,L.,  
Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,  
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,  
Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A.,  
Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S.,  
Davis,R.W., Theologis,A., and Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to  
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)  
contributed equally to this work as PIs.

FEATURES

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3'UTR

ORIGIN

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Query Match: 38.7% Indels: 2  
DB: 15 Gaps: 2

US-10-628-525A-35 (1-58) x AF428461 (1-1473)

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Db 165 GTCATTGTCATCA---TCATCCCAAGTTATGAGCTCTGTGTGTTGAAACAGAGAGCAG 221  
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Qy 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluHsnGlyThr 58  
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RESULT 27

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LOCUS

DEFINITION

ACCESSION

VERSION

FLI CDNA.

KEYWORDS

SOURCE

ORGANISM

AY081252 1519 bp mRNA linear PLN 24-MAR-2002  
Arabidopsis thaliana glutamate-ammonia ligase, chloroplast  
(AT5g35630) mRNA, complete cds.

AY081252

AY081252.1 GI:19698810

FLI CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

REFERENCE	rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 1519) Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M., Palm, C. J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S. X., Narusaka, M., Pham, P. K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shim, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R. W.
TITLE	Direct Submission
JOURNAL	Submitted (26-FEB-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT	e-mail for correspondence: arab@sequence.stanford.edu
	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
	The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAPL cDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C. J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M. K., Kim, C., Lin, J., Liu, S. X., Pham, P. K., Sakano, H., Shim, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R. W.
	Nguyen, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R. W. (SSP/Stanford) contributed equally to this work as PIs.
FEATURES	Location/Qualifiers
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	Db 119 GTCAATGTCATCA---TCATCCAAAGTTATGAGGCTCTGTGTGTTGAACAGAGAGCAG 175 QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr 58       Db 176 AGCAACAAACAAAGTCAGAGCTTTAGAGTTCTTGCTCTCCAAATCTGATAAGACTACT 232 RESULT 28 S69727 LOCUS DEFINITION light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, mRNA, 1548 nt]. ACCESSION S69727.1 GI:240069 VERSION S69727.1 GI:240069 KEYWORDS Arabidopsis thaliana (thale cress) SOURCE Arabidopsis thaliana ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis. REFERENCE AUTHORS Peterman, T. K. and Goodman, H. M. TITLE The glutamine synthetase gene family of Arabidopsis thaliana: light-regulation and differential expression in leaves, roots and seeds Mol. Gen. Genet. 230 (1-2), 145-154 (1991) JOURNAL PUBMED 1684022 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsg 69727] from the original journal article. FEATURES source 1..1548 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" 1..1548 /gene="light-regulated glutamine synthetase isoenzyme" 72..1364 /gene="light-regulated glutamine synthetase isoenzyme" /product="light-regulated glutamine synthetase isoenzyme" /codon_start=1 /protein_id="AAB20558.1" /db_xref="GI:240070" /translation="MAQILAASTCOMRVKHSVIASSKLSWVVKQKQSNKKV RGRFVLALQSDNSTVNRVETLLNLTDPKYSDDRIAYIWIIGSGIDLRKSRITKPV EDPSLPKNYDGSSTGQAPGDSVILYPOAIFRDPFRGNNILICDTWTAPGPI PTNKRAAAEISFNKVSQGVFWFIEQYTLQQNVKPLGWPVGFPGQPPYCG VGADKTIGRDISDAHYKACLYAGINISGTNGVMPQGVFGVPSVIGIDAGDHWCAR YLLERITEQAGVVLIDPKPIEGDWNAGCHTNYSTKSMREGGFVVKAILNLSLR HKEHISAYGEGNERLITGKHETASIDQPSGWNARCCSIRVRGDTAKGKGYLEDRRP ASNMDPYIVTSLAETLLWEPTLEAALAAQKLSLV"
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LOCUS	Arabidopsis thaliana AT5g35630/MJE4_9	mRNA, complete cds.			
DEFINITION	AF428319				
ACCESSION	AF428319.1	GI:16226743			
VERSION	FLI CDNA.				
KEYWORDS	Arabidopsis thaliana (thale cress)				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	1 (bases 1 to 1570)				
AUTHORS	Cheuk,R., Chen,H., Kim,C.J., Koesema,B., Meyers,M.C., Banh,J., Bower,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu.G., Yu.S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.				
TITLE	Arabidopsis cDNA clones				
JOURNAL	2 (bases 1 to 1570)				
REFERENCE	Cheuk,R., Chen,H., Kim,C.J., Koesema,B., Meyers,M.C., Banh,J., Bower,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu.G., Yu.S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.				
AUTHORS	Direct Submission				
TITLE	Submitted (05-OCT-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA				
JOURNAL	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-length CDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.				
COMMENT	The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Koesema,B., Meyers,M.C., Shinn,P., Banh,J., Bower,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu.G., Yu.S., Davis,R.W., Theologis,A., and Ecker,J.R.				
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ORIGIN	3'UTR				
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Percent Similarity:	47.5%	Mismatches:	18		
Best Local Similarity:	38.7%	Indels:	2		
Query Match:	15	Gaps:	2		
DB:	US-10-628-525A-35 (1-58) x AF428319 (1-1570)				
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Db	105 ATGGCTCAGATCTTAGCAGCTTCTCCACATGTCAGATGAGAGTGCCTAAACACTCATCA 164				
QY	21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40				
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LOCUS	Arabidopsis thaliana putative glutamate-ammonia ligase precursor, chloroplast (At5g35630) mRNA, complete cds.				
DEFINITION	AY091114				
ACCESSION	AY091114.1	GI:20268720			
VERSION	FLI CDNA.				
KEYWORDS	Arabidopsis thaliana (thale cress)				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	1 (bases 1 to 1580)				
AUTHORS	Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu.G., Bower,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.				
TITLE	Arabidopsis Full Length cDNA Clones				
JOURNAL	2 (bases 1 to 1580)				
REFERENCE	Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu.G., Bower,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.				
AUTHORS	Direct Submission				
TITLE	Submitted (20-MAR-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA				
JOURNAL	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-length CDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.				
COMMENT					



The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

Search completed: April 1, 2006, 15:18:40  
Job time : 1178.21 secs

Yamada, K. (SSP/PGECC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGECC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

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#### ORIGIN

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Percent Similarity:	66.1%	Conservative:	11	
Best Local Similarity:	47.5%	Mismatches:	18	
Query Match:	38.7%	Indels:	2	
DB:	15	Gaps:	2	

US-10-628-525A-35 (1-58) x AY091114 (1-1580)

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Qy	21	CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys	40
Db	167	GTCATTGCATCA---TCATCCAAAGTTATGGAGCTCTGTGTGTGTTGAACACAGAGAAGCAG	223
Qy	41	ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr	58
Db	224	AGCAACACAAAGTCAGAGCTTTAGAGTTCITGTGCTCTCCATCTGATAACAGTACT	280

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 00:15:06 ; Search time 136.553 Seconds  
(without alignments)  
2830.777 Million cell updates/sec

Title: US-10-628-525a-35

Perfect score: 297

Sequence: 1 MAQILAPSTQWQRIITKTP.....KKVAHSAKFRVMAVNSENGT 58

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abas/ABSSWEB spool/US10628525/runat\_31032006\_095109\_16557/app\_query.fasta\_1  
-DB=N Geneseq -QMT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blowsum2 -TRANS=human40.cdi -LIST=150  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs06h  
-USER=US10628525 @CGN 1.1 1404 @runat\_31032006\_095109\_16557 -NCPU=6 -ICPU=3  
-NO MAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 21:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271	91.2	1589	2 AAO12539	Aaql2539 GS2 promo
2	268	90.2	1601	2 AAO34621	Aaql34621 Chloropla
3	199	67.0	589	10 ADK54299	Adk54299 Plant DNA
4	199	67.0	1633	10 ADK58446	Adk58446 Plant DNA

5	174.5	58.8	1508	13	ADR65314	Adr65314 Cotton cd
6	155.5	52.4	1519	10	ADD17886	Add17886 DNA (Seqi
7	155.5	52.4	3895	10	ADK58449	Adk58449 Plant DNA
8	115	38.7	487	10	ADR82003	Adr82003 Arabidops
9	115	38.7	1598	3	AAC46992	Aac46992 Arabidops
10	115	38.7	2103	3	AAC49096	Aac49096 Arabidops
11	73	24.6	1543	6	ABL53628	Ab153628 Breast pr
12	73	24.6	2418	6	ABL53629	Ab153629 Breast pr
13	73	24.6	2445	6	ABL53627	Ab153627 Breast pr
C 14	70.5	23.7	386	10	AD856392	Ad856392 Toxicity-
C 15	70.5	23.7	386	10	AD850884	Ad850884 Primary r
C 16	70.5	23.7	386	14	AD25897	Ad25897 Novel cel
C 17	70.5	23.7	460	10	AD858674	Ad858674 Rat gene
C 18	70.5	23.7	460	10	AD858670	Ad858670 Rat gene
C 19	69.5	23.4	347	8	ABX44826	Abx44826 Bovine ES
C 20	69.5	23.4	1062	5	AAH66383	Aah66383 C glutami
C 21	69.5	23.4	1192	11	AD165758	Ad165758 C. glutam
C 22	69.5	23.4	1539	4	AAF71202	Aaf71202 Corynebac
C 23	69.5	23.4	1539	4	AAF71203	Aaf71203 Corynebac
C 24	69.5	23.4	34980	5	AAH68528	Aah68528 C glutami
C 25	69	23.2	1950	12	ADQ37186	Adq37186 Cell prol
C 26	68	22.9	86149	12	ADQ97278	Adq97278 Human can
C 27	68	22.9	110000	14	AEA61124_0	Aea61124 Human SLC
C 28	67.5	22.7	421	9	ACH47744	Ach47744 Human inf
C 29	67.5	22.7	939	4	AAI63931	Aai63931 Human pol
C 30	67.5	22.7	939	4	AAI63932	Aai63932 cDNA enco
C 31	67.5	22.7	939	4	ABK43906	Abk43906 DNA enco
C 32	67.5	22.7	939	12	AD154293	Ad154293 cDNA enco
C 33	67.5	22.7	939	12	ADM24482	Adm24482 Human PRO
C 34	67.5	22.7	1338	3	AAZ39568	Aaz39568 Human cal
C 35	67.5	22.7	1339	4	ABK43612	Abk43612 DNA enco
C 36	67.5	22.7	1339	12	ADI53999	Adi53999 cDNA enco
C 37	67.5	22.7	1346	4	AAI63854	Aai63854 Human pol
C 38	67.5	22.7	1346	12	ADM24405	Adm24405 Human PRO
C 39	67.5	22.7	1658	3	AACT7159	Aac77159 Human ORF
C 40	67.5	22.7	2103	4	AAH4175	Aah4175 Human ORF
C 41	67.5	22.7	3739	4	AACT75928	Aac75928 Human ORF
C 42	67.5	22.7	174424	6	ABL68122	Ab168122 Ovary can
C 43	67.5	22.7	181343	12	ADQ19573	Adq19573 Human sof
C 44	67	22.6	381	8	ABX41787	Abx41787 Bovine ES
C 45	67	22.6	1366	6	ABK63620	Abk63620 Rat seque
C 46	67	22.6	1366	12	ADP73022	Adp73022 Renal tox
C 47	67	22.6	1926	11	ADJ27276	Adj27276 Mouse HSP
C 48	67	22.6	1929	4	AAI10678	Aai10678 Murine hs
C 49	67	22.6	1929	11	ADJ27274	Adj27274 Mouse HSP
C 50	67	22.6	3783	10	ADP30533	Adp30533 Rat angio
C 51	67	22.6	76994	12	ADP64454	Adp64454 Sorangium
C 52	67	22.6	158405	13	ADV35010	Adv35010 Murine CD
C 53	67	22.6	158405	13	ADV35010	Adv35010 Murine CD
C 54	66.5	22.4	1167	6	ABL53626	Ab153626 Breast pr
C 55	66.5	22.4	1596	3	AAZ53282	Aaz53282 Neisseria
C 56	66.5	22.4	49646	3	AAA81457	Aaa81457 N. mening
C 57	66.5	22.4	110000	3	AAA81490_06	Continuation (7 of
C 58	66.5	22.4	34980	3	AAF21608	Aaf21608 Neisseria
C 59	66	22.2	503	10	ADK12028	Adk12028 Breast ca
C 60	66	22.2	525	6	ABL63576	Ab163576 Breast ca
C 61	66	22.2	525	6	ABL67454	Ab167454 Thyroid c
C 62	66	22.2	525	6	ABN97056	Abn97056 Gene #355
C 63	66	22.2	604	6	ABT10312	Abt10312 Human bre
C 64	66	22.2	1172	12	ADO42254	Ado42254 Human NOV
C 65	66	22.2	1189	12	ADO42252	Ado42252 Human NOV
C 66	66	22.2	1189	12	ADO42258	Ado42258 Human NOV
C 67	66	22.2	1191	12	ADO42248	Ado42248 Human NOV
C 68	66	22.2	1191	12	ADO42244	Ado42244 Human NOV
C 69	66	22.2	1198	12	ADO42256	Ado42256 Human NOV
C 70	66	22.2	1207	12	ADO42250	Ado42250 Human NOV
C 71	66	22.2	1230	12	ADO42246	Ado42246 Human NOV
C 72	66	22.2	1230	12	ADO42679	Ado42679 Human NOV
C 73	66	22.2	1231	12	AD46541	Aad46541 Human dia
C 74	66	22.2	1231	12	AD46541	Aad46541 Human DGA
C 75	66	22.2	1233	6	AD46549	Aad46549 Human DGA
C 76	66	22.2	1233	6	AD46549	Aad46549 Human DGA
C 77	66	22.2	1303	2	AAZ33556	Aaz33556 Human bre

78	66	22.2	1459	2	AAT29043	Aat29043 Oerskovia
79	66	22.2	1510	13	ADR26804	Adr26804 Breast ca
80	66	22.2	1570	3	AAA37103	Aaa37103 Human PRO
81	66	22.2	1570	4	AAE54409	Aaf54409 Primer #8
82	66	22.2	1570	4	AAS46092	Aaa46092 Human DNA
83	66	22.2	1570	8	ACA89542	ACA89542 cDNA enco
84	66	22.2	1570	8	ACA73552	ACA73552 Human sec
85	66	22.2	1570	8	ACA05867	ACA05867 Human sec
86	66	22.2	1570	8	ACA66701	ACA66701 cDNA enco
87	66	22.2	1570	8	ACF20276	Acf20276 Human sec
88	66	22.2	1570	8	ACFI19662	Acfi19662 Human sec
89	66	22.2	1570	8	ACD21950	Acdd21950 Human sec
90	66	22.2	1570	8	ACFI13115	Acfi13115 Human sec
91	66	22.2	1570	8	ACD25218	Acdd25218 Human sec
92	66	22.2	1570	8	ACF00267	Acf00267 Human sec
93	66	22.2	1570	8	ACA72334	Acad72334 Novel hum
94	66	22.2	1570	8	ACD04848	Acdd04848 Novel hum
95	66	22.2	1570	8	ACD18309	Acdd18309 Human sec
96	66	22.2	1570	8	ACD08316	Acdd08316 Human sec
97	66	22.2	1570	8	ACA88750	ACA88750 Novel hum
98	66	22.2	1570	8	ACA70192	ACA70192 Human sec
99	66	22.2	1570	8	ACD12414	Acdd12414 Novel hum
100	66	22.2	1570	8	ACC74329	Acc74329 Human sec
101	66	22.2	1570	8	ACD15957	Acdd15957 Human sec
102	66	22.2	1570	8	ACD25525	Acdd25525 Novel hum
103	66	22.2	1570	8	ACD18002	Acdd18002 Human sec
104	66	22.2	1570	8	ACC88289	Acc88289 Human sec
105	66	22.2	1570	8	ACD21643	Acdd21643 Human sec
106	66	22.2	1570	8	ACD18710	Acdd18710 Human sec
107	66	22.2	1570	8	ABX98320	Abx98320 Human cDN
108	66	22.2	1570	8	ACD14071	Acdd14071 Human PRO
109	66	22.2	1570	8	ACD09851	Acdd09851 Human sec
110	66	22.2	1570	8	ACC88596	Acc88596 Human sec
111	66	22.2	1570	8	ACD21336	Acdd21336 Human sec
112	66	22.2	1570	8	ABX75708	Abx75708 Human cDN
113	66	22.2	1570	8	ABX97911	Abx97911 Human PRO
114	66	22.2	1570	8	ACA97387	ACA97387 Novel hum
115	66	22.2	1570	8	ACA57850	ACA57850 Human PRO
116	66	22.2	1570	8	ACD14378	Acdd14378 Human PRO
117	66	22.2	1570	8	ACC91161	Acc91161 Human sec
118	66	22.2	1570	8	ACC88903	Acc88903 Human sec
119	66	22.2	1570	8	ACD07100	Acdd07100 Human PRO
120	66	22.2	1570	8	ACA67551	ACA67551 Human PRO
121	66	22.2	1570	8	ACC81606	Acc81606 Human sec
122	66	22.2	1570	8	ACC89210	Acc89210 Human sec
123	66	22.2	1570	8	ACC86566	Acc86566 Human sec
124	66	22.2	1570	8	ACC89824	Acc89824 Human sec
125	66	22.2	1570	8	ACC93003	Acc93003 Human sec
126	66	22.2	1570	8	ACA72631	ACA72631 Human PRO
127	66	22.2	1570	8	ACA89149	ACA89149 Human sec
128	66	22.2	1570	8	ACA69885	ACA69885 Human sec
129	66	22.2	1570	8	ACA97028	ACA97028 Novel hum
130	66	22.2	1570	8	ACA91024	ACA91024 Novel hum
131	66	22.2	1570	8	ACA70806	ACA70806 Human sec
132	66	22.2	1570	8	ACA95316	ACA95316 Novel hum
133	66	22.2	1570	8	ACC86259	Acc86259 Human sec
134	66	22.2	1570	8	ACC90131	Acc90131 Human sec
135	66	22.2	1570	8	ACD12739	Acdd12739 Human sec
136	66	22.2	1570	8	ACFI19969	Acfi19969 Human sec
137	66	22.2	1570	8	ABX76913	Abx76913 Human PRO
138	66	22.2	1570	8	ACA73245	ACA73245 Novel hum
139	66	22.2	1570	8	ACA68788	ACA68788 Novel hum
140	66	22.2	1570	8	ACA74632	ACA74632 cDNA enco
141	66	22.2	1570	8	ACA70499	ACA70499 Human sec
142	66	22.2	1570	8	ACD14685	Acdd14685 Human PRO
143	66	22.2	1570	8	ACA68357	ACA68357 Novel hum
144	66	22.2	1570	8	ABX98822	Abx98822 Novel hum
145	66	22.2	1570	8	ACC81299	Acc81299 Human sec
146	66	22.2	1570	8	ACA95623	ACA95623 Novel hum
147	66	22.2	1570	8	ACD04541	Acdd04541 Novel hum
148	66	22.2	1570	8	ACC87982	Acc87982 Human sec
149	66	22.2	1570	8	ACFI12644	Acfi12644 Human sec
150	66	22.2	1570	8	ACA96359	ACA96359 Human PRO

ALIGNMENTS

RESULT 1

AAQ12539

AAQ12539 standard; DNA; 1589 BP.

ID AAQ12539

XX AAQ12539;

AC AAQ12539;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 25-SEP-1991 (first entry)

XX

DE GS2 promoter element.

XX

KW Glutamine synthetase isoenzyme; photosynthesis; light induction;

KW tissue specific; transgenic plants; transcription; ss.

XX

OS Pisum sativum; cv "Sparkle".

XX

PN WO9109050-A.

XX

PD 27-JUN-1991.

XX

PF 08-DEC-1989; 89US-00448036.

XX

PR 08-DEC-1989; 89US-00448036.

XX

(UYRQ ) UNIV ROCKEFELLER.

XX

PI Coruzzi G, Edwards J, Walker EI;

XX

DR WPI; 1991-208085/28.

XX

PT Organ-specific, light-inducible plant promoter sequences - from Pisum

PT sativum glutamine synthetase isoenzyme(s), used to introduce herbicide

PT and pathogen resistance.

XX

PS Claim 1; Fig 5A; 70pp; English.

XX

CC The promoter was isolated from the nuclear gene for chloroplast GS2

CC glutamine synthetase. It is specific for photosynthetically active cells

CC and is light inducible. It can be used to control the expression of

CC glutamine synthetase as well as heterologous proteins in a tissue

CC specific and/or light inducible manner. This control can be applied to

CC e.g. manipulation of nutritional requirements or to induction of

CC resistance to herbicides, or viral or pathogen infection. See also

CC AAQ12540 and AAQ12541. (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 1589 BP; 548 A; 252 C; 219 G; 570 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:

Score:

Length: 1589

Matches: 53

Conservative: 0

Percent Similarity: 100.0%

Mismatches: 0

Best Local Similarity: 100.0%

Indels: 0

Query Match: 91.2%

Gaps: 0

DB:

US-10-628-525A-35 (1-58) x AAQ12539 (1-1589)

OY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20

DB 1431 ATGGCGCGAGATTTTGGCACCTTCGACGCAATGGCAGATGAGAAATCACAAAACCTCTCT 1490

OY 21 CysAlaThrProIleThrSerIysMetTrpSerSerLeuValMetIysGlnThrIysLys 40

DB 1491 TGTGCAATCCCAATCACATCAAGATGGAGTTCTTTGGTTATGAAACAATAAGAAA 1550

OY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsn 53

Db 1551 GTTGGCAGTTCTGCTAAATTTAGATTATGGCAGTCAAC 1589

RESULT 2  
AAQ34621 standard; DNA; 1601 BP.

ID AAQ34621 standard; DNA; 1601 BP.  
XX XX  
AC AAQ34621;  
XX XX  
25-MAR-2003 (revised)  
DT DT  
12-MAY-1993 (first entry)  
XX XX  
DE Chloroplast GS2 glutamine synthase promoter element.  
XX XX  
KW Plant organ specific; light inducible; heterologous protein; expression.  
XX XX  
OS Pisum sativum.  
XX XX  
PN WO9222582-A1.  
XX XX  
PD 23-DEC-1992.  
XX XX  
PF 12-JUN-1992; 92WO-US005170.  
XX XX  
PR 13-JUN-1991; 91US-00715751.  
XX XX  
PA (UYRQ ) UNIV ROCKEFELLER.  
XX XX  
PI Coruzzi GM, Edwards JW, Walker EL, Brears T;  
XX XX  
DR WPI; 1993-018084/02.  
XX XX  
PT Pure GS2, GS3A and GS3B promoter elements - which are light inducible or  
PT phloem active, used, e.g. to impart herbicide or pathogen resistance.  
XX XX  
PS Claim 1; Page 54; 104pp; English.  
XX XX  
CC The sequence is that of the chloroplast GS2 glutamine synthetase promoter  
CC element. It is inducible by light and directs levels of transcription in  
CC photosynthetic cells of leaves and in non-photosynthetic cells of leaves  
CC and in non-photosynthetic cells of the root tip. It may also be used to  
CC control expression of heterologous proteins, e.g. for the manipulation of  
CC nutritional requirements and the induction of resistance to herbicides  
CC and pathogens, e.g. viruses. It may be used to design optimal gene fusion  
CC systems and in the identification of promoter elements associated with  
CC glutamine synthetase genes from any species of plant, bacteria or virus  
XX XX  
SQ Sequence 1601 BP; 551 A; 259 C; 217 G; 574 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.41e-25 Length: 1601  
Score: 268.00 Matches: 52  
Percent Similarity: 100.0% Conservative: 1  
Best Local Similarity: 98.1% Mismatches: 0  
Query Watch: 90.2% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x AAQ34621 (1-1601)

Cy 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 1443 ATGGCGCAGATTTTGCCACCTTCGACGCAATGCCAGATGAGCATCACAAAACCTCTCCT 1502  
Cy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 1503 TGTCGAACCTCCAATCACATCAAAGATGTGGACTCTTTGGTTATGAACAACAACTAAGAAA 1562  
Cy 41 ValAlaHisSerAlaLysPheArgValMetAlaValAen 53  
Db 1563 GTTGGCAGTTCTGCTAAATTTAGATTATGGCAGTCAAC 1601

RESULT 3  
ADK54299

ID	ADK54299 standard; DNA; 589 BP.
XX	
AC	ADK54299;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Plant DNA sequence which confers altered metabolic characteristic #1682.
XX	
KW	altered metabolic characteristic; plant; acid metabolism;
KW	alcohol metabolism; fatty acid metabolism;
KW	branched fatty acid metabolism; alkalioid metabolism;
KW	amino acid metabolism; ester metabolism; glyceride metabolism;
KW	phenolic metabolism; carbohydrate metabolism; sterol metabolism;
KW	terpene metabolism; isoprenoid metabolism; alkene metabolism;
KW	alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
KW	quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX	
OS	Unidentified.
XX	
XX	
PN	WO2003020936-A1.
XX	
PD	13-MAR-2003.
XX	
PF	30-AUG-2002; 2002WO-US027884.
XX	
PR	31-AUG-2001; 2001US-0316471P.
XX	
PA	(DOWC ) DOW CHEM CO.
PA	(DOWC ) DOW AGROSCIENCES LLC.
PI	Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
PI	Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX	
DR	WPI; 2003-313091/30.
XX	
PT	Novel genes that confer altered metabolic characteristics in Nicotiana
PT	glauca plants, useful for altering the levels of metabolites e.g.
PT	acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols
XX	
PS	Claim 1; SEQ ID NO 1682; 2576pp; English.
XX	
CC	The invention comprises DNA sequences which confer an altered metabolic
CC	characteristic when they are expressed in a plant. The DNA sequences of
CC	the invention are useful for producing plants with an altered metabolic
CC	characteristic such as: altered acid metabolism, alcohol metabolism,
CC	fatty acid metabolism, branched fatty acid metabolism, alkalioid or other
CC	base metabolism, altered amino acid metabolism, altered ester metabolism
CC	altered glyceride metabolism, altered phenolic metabolism, altered
CC	carbohydrate metabolism, altered sterol, oxygenated terpene, or
CC	isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC	metabolism, ketone or quinone metabolism. The DNA sequences of the
CC	invention may be used to provide disease resistance in a plant and gene
CC	shuffling or sexual PCR procedures. The present nucleic acid represents a
CC	DNA sequence of the invention.
XX	
SQ	Sequence 589 BP; 181 A; 127 C; 127 G; 154 T; 0 U; 0 Other;

```

US-10-628-525A-35 (1-58) x AAQ34621 (1-1601)

Qy 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
    |||||
Db 1443 ATGGCGCAGATTTTGGCACCTTCACACGCNATGGCAGATGAGNATCACAAAACCTCTCCT 1502
    |||||

Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
    |||||:::
Db 1503 TGTGCAACTCCAAATCACATCAAGNATGGGACTCTTTGGTTATGAAACAACAACTAAGAAA 1562
    |||||

Qy 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsn 53
    |||||
Db 1563 GTTGGGCATCTCGTTAAATTTAGAGTTATGGCAGTCAAC 1601
    |||||

RESULT 3
ADKS4299

```

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Alignment Scores:
Pred. No.:      6.24e-17      Length:      589
Score:          199.00      Matches:      40
Percent Similarity: 83.3%      Conservative: 10
Best Local Similarity: 66.7%      Mismatches:  8
Query Match:      67.0%      Indels:      2
DB:              10      Gaps:        1

US-10-628-525A-35 (1-58) x ADK54299 (1-589)

Qy      1  MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
      |||||
Db      60  ATGGCTCAGATCTTGGCTCCATCTGGCAATGGCAGATGAGTACAAAGAGCTCAACA 11
      |||||

Qy      21  CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
      |||||

```



CC and/or content, improving yield by modification of carbohydrate, nitrogen  
 CC or phosphorus use and/or uptake, or improving yield by providing improved  
 CC plant growth and development under at least one stress condition. The  
 CC polynucleotide and polypeptide may also be used in recombinant DNA  
 CC constructs, in physical arrays of molecules, as plant breeding markers,  
 CC or in computer-based storage and analysis systems. The present sequence  
 CC is a cotton plant cDNA of the invention. NOTE: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequences.html?DocID=20040181830. However only 6585  
 CC polynucleotide sequences were available, the remaining 52213  
 CC polynucleotides and all 58798 protein sequences were not present.

SQ Sequence 1508 BP; 426 A; 343 C; 360 G; 379 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4.12e-13 Length: 1508  
 Score: 174.50 Matches: 38  
 Percent Similarity: 76.7% Conservatives: 8  
 Best Local Similarity: 63.3% Mismatches: 11  
 Query Match: 58.8% Indels: 3  
 DB: 13 Gaps: 2

US-10-628-525A-35 (1-58) x ADR65314 (1-1508)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 DB 135 ATGGCACAGCTTTTAGCACCTCAACTCAATGGCAATGACACTACCAAGACCTCAACC 194  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 DB 195 TATGGAAAGTCCCAATGCAAAAATGTGGAGTCTCTGTACTGAAACAGAACAGAA 254  
 QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaSerGluAenGlyThr 58  
 DB 255 GGAGCTGCTAAAGCTCTGCAAGTTTAAAGTGGTTCCTG---ICTGAACACGCACT 311

# RESULT 6

ADL17886  
 ID ADD17886 standard; DNA; 1519 BP.

AC ADD17886;

DT 15-JAN-2004 (first entry)

DE DNA (SeqID 1954) that confers an altered visual phenotype in plants.  
 KW ds: visual phenotype; plant; architecture; leaf surface; chlorotic;  
 KW bleaching; etching; wet leaf; stunting; elongation; texture;  
 KW agronomic trait; growth regulation; dwarf variety; insect resistance;  
 KW heat stress; transgenic.

OS Unidentified.

PN WO2003020741-A1.

PD 13-MAR-2003.

PF 30-AUG-2002; 2002WO-US027880.

PR 31-AUG-2001; 2001US-0316326P.

PA (DOWC) DOW CHEM CO.

PA (DOWC) DOW AGROSCIENCES LLC.

PI Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;

XX WPI; 2003-300858/29.

XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae  
 PT sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for  
 PT conferring altered visual phenotypes in plants.

XX

PS Claim 1; SEQ ID NO 1954; 517pp; English.

XX This invention relates to the identification and isolation of novel  
 CC nucleic acid molecules that confer altered visual phenotypes in plants.  
 CC Specifically, it refers to modifications of plant architecture and/or  
 CC leaf surface features in plants, such as chlorotic, bleaching, etching,  
 CC wet leaf, stunting, elongation and texture phenotypes, which are thought  
 CC will be agronomic traits beneficial to the farmer. As such, these novel  
 CC phenotypes can affect growth regulation i.e. useful for creating dwarf  
 CC varieties, exhibit resistance to insects or heat stress, confer changes  
 CC in pigment content such that plants have enhanced vitamin production or  
 CC delayed senescence and also for example produce plants that control the  
 CC production of ethylene. Furthermore, the present invention comprises  
 CC generating transgenic plants, as well as reproducibly altering the visual  
 CC phenotype of plant seeds, plant tissues and plant cells containing the  
 CC polynucleotides described herein. This polynucleotide is a homologue of a  
 CC DNA sequence that confers an altered visual phenotype when expressed in  
 CC plants, the method of the invention.

XX SQ Sequence 1519 BP; 467 A; 311 C; 372 G; 369 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.44e-10 Length: 1519  
 Score: 155.50 Matches: 34  
 Percent Similarity: 72.1% Conservatives: 10  
 Best Local Similarity: 55.7% Mismatches: 14  
 Query Match: 52.4% Indels: 3  
 DB: 10 Gaps: 2

US-10-628-525A-35 (1-58) x ADD17886 (1-1519)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 DB 70 ATGGCACAGCTTTTAGCACCTTCACATGTCAGATGAGATACAAATACACCACT 129  
 QY 21 ---CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 39  
 DB 130 AATGCTGCAAGCCCAATTACTACAAAGATGTGGGGTCTCTAATGTTTAAACCAAGAA 189  
 QY 40 Lys-----ValAlaHisSerAlaLysPheArgValMetAlaValAlaSerGluAenGly 57  
 DB 190 AGTGGACTTACTTAAAAACGCTTCTAAATCAAGTTATGTTGTTAAATCGGAACGGT 249

QY 58 Thr 58

DB 250 ACC 252

# RESULT 7

ADK58449

ID ADK58449 standard; DNA; 3895 BP.

AC ADK58449;

DT 06-MAY-2004 (first entry)

DE Plant DNA sequence which confers altered metabolic characteristic #5832.

XX altered metabolic characteristic; plant; acid metabolism;

XX alcohol metabolism; fatty acid metabolism;

XX branched fatty acid metabolism; alkaloid metabolism;

XX amino acid metabolism; ester metabolism; glyceride metabolism;

XX phenolic metabolism; carboxylate metabolism; sterol metabolism;

XX terpene metabolism; isoprenoid metabolism; alkene metabolism;

XX alkyne metabolism; hydrocarbon metabolism; ketone metabolism;

XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.

OS Unidentified.

XX WO2003020936-A1.

XX 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027884.

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XX PR 31-AUG-2001; 2001US-0316471P.
XX PA (DOWC ) DOW CHEM CO.
XX PA (DOWC ) DOW AGROSCIENCES LLC.
XX PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
XX PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX DR WPI; 2003-313091/30.
XX XX
XX PT Novel genes that confer altered metabolic characteristics in Nicotiana
XX PT benthamiana plants, useful for altering the levels of metabolites e.g.
XX PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX PS Claim 1; SEQ ID NO 5932; 2576pp; English.
XX CC
XX CC The invention comprises DNA sequences which confer an altered metabolic
XX CC characteristic when they are expressed in a plant. The DNA sequences of
XX CC the invention are useful for producing plants with an altered metabolic
XX CC characteristic, such as: altered acid metabolism, alcohol metabolism,
XX CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
XX CC base metabolism, altered amino acid metabolism, altered ester metabolism,
XX CC altered glyceride metabolism, altered phenolic metabolism, altered
XX CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
XX CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
XX CC metabolism, ketone or quinone metabolism. The DNA sequences of the
XX CC invention may be used to provide disease resistance in a plant and gene
XX CC shuffling or sexual PCR procedures. The present nucleic acid represents a
XX CC DNA sequence of the invention.
XX SQ Sequence 3895 BP; 1123 A; 853 C; 950 G; 969 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,07e-10 Length: 3895
Score: 155.50 Matches: 34
Percent Similarity: 72.1% Conservative: 10
Best Local Similarity: 55.7% Mismatches: 14
Query Match: 52.4% Indels: 3
DB: 10 Gaps: 2

US-10-628-525A-35 (1-58) x ADK58449 (1-3895)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 318 ATGGCACAGTTTACGACCTTCACGCAATGTCAGATGAGTACAAATACACAAACA 377
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 21 ---CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 39
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 378 AATGCTGCAAGCCCAATTACTACMAAGATGGGGTCTCTAATGTTTAAACCAAGAAAGA 437
QY 40 Lys-----ValAlaHisSerAlaLysPheArgValMetAlaValAsnSerGluEngly 57
Db |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 438 ATGGAGCTTACTAAACACGCTTCTAATTAATCAAGTTATGTTGTTAAATCGGAACCGGT 497
QY 58 Thr 58
Db ||||
QY 498 ACC 500
Db ||||

RESULT 8
ADE82003
ID ADE82003 standard; cDNA; 487 BP.
XX AC ADE82003;
XX XX
XX DT 29-JAN-2004 (first entry)
XX DE Arabidopsis thaliana expressed polynucleotide seq id 774.
XX KW genetically modified organism; transgenic organism; plant;
XX KW inhibitor testing; activator testing; modifier testing; fungicide;
XX KW insecticide; genetic function; genetic regulation; cellular metabolism;
XX KW gene; ss.

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XX OS Arabidopsis thaliana.
XX PN US2003115639-A1.
XX PD 19-JUN-2003.
XX PF 26-JAN-2001; 2001US-00770961.
XX PR 27-JAN-2000; 2000US-0178466P.
XX XX
XX PA (GORL/) GORLACH J.
XX PA (ANY/) AN Y.
XX PA (HAM/) HAMILTON C M.
XX PA (PRIC/) PRICE J L.
XX PA (RAIN/) RAINES T M.
XX PA (YUY/) YU Y.
XX PA (RAME/) RAMEAKA J G.
XX PA (PAGE/) PAGE A.
XX PA (MATH/) MATHW A V.
XX PA (LEDF/) LEDFORD B L.
XX PA (WOES/) WOESSNER J P.
XX PA (HAAS/) HAAS W D.
XX PA (KRIC/) KRICKER M.
XX PA (SLAT/) SLATER T.
XX PA (DAVI/) DAVIS K R.
XX PA (ALLE/) ALLEN K.
XX PA (HOFF/) HOFFMAN N.
XX PA (HURB/) HURBAN P.
XX PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
DR WPI; 2003-810930/76.
XX PT Novel Arabidopsis thaliana nucleic acids useful for generating
XX PT genetically modified transgenic organisms, for screening biologically
XX PT active agents such as fungicides, insecticides.
XX PS Claim 1; SEQ ID NO 774; 4pp; English.
XX CC The invention describes a nucleic acid (I) comprising a sequence capable
XX CC of hybridising under stringent conditions to any one of 993 fully defined
XX CC Arabidopsis thaliana sequences (I) as given in specification e.g., 360,
XX CC 1137, 455, 219, 472 nucleotides, etc, or its fragment. (I) is useful as a
XX CC hybridisation probe to complementary molecules in a cDNA library. (I) is
XX CC also useful for generating genetically modified and transgenic organisms,
XX CC usually plant cells and plants. A protein encoded by (I) is useful in
XX CC screening assays to determine the effect of candidate inhibitors,
XX CC activators or modifiers of the gene product. The protein is also useful
XX CC for screening biologically active agents e.g., fungicides and
XX CC insecticides. A genetically modified cell, comprising an exogenous
XX CC nucleic acid, where the nucleic acid comprises transcription regulatory
XX CC sequences operably linked to a sequence capable of hybridising under
XX CC stringent conditions to (I) is useful in the study of genetic function
XX CC and regulation, for alteration of the cellular metabolism and for
XX CC screening compounds that may affect the biological function of the gene
XX CC or gene product. This sequence represents an Arabidopsis thaliana
XX CC polynucleotide of the invention.
XX SQ Sequence 487 BP; 145 A; 106 C; 104 G; 132 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8,22e-06 Length: 487
Score: 115.00 Matches: 28
Percent Similarity: 66.1% Conservative: 11
Best Local Similarity: 47.5% Mismatches: 18
Query Match: 38.7% Indels: 2
DB: 10 Gaps: 2

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PR 06-AUG-1999;	99US-0147303P.	Score: 115.00	Matches: 28
PR 06-AUG-1999;	99US-0147416P.	Percent Similarity: 66.1%	Conservative: 11
PR 09-AUG-1999;	99US-0147493P.	Best Local Similarity: 47.5%	Mismatches: 18
PR 09-AUG-1999;	99US-0147935P.	Query Match: 38.7%	Indels: 2
PR 10-AUG-1999;	99US-0148171P.	DB: 3	Gaps: 2
PR 11-AUG-1999;	99US-0148319P.	US-10-628-525A-35 (1-58) x AAC46992 (1-1598)	
PR 12-AUG-1999;	99US-0148341P.		
PR 13-AUG-1999;	99US-0148565P.		
PR 13-AUG-1999;	99US-0148684P.		
PR 16-AUG-1999;	99US-0149368P.		
PR 17-AUG-1999;	99US-0149175P.		
PR 18-AUG-1999;	99US-0149426P.		
PR 20-AUG-1999;	99US-0149722P.		
PR 20-AUG-1999;	99US-0149723P.		
PR 20-AUG-1999;	99US-0149829P.		
PR 23-AUG-1999;	99US-0149902P.		
PR 23-AUG-1999;	99US-0149930P.		
PR 25-AUG-1999;	99US-0150566P.		
PR 26-AUG-1999;	99US-0150884P.		
PR 27-AUG-1999;	99US-0151065P.		
PR 27-AUG-1999;	99US-0151066P.		
PR 27-AUG-1999;	99US-0151080P.		
PR 30-AUG-1999;	99US-0151303P.		
PR 31-AUG-1999;	99US-0151438P.		
PR 01-SEP-1999;	99US-0151930P.		
PR 07-SEP-1999;	99US-0152363P.		
PR 10-SEP-1999;	99US-0153070P.		
PR 13-SEP-1999;	99US-0153758P.		
PR 15-SEP-1999;	99US-0154018P.		
PR 16-SEP-1999;	99US-0154039P.		
PR 20-SEP-1999;	99US-0154779P.		
PR 22-SEP-1999;	99US-0155139P.		
PR 23-SEP-1999;	99US-0155486P.		
PR 24-SEP-1999;	99US-0155659P.		
PR 28-SEP-1999;	99US-0156458P.		
PR 29-SEP-1999;	99US-0156596P.		
PR 04-OCT-1999;	99US-0157117P.		
PR 05-OCT-1999;	99US-0157753P.		
PR 06-OCT-1999;	99US-0157865P.		
PR 07-OCT-1999;	99US-0158029P.		
PR 08-OCT-1999;	99US-0158232P.		
PR 12-OCT-1999;	99US-0158369P.		
PR 13-OCT-1999;	99US-0159293P.		
PR 13-OCT-1999;	99US-0159294P.		
PR 13-OCT-1999;	99US-0159295P.		
PR 14-OCT-1999;	99US-0159329P.		
PR 14-OCT-1999;	99US-0159330P.		
PR 14-OCT-1999;	99US-0159331P.		
PR 14-OCT-1999;	99US-0159637P.		
PR 18-OCT-1999;	99US-0159638P.		
PR 21-OCT-1999;	99US-0159584P.		
PR 21-OCT-1999;	99US-0160741P.		
PR 21-OCT-1999;	99US-0160767P.		
PR 21-OCT-1999;	99US-0160768P.		
PR 21-OCT-1999;	99US-0160770P.		
PR 21-OCT-1999;	99US-0160814P.		
PR 22-OCT-1999;	99US-0160815P.		
PR 22-OCT-1999;	99US-0160980P.		
PR 22-OCT-1999;	99US-0160981P.		
PR 25-OCT-1999;	99US-0161404P.		
PR 25-OCT-1999;	99US-0161405P.		
PR 25-OCT-1999;	99US-0161406P.		
PR 26-OCT-1999;	99US-0161359P.		
PR 26-OCT-1999;	99US-0161360P.		
PR 26-OCT-1999;	99US-0161361P.		
PR 28-OCT-1999;	99US-0161920P.		
PR 28-OCT-1999;	99US-0161992P.		
PR 28-OCT-1999;	99US-0161993P.		
PR 29-OCT-1999;	99US-0162142P.		
Alignment Scores:		4.01e-05	Length: 1598
Pred. No.:			

Score:	115.00	Matches:	28
Percent Similarity:	66.1%	Conservative:	11
Best Local Similarity:	47.5%	Mismatches:	18
Query Match:	38.7%	Indels:	2
DB:	3	Gaps:	2
US-10-628-525A-35 (1-58) x AAC46992 (1-1598)			
QY	1	MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro	20
Db	138	ATGGCTCAGATCTTAGCAGCTTCTCCACATGTCAGATGAGATGCTTAACACTCATCA	197
QY	21	CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys	40
Db	198	GTCATTGCATCA---TCATCCAGTTATGGAGCTCTGTTGTGTTGAAACAGAGAAGCAG	254
QY	41	ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr	58
Db	255	AGCAACAACAAGTCAGAGGCTTTAGAGTTCCTGCTCTCCAATCTGATAACAGTACT	311
RESULT 10			
AAC49096			
ID	AAC49096 standard; DNA; 2103 BP.		
XX	AAC49096;		
XX	18-OCT-2000 (first entry)		
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 59909.		
XX	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway; metabolic pathway;		
KW	promoter; termination sequence; ss.		
OS	Arabidopsis thaliana.		
XX	EP1033405-A2.		
XX	06-SEP-2000.		
XX	25-FEB-2000; 2000EP-00301439.		
XX	25-FEB-1999;	99US-0121825P.	
PR	05-MAR-1999;	99US-0123180P.	
PR	09-MAR-1999;	99US-0123548P.	
PR	23-MAR-1999;	99US-0125788P.	
PR	25-MAR-1999;	99US-0126264P.	
PR	29-MAR-1999;	99US-0126785P.	
PR	01-APR-1999;	99US-0127462P.	
PR	06-APR-1999;	99US-0128234P.	
PR	08-APR-1999;	99US-0128714P.	
PR	16-APR-1999;	99US-0129845P.	
PR	19-APR-1999;	99US-0130077P.	
PR	21-APR-1999;	99US-0130449P.	
PR	23-APR-1999;	99US-0130510P.	
PR	23-APR-1999;	99US-0130891P.	
PR	28-APR-1999;	99US-0131449P.	
PR	30-APR-1999;	99US-0132048P.	
PR	30-APR-1999;	99US-0132407P.	
PR	04-MAY-1999;	99US-0132484P.	
PR	05-MAY-1999;	99US-0132485P.	
PR	06-MAY-1999;	99US-0132486P.	
PR	06-MAY-1999;	99US-0132487P.	
PR	07-MAY-1999;	99US-0132863P.	
PR	11-MAY-1999;	99US-0134256P.	
PR	14-MAY-1999;	99US-0134218P.	
PR	14-MAY-1999;	99US-0134219P.	
PR	14-MAY-1999;	99US-0134221P.	
PR	14-MAY-1999;	99US-0134370P.	
PR	18-MAY-1999;	99US-0134768P.	
PR	19-MAY-1999;	99US-0134941P.	
PR	20-MAY-1999;	99US-0135124P.	
PR	21-MAY-1999;	99US-0135353P.	

PR 24-MAY-1999; 99US-0135629P.  
 PR 25-MAY-1999; 99US-0136021P.  
 PR 27-MAY-1999; 99US-0136332P.  
 PR 28-MAY-1999; 99US-0136782P.  
 PR 01-JUN-1999; 99US-0137222P.  
 PR 03-JUN-1999; 99US-0137528P.  
 PR 04-JUN-1999; 99US-0137502P.  
 PR 07-JUN-1999; 99US-0137724P.  
 PR 08-JUN-1999; 99US-0138094P.  
 PR 10-JUN-1999; 99US-0138540P.  
 PR 10-JUN-1999; 99US-0138847P.  
 PR 14-JUN-1999; 99US-0139119P.  
 PR 16-JUN-1999; 99US-0139452P.  
 PR 17-JUN-1999; 99US-0139453P.  
 PR 18-JUN-1999; 99US-0139452P.  
 PR 18-JUN-1999; 99US-0139454P.  
 PR 18-JUN-1999; 99US-0139455P.  
 PR 18-JUN-1999; 99US-0139456P.  
 PR 18-JUN-1999; 99US-0139457P.  
 PR 18-JUN-1999; 99US-0139458P.  
 PR 18-JUN-1999; 99US-0139459P.  
 PR 18-JUN-1999; 99US-0139460P.  
 PR 18-JUN-1999; 99US-0139461P.  
 PR 18-JUN-1999; 99US-0139462P.  
 PR 18-JUN-1999; 99US-0139463P.  
 PR 18-JUN-1999; 99US-0139750P.  
 PR 18-JUN-1999; 99US-0139763P.  
 PR 21-JUN-1999; 99US-0139817P.  
 PR 22-JUN-1999; 99US-0139899P.  
 PR 23-JUN-1999; 99US-0140353P.  
 PR 23-JUN-1999; 99US-0140354P.  
 PR 24-JUN-1999; 99US-0140695P.  
 PR 28-JUN-1999; 99US-0140823P.  
 PR 29-JUN-1999; 99US-0140991P.  
 PR 30-JUN-1999; 99US-0141287P.  
 PR 01-JUL-1999; 99US-0141842P.  
 PR 01-JUL-1999; 99US-0142154P.  
 PR 02-JUL-1999; 99US-0142055P.  
 PR 06-JUL-1999; 99US-0142390P.  
 PR 08-JUL-1999; 99US-0142803P.  
 PR 09-JUL-1999; 99US-0142920P.  
 PR 12-JUL-1999; 99US-0142977P.  
 PR 13-JUL-1999; 99US-0143542P.  
 PR 14-JUL-1999; 99US-0143624P.  
 PR 15-JUL-1999; 99US-0144005P.  
 PR 16-JUL-1999; 99US-0144085P.  
 PR 16-JUL-1999; 99US-0144086P.  
 PR 19-JUL-1999; 99US-0144325P.  
 PR 19-JUL-1999; 99US-0144331P.  
 PR 19-JUL-1999; 99US-0144332P.  
 PR 19-JUL-1999; 99US-0144333P.  
 PR 19-JUL-1999; 99US-0144334P.  
 PR 19-JUL-1999; 99US-0144335P.  
 PR 20-JUL-1999; 99US-0144352P.  
 PR 20-JUL-1999; 99US-0144632P.  
 PR 20-JUL-1999; 99US-0144884P.  
 PR 21-JUL-1999; 99US-0144814P.  
 PR 21-JUL-1999; 99US-0145086P.  
 PR 21-JUL-1999; 99US-0145088P.  
 PR 22-JUL-1999; 99US-0145085P.  
 PR 22-JUL-1999; 99US-0145087P.  
 PR 22-JUL-1999; 99US-0145089P.  
 PR 22-JUL-1999; 99US-0145192P.  
 PR 23-JUL-1999; 99US-0145145P.  
 PR 23-JUL-1999; 99US-0145218P.  
 PR 23-JUL-1999; 99US-0145224P.  
 PR 26-JUL-1999; 99US-0145276P.  
 PR 27-JUL-1999; 99US-0145913P.  
 PR 27-JUL-1999; 99US-0145918P.  
 PR 27-JUL-1999; 99US-0145919P.  
 PR 28-JUL-1999; 99US-0145951P.  
 PR 02-AUG-1999; 99US-0146386P.  
 PR 02-AUG-1999; 99US-0146388P.

PR 02-AUG-1999; 99US-0146389P.  
 PR 03-AUG-1999; 99US-0147038P.  
 PR 04-AUG-1999; 99US-0147204P.  
 PR 04-AUG-1999; 99US-0147302P.  
 PR 05-AUG-1999; 99US-0147192P.  
 PR 05-AUG-1999; 99US-0147260P.  
 PR 06-AUG-1999; 99US-0147303P.  
 PR 06-AUG-1999; 99US-0147416P.  
 PR 09-AUG-1999; 99US-0147493P.  
 PR 09-AUG-1999; 99US-0147935P.  
 PR 10-AUG-1999; 99US-0148171P.  
 PR 11-AUG-1999; 99US-0148319P.  
 PR 12-AUG-1999; 99US-0148341P.  
 PR 13-AUG-1999; 99US-0148565P.  
 PR 13-AUG-1999; 99US-0148684P.  
 PR 16-AUG-1999; 99US-0149368P.  
 PR 17-AUG-1999; 99US-0149175P.  
 PR 18-AUG-1999; 99US-0149426P.  
 PR 20-AUG-1999; 99US-0149722P.  
 PR 20-AUG-1999; 99US-0149723P.  
 PR 20-AUG-1999; 99US-0149929P.  
 PR 23-AUG-1999; 99US-0149902P.  
 PR 23-AUG-1999; 99US-0149930P.  
 PR 25-AUG-1999; 99US-0150566P.  
 PR 26-AUG-1999; 99US-0150884P.  
 PR 27-AUG-1999; 99US-0151065P.  
 PR 27-AUG-1999; 99US-0151066P.  
 PR 27-AUG-1999; 99US-0151080P.  
 PR 30-AUG-1999; 99US-0151303P.  
 PR 31-AUG-1999; 99US-0151438P.  
 PR 01-SEP-1999; 99US-0151930P.  
 PR 07-SEP-1999; 99US-0152363P.  
 PR 10-SEP-1999; 99US-0153070P.  
 PR 13-SEP-1999; 99US-0153758P.  
 PR 15-SEP-1999; 99US-0154018P.  
 PR 16-SEP-1999; 99US-0154039P.  
 PR 20-SEP-1999; 99US-0154779P.  
 PR 22-SEP-1999; 99US-0155139P.  
 PR 23-SEP-1999; 99US-0155486P.  
 PR 24-SEP-1999; 99US-0155659P.  
 PR 28-SEP-1999; 99US-0156458P.  
 PR 29-SEP-1999; 99US-0156596P.  
 PR 04-OCT-1999; 99US-0157117P.  
 PR 05-OCT-1999; 99US-0157753P.  
 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
 PR 08-OCT-1999; 99US-0158232P.  
 PR 12-OCT-1999; 99US-0158369P.  
 PR 13-OCT-1999; 99US-0159293P.  
 PR 13-OCT-1999; 99US-0159294P.  
 PR 13-OCT-1999; 99US-0159295P.  
 PR 14-OCT-1999; 99US-0159329P.  
 PR 14-OCT-1999; 99US-0159330P.  
 PR 14-OCT-1999; 99US-0159331P.  
 PR 14-OCT-1999; 99US-0159637P.  
 PR 14-OCT-1999; 99US-0159638P.  
 PR 18-OCT-1999; 99US-0159584P.  
 PR 21-OCT-1999; 99US-0160741P.  
 PR 21-OCT-1999; 99US-0160767P.  
 PR 21-OCT-1999; 99US-0160768P.  
 PR 21-OCT-1999; 99US-0160770P.  
 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
 PR 22-OCT-1999; 99US-0160980P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0160989P.  
 PR 25-OCT-1999; 99US-0161404P.  
 PR 25-OCT-1999; 99US-0161405P.  
 PR 25-OCT-1999; 99US-0161406P.  
 PR 26-OCT-1999; 99US-0161359P.  
 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.

PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.  
Alignment Scores:  
Pred. No.: 5.78e-05 Length: 2103  
Score: 115.00 Matches: 28  
Percent Similarity: 66.1% Conservative: 11  
Best Local Similarity: 47.5% Mismatches: 18  
Query Match: 38.7% Indels: 2  
DB: 2 Gaps: 2  
US-10-628-525A-35 (1-58) x AAC49096 (1-2103)  
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 1 ATGGCTCAGATCTTAGCAGCTTCTCCAAATGTCAGATGAGTGCCTAAACACTCATCA 60  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 61 GTCATTGCATCA---TCATCCCAAGTTATGGAGCTCTGTTGTTGAAACAGAGAGCAG 117  
QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr 58  
Db 118 AGCAACACAAAGTCAGAGGCTTTAGAGTTCTTGCTCTCCTCAATCTGTATAACAGTACT 174  
RESULT 11  
ABLS3628  
ID ABL53628 standard; cDNA; 1543 BP.  
XX ABL53628;  
XX 17-JUN-2002 (first entry)  
DE Breast protein-eukaryotic conserved gene 1 (BSTP-ECG1) cDNA.  
XX BSTP-ECG1; breast cancer; diagnosis; gene therapy; antitumour;  
KW cytostatic; differential expression; gene; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 228..1394  
FT /\*tag= a  
FT /\*product= "BSTP-ECG1"  
XX  
PN WO200208260-A2.  
XX  
XX 31-JAN-2002.  
XX 26-JUL-2001; 2001WO-US023439.  
XX 26-JUL-2000; 2000US-0220967P.  
PR 06-DEC-2000; 2000US-0251669P.  
XX (STRD ) UNIV STANFORD.  
PA (GENO-) APPLIED GENOMICS INC.  
XX Botstein D, Brown PO, Perou C, Ross D, Seitz R;  
PI WPI; 2002-315251/35.  
XX P-PSDB; ABB75677.  
XX Novel substantially purified polypeptide encoded by breast protein-eukaryotic conserved gene 1, useful for diagnosing, treating or preventing breast cancer, and for classifying cancer.  
XX Disclosure; Fig 1b; 127pp; English.  
XX The present sequence is that of a BSTP-ECG1 (breast protein-eukaryotic conserved gene 1) cDNA sequence, encoding a 388-amino acid protein (see ABB75677). The cDNA corresponds to a 1.5 kb mRNA isoform detected in liver tumour-derived HepG2 cells (ATCC HB-8065), colon tumour-derived

CC COLO205 cells (ATCC CCL-222) and breast adenocarcinoma-derived MCF-7 cells (ATCC HTB-22) using Northern blotting. Multiple isoforms of BSTP-ECG1 mRNA are predicted resulting from alternative 3' processing. BSTP-ECG1 is differentially expressed among breast tumours, making it useful for the diagnosis, treatment, prevention, prognosis and classification of cancer, especially breast cancer, and a target for therapeutic intervention. The invention provides BSTP-ECG1 polypeptides and polynucleotides, expression vectors, host cells, antibodies, agonists and antagonists. It also provides methods for treating or preventing disorders of cell proliferation, polynucleotide or antibody of the invention. CC administering a polypeptide, polynucleotide or antibody of BSTP-ECG1 or a CC Also provided are methods of classifying diseases, particularly breast cancer, by detecting expression of BSTP-ECG1 or a polynucleotide encoding it, and of providing diagnostic, prognostic and/or predictive information for a patient based on the detection and/or measurement of BSTP-ECG1 or a CC polynucleotide encoding BSTP-ECG1. Since BSTP-ECG1 mRNA can be detected in CC a variety of tumour-derived cell lines, these methods may also be CC applicable to additional tumour types  
XX Sequence 1543 BP; 321 A; 452 C; 441 G; 329 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 15.8 Length: 1543  
Score: 73.00 Matches: 19  
Percent Similarity: 43.3% Conservative: 7  
Best Local Similarity: 31.7% Mismatches: 26  
Query Match: 24.6% Indels: 8  
DB: 2 Gaps: 2  
US-10-628-525A-35 (1-58) x ABL53628 (1-1543)  
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
Db 1252 TCACCATCCCAAGCTGGAGACCCCAACCCAGACATCCGCTGTACCACCATGT 1311  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45  
Db 1312 ACATGGAGGCCCTGTGAGACTTT---TCGACACGACACAGCAAGTTCGGCTCCCG 1368  
QY 46 LysPheArg-----ValMetAlaValAsnSerGluAsnGlyThr 58  
Db 1369 AGACTGAGGTCCTGGAGGTGAACCTGAGCAGCCTTCGGGGCCAATTCCTCGAGGAACC 1428  
RESULT 12  
ABLS3629  
ID ABL53629 standard; cDNA; 2418 BP.  
XX ABL53629;  
XX 17-JUN-2002 (first entry)  
DE Breast protein-eukaryotic conserved gene 1 (BSTP-ECG1) consensus.  
XX BSTP-ECG1; breast cancer; diagnosis; gene therapy; antitumour;  
KW cytostatic; differential expression; ss.  
XX Homo sapiens.  
OS  
XX WO200208260-A2.  
XX 31-JAN-2002.  
XX 26-JUL-2001; 2001WO-US023439.  
PF 26-JUL-2000; 2000US-0220967P.  
PR 06-DEC-2000; 2000US-0251669P.  
XX (STRD ) UNIV STANFORD.  
PA (GENO-) APPLIED GENOMICS INC.  
XX Botstein D, Brown PO, Perou C, Ross D, Seitz R;  
PI WPI; 2002-315251/35.  
XX

XX Novel substantially purified polypeptide encoded by breast protein-  
PT eukaryotic conserved gene 1, useful for diagnosing, treating or  
PT preventing breast cancer, and for classifying cancer.  
XX  
XX Disclosure; Fig 2; 127pp; English.  
XX  
XX The present sequence is that of a consensus of cDNA clones for BSTP-ECG1  
CC (breast protein-eukaryotic conserved gene 1). In order to identify genes  
CC that are differentially expressed in breast tumours, cDNA microarrays  
CC were produced, each representing the same set of approximately 8100  
CC different human genes. Variations in patterns of gene expression were  
CC characterised in 62 breast tumour samples from 40 patients, 3 normal  
CC breast tissue samples and 19 samples from 17 human cell lines. IMAGE  
CC clone 161484 was identified based on the expression pattern of its mRNA  
CC among these 84 samples. Overlapping IMAGE clones 48805, 1276329, 1343900  
CC and 1560906 were identified in a database search. The present consensus  
CC sequence was produced from the 5 IMAGE clones, and a coding region (see  
CC ABL53626) was derived. BSTP-ECG1 is differentially expressed among breast  
CC tumours, making it useful for the diagnosis, treatment, prevention,  
CC prognosis and classification of cancer, especially breast cancer, and  
CC also a potential therapeutic target. The invention provides BSTP-ECG1  
CC polypeptides and polynucleotides, expression vectors, host cells,  
CC antibodies, agonists and antagonists. It also provides methods for  
CC treating or preventing disorders of cell proliferation, particularly  
CC breast cancer, by administering a polypeptide, polynucleotide or antibody  
CC of the invention. Also provided are methods of classifying diseases,  
CC particularly breast cancer by detecting expression of BSTP-ECG1 or a  
CC polynucleotide encoding it, and of providing diagnostic, prognostic  
CC and/or predictive information for a patient based on the detection and/or  
CC measurement of BSTP-ECG1 or polynucleotide encoding BSTP-ECG1  
XX  
SQ Sequence 2418 BP; 590 A; 624 C; 604 G; 582 T; 0 U; 18 Other;

Alignment Scores:  
Pred. No.: 28.7 Length: 2418  
Score: 73.00 Matches: 19  
Percent Similarity: 43.3% Conservative: 7  
Best Local Similarity: 31.7% Mismatches: 26  
Query Match: 24.6% Indels: 8  
DB: 6 Gaps: 2

US-10-628-525A-35 (1-58) x ABL53629 (1-2418)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
Db 1225 TCACCATCCCAAGCTGGAGACCCCAACCCAGCAGACATCGACCTGTACCACCATGT 1284  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45  
Db 1285 ACATGGAGGCCCTGGTGAAGCTTT---TCGACAAAGCAGCAAGACCAAGTTCCGGCTCCCGG 1341  
QY 46 LysPheArg-----ValMetAlaValAsnSerGluAsnGlyThr 58  
Db 1342 AGACTGAGGTCTCTGGAGGTGAAGTGAAGCCAGCCCTCGGGGCCAATTCCTCGGAGGAACC 1401

RESULT 13  
ABL53627  
ID ABL53627 standard; cDNA; 2445 BP.  
XX  
XX ABL53627;  
AC

XX 17-JUN-2002 (first entry)  
DT  
XX  
XX Breast protein-eukaryotic conserved gene 1 (BSTP-ECG1) cDNA.  
DE  
XX BSTP-ECG1; breast cancer; diagnosis; gene therapy; antitumour;  
KW cytostatic; differential expression; gene; ss.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH 228. .1394  
FT CDS

PT /\*tag= a  
XX /product= "BSTP-ECG1"  
PN WO200208260-A2.  
XX  
XX 31-JAN-2002.  
PD

XX 26-JUL-2001; 2001WO-US023439.  
PF

XX 26-JUL-2000; 2000US-0220967P.  
PR

XX 06-DEC-2000; 2000US-0251669P.  
PR

XX (STRD ) UNIV STANFORD.  
PA

XX (GENO-) APPLIED GENOMICS INC.  
PA

XX Botstein D, Brown PO, Perou C, Ross D, Seitz R;  
PI

XX WPI; 2002-315251/35.  
XX

XX P-PSDB; ABB75677.  
DR

XX Novel substantially purified polypeptide encoded by breast protein-  
PT eukaryotic conserved gene 1, useful for diagnosing, treating or  
PT preventing breast cancer, and for classifying cancer.  
XX  
XX Disclosure; Fig 1C; 127pp; English.

XX The present sequence is that of a BSTP-ECG1 (breast protein-eukaryotic  
CC conserved gene 1) cDNA sequence, encoding a 388-amino acid protein (see  
CC ABB75677). The cDNA corresponds to a 2.2 kb mRNA isoform detected in  
CC liver tumour-derived HepG2 cells (ATCC HB-8065), colon tumour-derived  
CC COLO205 cells (ATCC CCL-222) and breast adenocarcinoma-derived MCF-7  
CC cells (ATCC HTB-22) using Northern blotting. Multiple isoforms of BST-  
CC ECG1 mRNA are predicted resulting from alternative 3' processing. BSTP-  
CC ECG1 is differentially expressed among breast tumours, making it useful  
CC for the diagnosis, treatment, prevention, prognosis and classification of  
CC cancer, especially breast cancer, and a target for therapeutic  
CC intervention. The invention provides BSTP-ECG1 polypeptides and  
CC polynucleotides, expression vectors, host cells, antibodies, agonists and  
CC antagonists. It also provides methods for treating or preventing  
CC disorders of cell proliferation, particularly breast cancer, by  
CC administering a polypeptide, polynucleotide or antibody of the invention.  
CC Also provided are methods of classifying diseases, particularly breast  
CC cancer, by detecting expression of BSTP-ECG1 or a polynucleotide encoding  
CC it, and of providing diagnostic, prognostic and/or predictive information  
CC for a patient based on the detection and/or measurement of BSTP-ECG1 or a  
CC polynucleotide encoding BSTP-ECG1. Since BST-ECG1 mRNA can be detected in  
CC a variety of tumour-derived cell lines, these methods may also be  
CC applicable to additional tumour types  
XX

SQ Sequence 2445 BP; 525 A; 678 C; 676 G; 563 T; 0 U; 3 Other;

Alignment Scores:  
Pred. No.: 29.1 Length: 2445  
Score: 73.00 Matches: 19  
Percent Similarity: 43.3% Conservative: 7  
Best Local Similarity: 31.7% Mismatches: 26  
Query Match: 24.6% Indels: 8  
DB: 6 Gaps: 2

US-10-628-525A-35 (1-58) x ABL53627 (1-2445)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
Db 1252 TCACCATCCCAAGCTGGAGACCCCAACCCAGCAGACATCGACCTGTACCACCATGT 1311  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45  
Db 1312 ACATGGAGGCCCTGGTGAAGCTTT---TCGACAAAGCAGCAAGACCAAGTTCCGGCTCCCGG 1368  
QY 46 LysPheArg-----ValMetAlaValAsnSerGluAsnGlyThr 58  
Db 1369 AGACTGAGGTCTCTGGAGGTGAAGTGAAGCCAGCCCTCGGGGCCAATTCCTCGGAGGAACC 1428

Qy	26 ThrSerLysMetTrp---SerSerLeuValMet 35
	:::     :::
Db	193 ACATGGAGGCCCTGGTGAAGCTCTTTGACAATC 161
RESULT 15	
ADBS0884/c	
ID	ADBS0884 standard; DNA; 386 BP.
XX	
AC	ADBS0884;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:1426.
XX	
KW	toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW	toxicity marker; toxicity progression; drug screening;
KW	primary rat hepatocyte toxicity modelling; gene; ds.
XX	
OS	Rattus norvegicus.
XX	
PN	WO2003065993-A2.
XX	
PD	14-AUG-2003..
XX	
PF	04-FEB-2003; 2003WO-US003482.
XX	
PR	04-FEB-2002; 2002US-0353171P.
PR	13-MAR-2002; 2002US-0363534P.
PR	08-APR-2002; 2002US-0370248P.
PR	10-APR-2002; 2002US-0371134P.
PR	10-APR-2002; 2002US-0371135P.
PR	10-APR-2002; 2002US-0371150P.
PR	11-APR-2002; 2002US-0371413P.
PR	19-APR-2002; 2002US-0373601P.
PR	19-APR-2002; 2002US-0373602P.
PR	22-APR-2002; 2002US-0374139P.
PR	08-MAY-2002; 2002US-0378370P.
PR	09-MAY-2002; 2002US-0378652P.
PR	09-MAY-2002; 2002US-0378653P.
PR	09-MAY-2002; 2002US-0378665P.
PR	09-JUL-2002; 2002US-0394230P.
PR	09-JUL-2002; 2002US-0394253P.
PR	04-SEP-2002; 2002US-0407688P.
PR	28-JAN-2003; 2003US-0442900P.
XX	
XX	(GENE-) GENE LOGIC INC.
PA	
XX	
PI	Mendrick D, Porter M, Johnson K, Higgs B, Caastle A, Orr M;
PI	Elashoff M;
XX	
DR	WPI; 2003-731472/69.
XX	
PT	Determining if a compound induces a toxic effect on a tissue or cell, for
PT	identifying hepatotoxic compounds, comprises comparing a gene expression
PT	profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT	mean values.
XX	
PS	Claim 44; SEQ ID NO 1426; 874pp; English.
XX	
CC	The present invention describes a method for determining whether a
CC	compound induces a toxic effect on a tissue or cell. The method comprises
CC	preparing a gene expression profile of a tissue or cell sample exposed to
CC	the compound, and comparing the gene expression profile to a database
CC	comprising data or information on the Tox mean and non-Tox mean value.
CC	The method is useful for predicting or identifying at least one toxic
CC	effect, particularly hepatotoxicity, of a test or unknown compound. The
CC	genes listed in the specification are useful as diagnostic or toxicity
CC	markers for the prediction or identification of the physiological state
CC	of tissue or cell sample that has been exposed to a compound, or to
CC	identify or predict the toxic effects of a compound or an agent. These
CC	may also be used as markers for monitoring toxicity progression or for
CC	drug screening. The present sequence represents a primary rat hepatocyte
CC	toxicity modelling related gene sequence from the present invention.

XX SQ Sequence 386 BP; 91 A; 98 C; 110 G; 87 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5.36 Length: 386

Score: 70.50 Matches: 15

Percent Similarity: 58.1% Conservative: 3

Best Local Similarity: 48.4% Mismatches: 12

Query Match: 23.7% Indels: 1

DB: 10 Gaps: 1

US-10-628-525A-35 (1-58) x ADB50894 (1-386)

Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProile 25

Db 253 TCACCGTCCCTAAGCTGGAGCACCAGCCGAGAAAGACATCGACCTGTACACCATGT 194

Qy 26 ThrSerLysMetTrp---SerSerLeuValMet 35

Db 193 ACATGGAGGCCCTGGTGAAGCTCTTTGACAATC 161

RESULT 16

ADX25897

ID ADX25897 standard; DNA; 386 BP.

XX AC ADX25897;

XX DT 05-MAY-2005 (first entry)

XX DE Novel cell pain response detection method-related human gene SeqID243.

XX KW pain; animal disease model; expression; analgesic; antiaddictive;

XX KW nootropic; anticonvulsant; vasotropic; neuroprotective; tranquilizer;

XX KW antiasthmatic; antirheumatic; antiarthritic; osteopathic;

XX KW ophthalmological; antinflammatory; antipruritic; dermatological;

XX KW antiulcer; gastrointestinal-Gen.; nephrotropic; gynecological;

XX KW hepatotropic; antiparkinsonian; neuroleptic; laxative; gene therapy;

XX KW neuropathic pain; Alzheimers disease; Parkinsons disease;

XX KW motor neurone disease; Huntingtons disease; schizophrenia; gene; ds.

XX OS Homo sapiens.

XX PN WO2005014849-A2.

XX XX WO2005014849-A2.

XX PD 17-FEB-2005.

XX PF 06-JUL-2004; 2004WO-US023166.

XX PR 03-JUL-2003; 2003US-0485101P.

XX PA (EURO-) EUROCELTIQUE SA.

XX PI Tong J, Jin G, Ji R, Xu Y, Chiang LW, Lavery DJ;

XX DR WPI; 2005-163258/17.

XX PT Detecting pain responses in a cell, useful in identifying potential

XX PT therapeutic and diagnostic candidates for treating pain, by identifying

XX PT genes that are differentially expressed in a model of neuropathic pain.

XX PS Claim 1; SEQ ID NO 243; 173pp; English.

XX CC This invention relates to a novel method of detecting a pain response in

XX CC a cell which comprises determining the expression level in a test cell of

XX CC at least one nucleic acid molecule and comparing the expression level to

XX CC a level in an animal model of pain, where similar or identical expression

XX CC levels indicate a pain response in the test cell. The invention may be

XX CC useful for the development of compounds with an analgesic, antiaddictive,

XX CC nootropic, anticonvulsant, vasotropic, neuroprotective, tranquilizer,

XX CC antiasthmatic, antirheumatic, antiarthritic, osteopathic,

XX CC ophthalmological, antinflammatory, antipruritic, dermatological,

XX CC antiulcer, gastrointestinal-Gen., nephrotropic, gynecological,

XX CC hepatotropic, antiparkinsonian, neuroleptic or laxative activity whilst

the disclosed sequences may prove useful for gene therapy. The methods and compositions of the present invention are useful for identifying agonists and antagonists for the gene or gene products as potential therapeutic and diagnostic candidates for treating pain, including neuropathic pain, nociceptive pain, chronic pain, inflammatory pain, pain associated with cancer, and pain associated with rheumatic disease, and also for addiction, seizure, stroke, ischemia, a neurodegenerative disorder, anxiety, depression, headache, asthma, rheumatic disease, osteoarthritis, retinopathy, inflammatory eye disorders, pruritus, ulcer, gastric lesions, uncontrollable urination, an inflammatory or unstable bladder disorder, inflammatory bowel disease, irritable bowel syndrome (IBS), irritable bowel disease (IBD), gastroesophageal reflux disease (GERD), functional dyspepsia, functional chest pain of presumed esophageal origin, functional dysphagia, non-cardiac chest pain, symptomatic gastroesophageal disease, gastritis, aerophagia, functional constipation, functional diarrhea, borbulence, chronic functional abdominal pain, recurrent abdominal pain (RAP), function abdominal bloating, functional biliary pain, functional incontinence, functional ano-rectal disorder, cholecystalgia, interstitial cystitis, dysmenorrhea, or dyspareunia. They can also be used diagnosing or treating Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease and schizophrenia. The present sequence is that of a human gene whose expression level analysed in the method of the invention.

XX SQ Sequence 386 BP; 87 A; 110 C; 98 G; 91 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5.36 Length: 386

Score: 70.50 Matches: 15

Percent Similarity: 58.1% Conservative: 3

Best Local Similarity: 48.4% Mismatches: 12

Query Match: 23.7% Indels: 1

DB: 14 Gaps: 1

US-10-628-525A-35 (1-58) x ADX25897 (1-386)

Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProile 25

Db 134 TCACCGTCCCTAAGCTGGAGCACCAGCCGAGAAAGACATCGACCTGTACACCATGT 193

Qy 26 ThrSerLysMetTrp---SerSerLeuValMet 35

Db 194 ACATGGAGGCCCTGGTGAAGCTCTTTGACAATC 226

RESULT 17

ADX58674/c

ID ADE58674 standard; DNA; 460 BP.

XX AC ADE58674;

XX DT 29-JAN-2004 (first entry)

XX DE Rat gene AA799889, SEQ ID NO 4550.

XX KW Rat; ds; gene; pain; neuronal tissue; gene therapy;

XX KW spinal segmental nerve injury; chronic constriction injury; CCI;

XX KW spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX XX WO2003016475-A2.

XX PN 27-FEB-2003.

XX PD 14-AUG-2002; 2002WO-US025765.

XX PF 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX XX (GEHO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX XX





Qy	31	SerSerLeuValMetLysGlnThrLyrsLyvsValAlaHisSerAlaLysPheArgValMet	50
Db	292	ACAGGTTTAACTTACCAGACAGCGCTCATATCAGT---	AGTCAGCCCTTGCGTTTATAC 236
Qy	51	AlaValAenSerglu	55
Db	235	CAAGTGAACACTCAGAA	221
RESULT	19		
ABX44826			
ID	ABX44826	standard; cDNA; 347 BP.	
XX	AC	ABX44826;	
XX	XX		
DT	21-FEB-2003	(first entry)	
XX	DE	Bovine EST associated with lactation/muscle/fat deposition #9991.	
XX	DE	Bovine; SS; EST; expressed sequence tag; lactation; LMFD;	
KW	KM	muscle deposition; fat deposition; genome mapping; gene identification;	
KW	KW	gene analysis; cattle breeding.	
XX	OS	Bos Taurus.	
XX	XX		
PN	US	US2002137139-A1.	
PD	26-SEP-2002.		
XX	XX		
XX	24-SEP-2001;	2001US-00960352.	
PF	12-JAN-1999;	99US-0115707P.	
PR	11-JAN-2000;	2000US-00480902.	
XX	(BYAT// BYATT J C.		
PA	(MATH// MATHIALAGAN N.		
PA	(TAON// TAO N.		
PA	(WARR// WARREN W C.		
XX	Byatt JC,	Mathialagan N, Tao N, Warren WC;	
PI	WPI;	2003-110599/10.	
DR			
XX	New nucleic acid associated with lactation, and muscle and fat		
PT	deposition, useful for genome mapping, gene identification and analysis,		
PT	cattle breeding, or for genetically improving cattle.		
XX	Claim 2; SEQ ID NO 9991; 245pp; English.		
PS	The invention relates to a purified nucleic acid molecule associated with		
XX	lactation or muscle and fat deposition (designated LMFD), derived from		
CC	cattle, and the LMFD nucleic acid can specifically hybridise to a second		
CC	nucleic acid molecule comprising any of 15112 nucleotide sequences,		
CC	appearing as ABX34836-ABX49947, or complements of them. Also included are		
CC	; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic		
CC	acid linked to a promoter and a 3' non-translated sequence that		
CC	functions in the cell to cause termination of transcription and addition		
CC	of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and		
CC	(2) determining a level or pattern of a molecule in a bovine cell or		
CC	tissue comprising: (a) incubating a marker nucleic acid (comprising any		
CC	of the 15112 nucleic acid sequences or its complement or fragment) with a		
CC	complementary nucleic acid molecule obtained from the bovine cell or		
CC	tissue, where hybridisation between the marker nucleic acid and the		
CC	complementary nucleic acid permits the detection of the molecule; and (b)		
CC	detecting the level or pattern of the complementary nucleic acid, where		
CC	the detection of the complementary nucleic acid is predictive of the		
CC	level or pattern of the molecule. The LMFD nucleic acid is used for		
CC	determining a level or pattern of a molecule in a bovine cell or tissue.		
CC	It is useful for genome mapping, gene identification and analysis, cattle		
CC	breeding, preparation of constructs for use in cattle gene expression, or		
CC	for genetically improving cattle. The present sequence is one of the		
CC	15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The		
CC	present sequence was not shown in the specification but was obtained in		

CC electronic format from the USPTO web site:  
CC seqdata.uspto.gov/sequence.html?DocID=20020137139  
XX  
SQ Sequence 347 BP; 93 A; 95 C; 91 G; 68 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.33 Length: 347  
Score: 69.50 Matches: 17  
Percent Similarity: 54.7% Conservative: 12  
Best Local Similarity: 32.1% Mismatches: 19  
Query Match: 23.4% Indels: 5  
DB: 8 Gaps: 2  
  
US-10-628-525A-35 (1-58) x ABX44826 (1-347)  
  
Qy 4 IleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLys-----ThrSerPro 20  
Db 39 TTGCTATCCGACGACCAACAGTCGGAGACCAAGATCCCGAAGAGAGATGTTGACCCGCC 98  
Qy 21 CysAla-----ThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThr 38  
Db 99 TGGAGCTGTGTGAACCCATTGACCAAGAGATTGGTCAATCAGTACCTTGTTACGAGCCCA 150  
Qy 39 LysLeuValAlaHisSerAlaLysPheArgValMetAla 51  
Db 159 TCGATGATGCTCCGAGAGCCAGGTGCCTGTTCTCTGCT 197  
  
RESULT 20  
AAH66383/c  
ID AAH66383 standard; DNA; 1062 BP.  
XX  
AC AAH66383;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DE C glutamicum coding sequence fragment SEQ ID NO: 1418.  
XX  
KW Corynebacterium; amino acid synthesis; vitamin; saccharide;  
XX organic acid synthesis; ds.  
XX  
OS Corynebacterium glutamicum.  
XX  
PN EP1108790-A2.  
XX  
PD 20-JUN-2001.  
XX  
PF 18-DEC-2000; 2000EP-00127688.  
XX  
PR 16-DEC-1999; 93JP-00377484.  
XX  
PR 07-APR-2000; 2000JP-00159162.  
XX  
PR 03-AUG-2000; 2000JP-00280988.  
XX  
XX (KYOW) KYOWA HAKKO KOGYO KK.  
XX  
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;  
XX  
XX WPI; 2001-376931/40.  
DR  
DR P-PSDB; AAG91164.  
XX  
XX  
PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying  
PT mutation point of a gene, measuring expression of a gene, analyzing  
PT expression profile or pattern of a gene and identifying homologous gene.  
XX  
XX Claim 8; SEQ ID NO 1418; 246pp + Sequence Listing; English.  
XX  
XX The present invention provides a number of nucleotide and protein  
CC sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These  
CC are useful for identifying the mutation point of a gene derived from a  
CC mutant of corynebacterium bacterium, measuring expression amount and analysing  
CC the expression profile or expression pattern of a gene derived from  
CC Corynebacterium bacterium, and identifying a homologue of a gene derived from  
CC corynebacterium bacterium. Corynebacterium bacteria are useful for producing amino  
XX acids.  
XX

CC acids, nucleic acids, vitamins, saccharides and organic acids,  
 CC particularly L-lysine. The present sequence is a nucleic acid described  
 CC in the exemplification of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from the European Patent Office

XX  
 SQ Sequence 1062 BP; 271 A; 266 C; 255 G; 270 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 28.1 Length: 1062  
 Score: 69.50 Matches: 17  
 Percent Similarity: 49.0% Conservatives: 7  
 Best Local Similarity: 34.7% Mismatches: 16  
 Query Match: 23.4% Indels: 9  
 DB: 5 Gaps: 2

US-10-628-525A-35 (1-58) x AAH6383 (1-1062)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 Db 296 ATGTCATCCTTTTGGCGGATTCA-----ATGGACTCAAGCGCGCT 255  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 Db 254 TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAAAATACCCAAAGCGCA 204  
 QY 41 ValAlaHisSerAlaLysPheArgVal 49  
 Db 203 ACTGCTAATTCACGAGTTTAGATTG 177

RESULT 21  
 ID ADL65758/7c  
 ADL65758 standard; DNA; 1192 BP.

XX AC ADL65758;  
 XX  
 XX 20-MAY-2004 (first entry)  
 XX  
 XX C. glutamicum RXA-associated DNA #58.  
 XX  
 XX fine chemical production; lysine production; nucleotide; nucleoside;  
 KW lipid; fatty acid; diol; carbohydrate; aromatic compound; vitamin;  
 KW co-factor; enzyme; food; animal feed; cosmetic; pharmaceutical; gene; ds.  
 XX  
 XX Corynebacterium glutamicum.  
 OS  
 FN DE10154177-A1.  
 XX  
 XX 08-MAY-2003.  
 XX  
 XX 05-NOV-2001; 2001DE-01054177.  
 XX  
 XX 05-NOV-2001; 2001DE-01054177.  
 XX  
 XX (BADI ) BASF AG.  
 XX  
 XX Zelder O, Pompejus M, Schroeder H, Kroeger B, Klopffrogge C;  
 PI Habershauer G;  
 XX  
 XX WPI; 2003-431900/41.  
 DR P-PSDB; ADL65759.

XX  
 XX New nucleic acid encoding variant forms of marker and fine chemical-  
 PT production proteins, useful for production of fine chemicals,  
 PT specifically lysine, in microorganisms.  
 XX  
 XX Claim 1; Page; 20pp; German.  
 PS  
 XX This invention describes novel polynucleotides that encode protein  
 CC markers and fine chemical-production proteins from Corynebacterium  
 CC glutamicum. The polynucleotides are isolated from a nucleic acid library  
 CC of C. glutamicum then mutated at the specified positions, cloned and  
 CC expressed by standard methods. Cells, especially Corynebacterium

CC glutamicum, containing vectors that express the polynucleotides are used  
 CC for production of fine chemicals, preferably amino acids and specifically  
 CC lysine, but more generally nucleotides, nucleosides, lipids, fatty acids,  
 CC diols, carbohydrates, aromatic compounds, vitamins, co-factors and  
 CC enzymes. These are useful in the food, animal feed, cosmetics and  
 CC pharmaceutical industries. The polynucleotides, optionally as primers and  
 CC probes, can also be used for identification and classification of C.  
 CC glutamicum and related species, e.g. for diagnosis, for genomic mapping,  
 CC functional or evolutionary studies, gene manipulation and modulation of  
 CC metabolic activity. Cells that containing the polynucleotides of the  
 CC invention may produce fine chemicals in better yields, with higher  
 CC productivity and/or more efficiently. NOTE: This sequence is not  
 CC represented in the printed specification but is available in electronic  
 CC format. The sequence represented in this record has been obtained from  
 CC WO2003046123.

XX  
 SQ Sequence 1192 BP; 323 A; 283 C; 285 G; 301 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 32.8 Length: 1192  
 Score: 69.50 Matches: 17  
 Percent Similarity: 49.0% Conservatives: 7  
 Best Local Similarity: 34.7% Mismatches: 16  
 Query Match: 23.4% Indels: 9  
 DB: 11 Gaps: 2

US-10-628-525A-35 (1-58) x ADL65758 (1-1192)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 Db 396 ATGTCATCCTTTTGGCGGATTCA-----ATGGACTCAAGCGCGCT 355  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 Db 354 TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAAAATACCCAAAGCGCA 304  
 QY 41 ValAlaHisSerAlaLysPheArgVal 49  
 Db 303 ACTGCTAATTCACGAGTTTAGATTG 277

RESULT 22  
 ID AAF71202  
 AAF71202 standard; DNA; 1539 BP.

XX AC AAF71202;  
 XX  
 XX 30-APR-2001 (first entry)  
 XX  
 XX Corynebacterium glutamicum HA protein nucleotide sequence SEQ ID NO:129.  
 XX  
 XX Corynebacterium glutamicum; homeostasis; adaptation; HA protein;  
 KW fine chemical production; organic acid; proteinogenic amino acid;  
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;  
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;  
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;  
 KW diagnosis; Corynebacterium diphtheriae; genetic engineering;  
 KW Brevibacterium; environmental condition; ds.  
 XX  
 XX Corynebacterium glutamicum.

XX  
 XX WO200100842-A2.  
 XX  
 XX 04-JAN-2001.  
 XX  
 XX 23-JUN-2000; 2000WO-IB000911.  
 XX  
 XX 25-JUN-1999; 99US-0141031P.  
 PR 08-JUL-1999; 99DE-01031636.  
 PR 09-JUL-1999; 99DE-0103125.  
 PR 09-JUL-1999; 99DE-0103126.  
 PR 09-JUL-1999; 99DE-0103127.  
 PR 09-JUL-1999; 99DE-0103128.  
 PR 09-JUL-1999; 99DE-0103129.

PR 09-JUL-1999; 99DE-01032226.  
PR 14-JUL-1999; 99DE-01032920.  
PR 14-JUL-1999; 99DE-01032922.  
PR 14-JUL-1999; 99DE-01032924.  
PR 14-JUL-1999; 99DE-01032928.  
PR 14-JUL-1999; 99DE-01032930.  
PR 14-JUL-1999; 99DE-01032933.  
PR 14-JUL-1999; 99DE-01032935.  
PR 14-JUL-1999; 99DE-01032973.  
PR 14-JUL-1999; 99DE-01033002.  
PR 14-JUL-1999; 99DE-01033003.  
PR 14-JUL-1999; 99DE-01033005.  
PR 14-JUL-1999; 99DE-01033006.  
PR 31-AUG-1999; 99DE-01041378.  
PR 31-AUG-1999; 99DE-01041379.  
PR 31-AUG-1999; 99DE-01041390.  
PR 03-SEP-1999; 99DE-01041391.  
PR 03-SEP-1999; 99DE-01042088.  
XX  
PA (BADI ) BASF AG.  
XX  
PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;  
XX  
DR WPI: 2001-061974/07.  
XX  
DR P-PSDB; AAB79087.  
XX  
XX New isolated Corynebacterium glutamicum nucleic acid for production or  
PT modulation of production of fine chemicals such as amino acids,  
PT nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins or  
PT enzymes.  
XX  
PS Claim 3; Page 324-326; 712pp; English.  
XX  
CC AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis  
CC and adaptation (HA) proteins given in AAB79023 to AAB79242. The C.  
CC glutamicum HA genes (I) can be used in vectors for expression in host  
CC cells and production of fine chemicals, such as, an organic acid,  
CC proteinogenic or nonproteinogenic amino acid (preferred), purine or  
CC pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated  
CC fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor,  
CC polyketide or enzyme. The amino acids produced can be lysine, glutamine,  
CC glutamate, alanine, aspartate, glycine, serine, threonine, methionine,  
CC cysteine, valine, leucine, isoleucine, arginine, proline, histidine,  
CC tyrosine, phenylalanine, or tryptophan. The fine chemical production can  
CC be modulated. The presence of (I) or HA proteins encoded by then are used  
CC for diagnosing the presence or activity of Corynebacterium diphtheriae.  
CC (I) can be used to map the C. glutamicum genome or can be used as markers  
CC for genetically engineered Corynebacterium or Brevibacterium. The HA  
CC proteins encoded by the (I) are used to maintain homeostasis in C.  
CC glutamicum or help the microorganism to adapt to different environmental  
CC conditions  
XX  
SQ Sequence 1539 BP; 344 A; 423 C; 434 G; 338 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 46.2 Length: 1539  
Score: 69.50 Matches: 19  
Percent Similarity: 50.8% Conservative: 14  
Best Local Similarity: 29.2% Mismatches: 21  
Query Match: 23.4% Indels: 11  
DB: 4 Gaps: 3  
XX  
US-10-628-525A-35 (1-58) x AAF71202 (1-1539)  
OY 3 GlnIleuAlaProSerThrGlnTTPGlnMetArgIleThrlySerProCysAla 22  
Db 32 CAGATACTGTGGCCCAAGGTGGGTACCCCGTTGAAGAAGACGGTGTGTAC 91  
OY 23 ThrProIleThrSerLysMet-----TTPSerSerLeuValMetLysGln----- 37  
Db 92 ACGAGCTGTAGAACGTTATTCACCTGGGTGGGACCACTCGTTCAGAAAGATTTCATC 151  
OY 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAen 53

Db 152 CTTTGTGGTTCGCCCTCCAGATC-----ACCTCTGAAGTACGGTGTCTCTTTTCGAC 205  
OY 54 SerGluAenGlyThr 58  
Db 206 CAGCCAGAGGGCACC 220  
RESULT 23  
AAF71203  
ID AAF71203 standard; DNA; 1539 BP.  
XX  
AC AAF71203;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Corynebacterium glutamicum HA protein nucleotide sequence SEQ ID NO:131.  
XX  
KW Corynebacterium glutamicum; homeostasis; adaptation; HA protein;  
KW fine chemical production; organic acid; proteinogenic amino acid;  
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;  
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;  
KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;  
KW diagnosis; Corynebacterium diphtheriae; genetic engineering;  
KW Brevibacterium; environmental condition; ds.  
XX  
OS Corynebacterium glutamicum.  
XX  
PN WO200100842-A2.  
XX  
PD 04-JAN-2001.  
XX  
PF 23-JUN-2000; 2000WO-IB000911.  
XX  
PR 25-JUN-1999; 99US-0141031P.  
PR 08-JUL-1999; 99DE-01031636.  
PR 09-JUL-1999; 99DE-01032125.  
PR 09-JUL-1999; 99DE-01032126.  
PR 09-JUL-1999; 99DE-01032127.  
PR 09-JUL-1999; 99DE-01032128.  
PR 09-JUL-1999; 99DE-01032129.  
PR 09-JUL-1999; 99DE-01032226.  
PR 14-JUL-1999; 99DE-01032920.  
PR 14-JUL-1999; 99DE-01032922.  
PR 14-JUL-1999; 99DE-01032924.  
PR 14-JUL-1999; 99DE-01032928.  
PR 14-JUL-1999; 99DE-01032930.  
PR 14-JUL-1999; 99DE-01032933.  
PR 14-JUL-1999; 99DE-01032935.  
PR 14-JUL-1999; 99DE-01032973.  
PR 14-JUL-1999; 99DE-01033002.  
PR 14-JUL-1999; 99DE-01033003.  
PR 14-JUL-1999; 99DE-01033005.  
PR 14-JUL-1999; 99DE-01033006.  
PR 31-AUG-1999; 99DE-01041378.  
PR 31-AUG-1999; 99DE-01041379.  
PR 31-AUG-1999; 99DE-01041390.  
PR 31-AUG-1999; 99DE-01041391.  
PR 03-SEP-1999; 99DE-01042088.  
XX  
PA (BADI ) BASF AG.  
XX  
PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;  
XX  
DR WPI: 2001-061974/07.  
XX  
DR P-PSDB; AAB79088.  
XX  
PT New isolated Corynebacterium glutamicum nucleic acid for production or  
PT modulation of production of fine chemicals such as amino acids,  
PT nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins or  
PT enzymes.  
XX  
PS Claim 3; Page 328-330; 712pp; English.  
XX



XX Cooper B;  
XX WPI; 2004-534388/51.  
XX  
XX New nucleic acid molecule encoding a cell proliferation-related  
PT polypeptide, useful for modulating cell proliferation, senescence,  
PT differentiation, development, and stress response in plants, and for  
PT producing enhanced food crops.  
XX  
XX Disclosure; SEQ ID NO 345; 408pp; English.  
XX  
XX The present invention relates to an isolated nucleic acid molecule  
CC encoding a cell proliferation-related polypeptide. The nucleic acid  
CC molecule and the encoded polypeptide, and methods are useful for  
CC modulating cell proliferation, senescence, differentiation, development,  
CC and stress response in plants, and for producing enhanced food crops. The  
CC present sequence represents a cell proliferation-related nucleic acid  
CC sequence. The present sequence is published separately from the main body  
CC of the specification as EPO data.  
XX  
XX Sequence 1950 BP; 468 A; 515 C; 561 G; 406 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 73.8 Length: 1950  
Score: 69.00 Matches: 18  
Percent Similarity: 63.6% Conservative: 10  
Best Local Similarity: 40.9% Mismatches: 10  
Query Match: 23.2% Indels: 6  
DB: 12 Gaps: 2  
US-10-628-525A-35 (1-58) x ADQ37186 (1-1950)  
QY 4 IleLeuAlaProSerThrGlnTrp---GlnMetArgIleThrLysThrSerPro----- 20  
DB 758 CTCTTGAATTCTTGCAACAAGTGGTTGACCATGGGTTGTCAAATCTTCACCAACAGA 699  
QY 21 -----CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGln 37  
DB 698 TGGGTGTCCACGCTGTGGCTTGACCTCAAGATACCTCTCTCAATGGTAAGGAGGAA 639  
QY 38 ThrLysLysVal 41  
DB 638 ACATCAAGGTA 627  
RESULT 26  
ADQ97278/c  
ID ADQ97278 standard; DNA; 86149 BP.  
XX  
AC ADQ97278;  
XX  
XX 07-OCT-2004 (first entry)  
XX  
XX Human cancer associated sequence HD08-025, SEQ ID 254.  
XX  
XX Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO2004060304-A2.  
XX  
XX 22-JUL-2004.  
XX  
XX 22-DEC-2003; 2003WO-US041389.  
XX  
XX 27-DEC-2002; 2002US-00330773.  
XX  
XX (SAGR-) SAGRES DISCOVERY INC.  
XX  
XX Morris DW, Malandro MS;  
XX  
XX WPI; 2004-543781/52.  
XX

PT New isolated cancer associated nucleic acids comprising at least 10  
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating  
XX cancers such as leukemia and lymphoma.  
XX  
XX Claim 1; SEQ ID NO 254; 199pp; English.  
XX  
XX The present invention relates to cancer associated sequences (ADQ97025-  
CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or  
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 86149 BP; 19445 A; 19457 C; 18668 G; 20667 T; 0 U; 7912 Other;  
SQ  
Alignment Scores:  
Pred. No.: 1.57e+04 Length: 86149  
Score: 68.00 Matches: 17  
Percent Similarity: 45.3% Conservative: 7  
Best Local Similarity: 32.1% Mismatches: 29  
Query Match: 22.9% Indels: 0  
DB: 12 Gaps: 0  
US-10-628-525A-35 (1-58) x ADQ97278 (1-86149)  
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
DB 46678 GCCCGCAGCTCACCATGGTAGATGTAATATATCTGGAGACCCCTGTTCAGGCTCAGAGATT 46619  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45  
DB 46618 TGCAGAGCCCATGGGGCGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 46559  
QY 46 LysPheArgValMetAlaValAsnSerGluAsnGlyThr 58  
DB 46558 AGATTTCAGCAGCTCAACGAGGAACTGGAGAAAGGCCT 46520  
RESULT 27  
AEA61124.0  
WP Sequence split into 4 fragments LOCUS AEA61124 Accession Aea61124  
WP Fragment Name Begin End  
WP AEA61124\_0 1 110000  
WP AEA61124\_1 100001 210000  
WP AEA61124\_2 200001 310000  
WP AEA61124\_3 300001 383432  
ID AEA61124 standard; DNA; 383432 BP.  
XX  
AC AEA61124;  
XX  
XX 25-AUG-2005 (first entry)  
XX  
XX Human SLC4A4 gene genomic sequence SEQ ID NO:34.  
XX  
XX DNA methylation; biomarker; cancer; gene; ds; SLC4A4.  
XX  
XX Homo sapiens.  
XX  
XX US2005130172-A1.  
XX  
XX 16-JUN-2005.  
XX  
XX 27-JAN-2004; 2004US-00765790.  
XX  
XX 16-DEC-2003; 2003US-00737082.  
XX  
XX (FARB ) BAYER CORP.  
XX  
XX Beard C, Burgess C, Gannon A, Harvey J, Lechner JF, Li Z;  
XX WPI; 2005-456991/46.  
XX GENBANK; AF011390, NM\_003759.  
XX  
XX Identifying nucleic acid sequences as biomarker for disease, by  
PT

PT identifying nucleic acid sequences comprising methylated CpG site and  
PT down-regulated in diseased cells and comparing its expression level with  
XX demethylated nucleic acid.

PS Claim 11; SEQ ID NO 34; 27pp; English.

XX The invention relates to a method (M1) for identifying one or more  
CC nucleic acid sequences useful as a biomarker for a disease to be  
CC detected. (M1) involves identifying nucleic acid sequences comprising  
CC methylated CpG site in promoter-first exon region and that are down-  
CC regulated in diseased cells, comparing expression level of nucleic acid  
CC sequences with that of demethylated nucleic acid sequences and  
CC identifying nucleic acid sequences exhibiting increase in expression  
CC after demethylation. Also described: (1) detecting (M2) the presence or  
CC stage of a disease in a subject, which involves determining the degree of  
CC methylation of one or more CpG sites on nucleic acid sequences in a  
CC biological sample obtained from the subject, and determining the presence  
CC of, predisposition to, or stage of the disease in the subject based on  
CC the degree of methylation; (2) monitoring the onset, progression, or  
CC regression of a disease in a subject; (3) determining the efficacy of a  
CC test compound for inhibiting a disease in a subject; and (4) a kit (I)  
CC useful for diagnosis, prognosis, staging, monitoring, and therapeutic  
CC treatment of a disease. (M1) is useful for identifying one or more  
CC nucleic acid sequences useful as a biomarker for a disease to be  
CC detected, where the nucleic acid sequences are useful for detecting, the  
CC presence or stage of a disease such as cancer e.g. colorectal cancer in a  
CC subject. The present sequence represents a specifically claimed human  
CC genomic sequence for use in the method of the invention. Note - The  
CC sequence data for this patent is not represented in the printed  
CC specification but was obtained in electronic format from the USPTO web  
CC site.

SQ Sequence 383432 BP; 113010 A; 59169 C; 74959 G; 126294 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.: 2.18e+04 Length: 110000  
Score: 68.00 Matches: 14  
Percent Similarity: 60.0% Conservative: 7  
Best Local Similarity: 40.0% Mismatches: 14  
Query Match: 22.9% Indels: 0  
DB: 14 Gaps: 0

US-10-628-525A-35 (1-58) x AEA61124\_0 (1-110000)

QY 14 ArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSerSerLeu 33  
Db 72417 CGTATTATATTCCTCCCTGCGCTTTCTCCCTTGGCACATAAAATCTGGCTT 72476  
QY 34 ValMetLysGlnThrLysLysValAlaHisSerAlaLysPheArg 48  
Db 72477 TTAATTATCCCACTTGGAAAGTGCTCATTTATTGTGTATCGC 72521

## RESULT 28

ACH47744  
ID ACH47744 standard; cDNA; 421 BP.

AC ACH47744;

DT 13-OCT-2003 (first entry)

DE Human infant brain cDNA #1807.

KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
KW Genome mapping; biodiversity; genetic disorder.

OS Homo sapiens.

PN US2003073623-A1.

PD 17-APR-2003.

PF 30-JUL-2001; 2001US-00918995.

XX

PR 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.

XX Claim 1; SEQ ID NO 34956; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH2789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030073623

SQ Sequence 421 BP; 120 A; 98 C; 92 G; 111 T; 0 U; 0 Other;

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Percent Similarity: 49.1% Conservative: 11  
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Query Match: 22.7% Indels: 9  
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QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44  
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## RESULT 29

AAI63931  
ID AAI63931 standard; cDNA; 939 BP.

AC AAI63931;

DT 22-OCT-2001 (first entry)

DE Human polynucleotide SEQ ID NO 139.

KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;  
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;

fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;  
neuroprotective; antiallergic; hepatotropic; antidiabetic;  
antiinflammatory; antitumor; vulnerary; anticonvulsant; antibacterial;  
antiparasitic; cardiant; gene therapy; cancer; immune disorder;  
cardiovascular disorder; neurological disease; infection; human; ss.

Homo sapiens.

WO200155308-A2.

02-AUG-2001.

17-JAN-2001; 2001WO-US001309.

31-JAN-2000; 2000US-0179065P.

04-FEB-2000; 2000US-0180628P.

24-FEB-2000; 2000US-0184664P.

02-MAR-2000; 2000US-0186350P.

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PR 08-DEC-2000; 2000US-0251989P.
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PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-488781/53.
XX P-PSDB; AAM43625.
DR
XX New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders.
XX
XX Claim 1; SEQ ID NO 139; 664pp + Sequence Listing; English.
PS
XX The invention relates to human polynucleotides (AAI63803-AAI64012) and
CC the encoded proteins (AAM434497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d)
CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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SQ Sequence 939 BP; 246 A; 199 C; 216 G; 273 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.: 44.2 Length: 939
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 4 Gaps: 1

US-10-628-525A-35 (1-58) x AAI63931 (1-939)
QY 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11
Db 159 ATGGGAGAGATCTTCCACCTCTAATGAACCGCGGTGTGCCCAAGTTTGGTGG 218
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ID AAS31627 standard; cDNA; 939 BP.
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AC AAS31627;
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DT 04-DEC-2001 (first entry)
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DE cDNA encoding novel human calcium-binding protein #51.
KW Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
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KW virucide; ss.
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OS Homo sapiens.
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PN WO200153304-A2.
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PD 02-AUG-2001.
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PF 17-JAN-2001; 2001WO-US001302.
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PR 31-JAN-2000; 2000US-0179065P.
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XX (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-465568/50.  
 XX P-PSDB; AAU19942.  
 PT Isolated nucleic acid molecule encoding a calcium-binding protein is used  
 in preventing, treating or ameliorating a medical condition.  
 XX Claim 4; SEQ ID NO 61; 542pp; English.  
 XX The present invention relates to the isolation of novel human calcium-  
 binding proteins (AAU19892-AAU19969), and cDNA and genomic sequences  
 encoding for these proteins. The sequences of the invention are useful in  
 the diagnosis, prevention and/or prognosis of diseases associated with  
 aberrant calcium flux. Such disorders include neurological diseases (e.g.  
 amyotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe  
 combined immunodeficiency, SCID), digestive disorders (e.g. irritable  
 bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders  
 (e.g. haemophilia), and/or infectious disease (e.g. acquired  
 immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are  
 also useful as screening tools to identify antagonists and/or agonists  
 that may enhance or inhibit activities mediated by calcium-binding  
 proteins. The polynucleotides of the invention are also useful in gene  
 therapy. AAS31577-AAS31654 represent cDNA sequences encoding for the  
 novel human calcium-binding proteins. Note: The sequence data for this  
 patent did not form part of the printed specification, but was obtained  
 in electronic format directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 939 BP; 246 A; 199 C; 216 G; 273 T; 0 U; 5 Other;  
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 Pred. No.: 44.2 Length: 939  
 Score: 67.50 Matches: 15  
 Percent Similarity: 49.1% Conservative: 11  
 Best Local Similarity: 28.3% Mismatches: 18  
 Query Match: 22.7% Indels: 9  
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

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Post-processing: Minimum Match 0%
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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4 223 75.1 428 2 BE323195 BE323195 NF001G02P
5 223 75.1 447 2 BP521090 BP521090 EST458564
6 223 75.1 454 2 BE317419 BE317419 NF069A11L
7 223 75.1 477 1 AM689288 AM689288 NF017E08S
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8	223	75.1	486	1	AM690855	AM690855	NF039G07S
9	223	75.1	488	3	BQ140918	BQ140918	NF055A10P
10	223	75.1	492	2	BE323101	BE323101	NF004A10P
11	223	75.1	541	2	BE316885	BE316885	NF056F08L
12	223	75.1	553	2	BE319151	BE319151	NF045C12L
13	223	75.1	562	2	BE321453	BE321453	NF025E10I
14	223	75.1	570	2	BF638827	BF638827	NF079C04P
15	223	75.1	580	8	CX526728	CX526728	813NF26A
16	223	75.1	582	1	AM688380	AM688380	NF006G01S
17	223	75.1	597	2	BE321399	BE321399	NF024E10I
18	223	75.1	614	2	BE326809	BE326809	NF117F10I
19	223	75.1	628	1	AM696250	AM696250	NF104E11S
20	223	75.1	642	2	BF642149	BF642149	NF058D06I
21	223	75.1	649	1	AM693739	AM693739	NF068B07S
22	223	75.1	650	2	BE325326	BE325326	NF120H12S
23	223	75.1	651	3	BQ139196	BQ139196	NF012F06P
24	223	75.1	656	1	AM691414	AM691414	NF044E06S
25	223	75.1	657	1	AM695784	AM695784	NF009B12S
26	223	75.1	688	2	BE322970	BE322970	NF025H10I
27	223	75.1	812	1	AM688552	AM688552	NF008H08S
28	220	74.1	406	2	BF639835	BF639835	NF026G07I
29	219	73.7	630	1	AM573676	AM573676	EST316267
30	218	73.4	457	1	AL572792	AL572792	MCBA53F02
31	218	73.4	458	2	BE323758	BE323758	NF007H06P
32	217	73.1	360	1	AV408180	AV408180	AV408180
33	217	73.1	381	1	AV423273	AV423273	AV423273
34	217	73.1	384	1	AV419708	AV419708	AV419708
35	217	73.1	387	1	AV426836	AV426836	AV426836
36	217	73.1	387	3	BI419883	BI419883	LJNEST17E
37	217	73.1	390	1	AV423048	AV423048	AV423048
38	217	73.1	402	1	AV407093	AV407093	AV407093
39	217	73.1	405	1	AV420900	AV420900	AV420900
40	217	73.1	413	1	AV416605	AV416605	AV416605
41	217	73.1	414	1	AV410112	AV410112	AV410112
42	217	73.1	414	1	AV416374	AV416374	AV416374
43	217	73.1	414	1	AV424686	AV424686	AV424686
44	217	73.1	416	1	AV412955	AV412955	AV412955
45	217	73.1	418	1	AV424625	AV424625	AV424625
46	217	73.1	423	1	AV408409	AV408409	AV408409
47	217	73.1	423	1	AV410960	AV410960	AV410960
48	217	73.1	423	1	AV425462	AV425462	AV425462
49	217	73.1	425	1	AV407495	AV407495	AV407495
50	217	73.1	425	1	AV416585	AV416585	AV416585
51	217	73.1	427	1	AV415839	AV415839	AV415839
52	217	73.1	429	1	AV410526	AV410526	AV410526
53	217	73.1	431	1	AV408612	AV408612	AV408612
54	217	73.1	431	1	AV409954	AV409954	AV409954
55	217	73.1	499	3	BI420133	BI420133	LJNEST53d
56	217	73.1	529	6	CB829301	CB829301	LJNEST96e
57	217	73.1	536	3	BI418594	BI418594	LJNEST43e
58	217	73.1	545	3	BI418791	BI418791	LJNEST48h
59	217	73.1	554	1	AW720158	AW720158	LJNEST16a
60	217	73.1	850	11	CR307348	CR307348	mtel-28C6
61	216	72.7	566	1	AM620695	AM620695	g108601.y
62	211	71.0	427	1	AV408762	AV408762	AV408762
63	210	70.7	273	1	AV429053	AV429053	AV429053
64	210	70.7	419	3	BQ273341	BQ273341	esol1a10.
65	210	70.7	525	1	AM596186	AM596186	6199a12.y
66	210	70.7	580	3	BI974110	BI974110	es196f08.
67	210	70.7	588	3	BM143687	BM143687	es196f08.
68	210	70.7	621	3	BM108015	BM108015	a05g10.cd
69	208	70.0	342	1	AV411599	AV411599	AV411599
70	206	69.4	658	8	CX178438	CX178438	C06_45-49
71	205	69.0	452	1	AJ645307	AJ645307	AJ645307
72	205	69.0	543	1	AW399670	AW399670	EST310170
73	205	69.0	580	1	AM399193	AM399193	EST309693
74	205	69.0	583	1	AM399118	AM399118	EST309618
75	205	69.0	585	2	BF053088	BF053088	EST438318
76	205	69.0	657	3	BQ047105	BQ047105	EST596223
77	205	69.0	691	7	CK273506	CK273506	EST719584
78	205	69.0	706	2	BG589824	BG589824	EST437666
79	205	69.0	730	2	BG591105	BG591105	EST498947
80	205	69.0	875	7	CK279059	CK279059	EST725137



ACCESSION BE323583  
 VERSION BE323583.2 GI:11965726  
 KEYWORDS EST.  
 SOURCE Medicago truncatula (barrel medic)  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.  
 REFERENCE 1 (bases 1 to 393)  
 AUTHORS Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D., and Harrison, M.J.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library  
 JOURNAL Unpublished (2000)  
 COMMENT On Jul 14, 2000 this sequence version replaced gi:9197360.  
 Contact: Harrison MJ  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7325  
 Fax: 580 221 7380  
 Email: mjharrison@noble.org  
 Medicago Genome Initiative accession: MGI:S:22731  
 Insert Length: 792 Std Error: 0.00  
 Plate: 016 row: C column: 08  
 Seq primer: TCACACGAGAAACAGCTATGAC.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:3880"  
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 /dev\_stage="trifoliolate"  
 /clone\_lib="Phosphate starved leaf"  
 /note="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.69e-18 Length: 393  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-628-525A-35 (1-58) x BE323583 (1-393)  
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 Db 92 ATGGCACAGATTTGGCTCTCTTACACAATGTGAGCAAGATCATCAAAATCTCTCCC 151  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
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 Db 152 GTTGCACACTCTCATCAAGATGTGGAGTCTTTGGTTATGAACAACAAAGAA 211  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
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 Db 212 GTGGCAGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 253  
 RESULT 3  
 BQ140352  
 LOCUS NF034F04PHIP1043 Phoma-infected Medicago truncatula cdna clone  
 DEFINITION NF034F04PH 5', mRNA sequence.  
 ACCESSION BQ140352  
 VERSION BQ140352.1 GI:20276478

KEYWORDS EST.  
 SOURCE Medicago truncatula (barrel medic)  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.  
 REFERENCE 1 (bases 1 to 399)  
 AUTHORS Watson, B.S., Shin, H.-S., Lopez-Meyer, M., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Imman, J.T., Waugh, M.E., Sullivan, J.P., May, G.D., and Paiva, N.L.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula Phoma-infected library  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Paiva NL  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7317  
 Fax: 580 221 7380  
 Email: nlpaiva@noble.org  
 Insert Length: 399 Std Error: 0.00  
 Plate: 034 row: P column: 04  
 Seq primer: TCACACGAGAAACAGCTATGAC.  
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 /clone="NF034F04PH"  
 /tissue\_type="leaf"  
 /dev\_stage="Pathogen-induced, young trifoliolate"  
 /clone\_lib="Phoma-infected"  
 /note="Vector: pBluescript SK(-); Young trifoliolate leaves of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and incubated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96 hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAmpist helper phage and the E. coli strain XL1-Blue MRP' (Stratagene). Excised plasmids were plated using SOLR cells."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.77e-18 Length: 399  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
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 Db 97 ATGGCACAGATTTGGCTCTCTTACACAATGTGAGCAAGATCATCAAAATCTCTCCC 156  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 157 GTTGCACACTCTCATCAAGATGTGGAGTCTTTGGTTATGAACAACAAAGAA 216  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
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 Db 217 GTGGCAGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 258  
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BE323195
LOCUS       BE323195                428 bp    mRNA    linear    EST 21-DEC-2000
DEFINITION   NF001G02PL1F1008 Phosphate starved leaf Medicago truncatula cDNA
clone NF001G02PL 5', mRNA sequence.
ACCESSION   BE323195
VERSION     BE323195.2  GI:11966519
KEYWORDS    Medicago truncatula (barrel medic)
SOURCE      Medicago truncatula
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1 (bases 1 to 428)
AUTHORS     Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
            Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
TITLE       Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula phosphate-starved leaf library
JOURNAL     Unpublished (2000)
COMMENT     On Jul 14, 2000 this sequence version replaced gi:9196972.
            Contact: Harrison MJ
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7325
            Fax: 580 221 7380
            Email: mjharrison@noble.org
            Medicago Genome Initiative accession: MGI:S:19371
            Insert length: 701 Std Error: 0.00
            Plate: 001 row: G column: 02
            Seq primer: TCACACAGGAACAGCTATGAC.
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                     /clone="NF001G02PL"
                     /tissue_type="leaf"
                     /dev_stage="trifoliolate"
                     /clone_lib="Phosphate starved leaf"
                     /note="Vector: Lambda Zap; At the trifoliolate stage, M.
                     truncatula plants were transplanted to phosphate-free sand
                     and grown for a further 30 days. During this 30 day
                     period, the plants were fertilized twice weekly with 1/2
                     Hoaglands solution containing only 20uM potassium
                     phosphate. RNA was prepared from above ground tissues."

ORIGIN
Alignment Scores:
Pred. No.:      4,14e-18      Length:      428
Score:          223.00      Matches:    47
Percent Similarity: 88.9%      Conservative: 1
Best Local Similarity: 87.0%      Mismatches: 6
Query Match:    75.1%      Indels:    0
DB:             2           Gaps:      0

US-10-628-525A-35 (1-58) x BE323195 (1-428)

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         |||||

QY      21 CysAlaThrProIleThrSerIlyMetTrpSerSerLeuValMetIlyGlnThrIlyLys 40
         |||||
Db      193 GTTGCACCTCCATCTCATCAAGATGTGGAGTTCTTTGGTTATGAAACAAACAGAAA 242
         |||||

QY      41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
         |||||
Db      243 GTCGCACGTTCTGTCTAAATTCAGAGTAATGGCAGTCAACTCT 284
         |||||

RESULT 5
BF521090
LOCUS       BF521090                447 bp    mRNA    linear    EST 08-DEC-2000
DEFINITION   EST458564 DSIL Medicago truncatula cDNA clone pDSIL-41114, mRNA
sequence.
ACCESSION   BF521090
VERSION     BF521090.1  GI:11609773
KEYWORDS    Medicago truncatula (barrel medic)
SOURCE      Medicago truncatula
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1 (bases 1 to 447)
AUTHORS     Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S.,
            Peng, H., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B.,
            Hansen, T.S., Holt, J.E. and Fraser, C.M.
TITLE       ESTs from leaves of Medicago truncatula after inoculation with
            Colletotrichum trifolii
JOURNAL     Unpublished (2000)
COMMENT     Contact: Deborah A. Samac
            Department of Plant Pathology
            University of Minnesota
            495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
            Tel: 612 625 1243
            Fax: 651 649 5058
            Email: debbys@umn.edu
            University of Minnesota name: M278533e
            TIGR sequence name: MTPD557K
            More information is available at: http://chrysis.tamu.edu/medicago
            Seq primer: SKmod (CTA GAA CTA Gtg GAR CC).
            Location/Qualifiers
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                     /db_xref="taxon:3880"
                     /clone="pDSIL-41114"
                     /tissue_type="leaves infected with Colletotrichum
                     trifolii"
                     /dev_stage="cotyledons and primary leaves harvested 5 and
                     8 days after inoculation with Colletotrichum trifolii"
                     /lab_host="E. coli strain XLOLR"
                     /clone_lib="DSIL"
                     /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
                     XhoI; cDNA was prepared from polyA+ enriched RNA from
                     cotyledons and primary leaves harvested 5 and 8 days after
                     inoculation with Colletotrichum trifolii. The cDNA was
                     directionally ligated into the Uni-ZAP XR vector from
                     Stratagene and packaged using Gigapack III Gold packaging
                     extracts. Plasmids containing cDNA inserts were excised
                     from the recombinant lambda-ZAP phage using Ex-Aestit
                     helper phage and propagated in XLOLR cells. Note: EST may
                     be of fungal origin."

ORIGIN
Alignment Scores:
Pred. No.:      4,38e-18      Length:      447
Score:          223.00      Matches:    47
Percent Similarity: 88.9%      Conservative: 1
Best Local Similarity: 87.0%      Mismatches: 6
Query Match:    75.1%      Indels:    0
DB:             2           Gaps:      0

US-10-628-525A-35 (1-58) x BF521090 (1-447)

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QY      21 CysAlaThrProIleThrSerIlyMetTrpSerSerLeuValMetIlyGlnThrIlyLys 40
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Db      150 GTTGCACCTCCATCTCATCAAGATGTGGAGTTCTTTGGTTATGAAACAAACAGAAA 209
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QY      41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
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Db      210 GTGCACGTTCTGCTAAATTCAGAGTAATGCAGTCAACTCT 251
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RBSULT 6
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LOCUS      BE317419
DEFINITION BE317419 454 bp mRNA linear EST 21-DEC-2000
            NF069A11LP 5', mRNA sequence.
ACCESSION BE317419
VERSION    BE317419.2 GI:11960851
KEYWORDS
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE 1 (bases 1 to 454)
AUTHORS   Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
            Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
TITLE      Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula leaf library
JOURNAL    Unpublished (2000)
COMMENT    On Jul 14, 2000 this sequence version replaced gi:9191196.
            Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 224 6650
            Fax: 580 224 6692
            Email: gdmay@noble.org
            Medicago Genome Initiative accession: MGI:S:21261
            Insert Length: 740 Std Error: 0.00
            Plate: 069 row: A column: 11
            Seq primer: TCACACAGGAACAGCTATGAC.
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            young, developing, mature and senescing leaves."
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Pred. No.: 4,47e-18 Length: 454
Score: 223.00 Matches: 47
Percent Similarity: 88.9% Conservative: 1
Best Local Similarity: 87.0% Mismatches: 6
Query Match: 75.1% Indels: 0
DB: 2 Gaps: 0
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Db 72 ATGGCAGATTGTGGCTCTCTACACAATGTGCAGGAAGATCAAAAATCTCTCCC 131
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 132 GTTGCAACTCCATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAAA 191
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
Db 192 GTGCACGTTCTGCTAAATTCAGAGTAATGCAGTCAACTCT 233
RBSULT 7
AW689288
LOCUS      AW689288
DEFINITION AW689288 477 bp mRNA linear EST 15-JUN-2000
            NF039G07ST 5', mRNA sequence.
ACCESSION AW689288
VERSION    AW689288.2 GI:11936565
KEYWORDS
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula

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DEFINITION NF017E08STIF1000 Developing stem Medicago truncatula cDNA clone
ACCESSION  AW689288
VERSION     AW689288.1 GI:7564024
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE 1 (bases 1 to 477)
AUTHORS   He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A.,
            Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and
            Dixon, R.A.
TITLE      Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula stem library
JOURNAL    Unpublished (2000)
COMMENT    Contact: Dixon RA
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7302
            Fax: 580 221 7380
            Email: radixon@noble.org
            Insert Length: 477 Std Error: 0.00
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            /dev_stage="Pooled developmental"
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            /note="Vector: Lambda Zap; Contains a mixture of
            internodal stem segments"
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Pred. No.: 4,78e-18 Length: 477
Score: 223.00 Matches: 47
Percent Similarity: 88.9% Conservative: 1
Best Local Similarity: 87.0% Mismatches: 6
Query Match: 75.1% Indels: 0
DB: 1 Gaps: 0
US-10-628-525A-35 (1-58) x AW689288 (1-477)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 62 ATGGCAGATTGTGGCTCTCTACACAATGTGCAGGAAGATCAAAAATCTCTCCC 121
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 122 GTTGCAACTCCATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAAA 181
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
Db 182 GTGCACGTTCTGCTAAATTCAGAGTAATGCAGTCAACTCT 223
RBSULT 8
AW690855
LOCUS      AW690855
DEFINITION AW690855 486 bp mRNA linear EST 21-DEC-2000
            NF039G07STIF1000 Developing stem Medicago truncatula cDNA clone
            NF039G07ST 5', mRNA sequence.
ACCESSION AW690855
VERSION    AW690855.2 GI:11936565
KEYWORDS
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 486)

He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Dixon, R.A.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library

Unpublished (2000)

On Apr 14, 2000 this sequence version replaced gi:7565679.

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 692 Std Error: 0.00

Plate: 039 row: G column: 07

Seq primer: TCACACAGGAACAGCTATGAC.

Location/Qualifiers

1. .486

/organism="Medicago truncatula"

/mol\_type="mRNA"

/db\_xref="taxon:3880"

/clone="NF039G07ST"

/tissue\_type="stem"

/dev\_stage="Pooled developmental"

/clone\_lib="Developing stem"

/note="Vector: Lambda Zap; Contains a mixture of

internodal stem segments"

# ORIGIN

## Alignment Scores:

Pred. No.: 4,9e-18 Length: 486  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 1 Gaps: 0

US-10-628-525A-35 (1-58) x AW690855 (1-486)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20  
|||||  
Db 66 ATGGCACAGATTTGGCTCTCTACCAATGTCAGGCAAGAAATCACAAAAATCTCTCCC 125

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrIysLys 40  
|||||  
Db 126 GTTGCACACTCCAAATCTCATCAAGATGTGGAGTTCTTTGGTTATGAAACAAACAGAAA 185

QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||  
Db 186 GTTCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 227

# RESULT 9

BQ140918  
LOCUS BQ140918 488 bp mRNA linear EST 26-APR-2002  
DEFINITION NF055A10PH1F1081 Phoma-infected Medicago truncatula cDNA clone  
NF055A10PH 5', mRNA sequence.

ACCESSION BQ140918.1 GI:20277044

VERSION BQ140918

KEYWORDS Medicago truncatula (barrel medic)

SOURCE Medicago truncatula

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 488)

Watson, B.S., Shin, H.-S., Lopez-Meyer, M., Scott, A.D., Harris, A.R.,

## TITLE

## JOURNAL

## COMMENT

Gonzales, R.A., Bell, C.J., Inman, J.T., Waugh, M.E., Sullivan, J.P., May, G.D. and Paiva, N.L.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula Phoma-infected library  
Unpublished (2002)  
Contact: Paiva NL

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The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7317

Fax: 580 221 7380

Email: nlpaiva@noble.org

Insert Length: 488 Std Error: 0.00

Plate: 055 row: A column: 10

Seq primer: TCACACAGGAACAGCTATGAC.

Location/Qualifiers

1. .488

/organism="Medicago truncatula"

/mol\_type="mRNA"

/db\_xref="taxon:3880"

/clone="NF055A10PH"

/tissue\_type="leaf"

/dev\_stage="Pathogen-induced, young trifoliolate"

/clone\_lib="Phoma-infected"

/note="Vector: pBluescript SK(-); Young trifoliolate leaves

of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and incubated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

## ORIGIN

Alignment Scores:  
Pred. No.: 4,92e-18 Length: 488  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x BQ140918 (1-488)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20  
|||||  
Db 88 ATGGCACAGATTTGGCTCTCTACCAATGTCAGGCAAGAAATCACAAAAATCTCTCCC 147

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrIysLys 40  
|||||  
Db 148 GTTGCACACTCCAAATCTCATCAAGATGTGGAGTTCTTTGGTTATGAAACAAACAGAAA 207

QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||

Db 208 GTTCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 249

## RESULT 10

## BE323101

## LOCUS

## DEFINITION

BE323101 492 bp mRNA linear EST 21-DEC-2000

NF004A10PL1F1069 Phosphate starved leaf Medicago truncatula cDNA clone NF004A10PL 5', mRNA sequence.

ACCESSION BE323101

VERSION BE323101.2 GI:11967028

KEYWORDS EST.

SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 492)

Liou, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula phosphate-starved leaf library  
Unpublished (2000)

## JOURNAL

## COMMENT

On Jul 14, 2000 this sequence version replaced gi:9196794.

Contact: Harrison MJ

Plant Biology Division

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Tel: 580 221 7325

Fax: 580 221 7380

Email: mjharrison@noble.org

Medicago Genome Initiative accession: MGI:S:20027

Insert Length: 693 Std Error: 0.00

Plate: 004 row: A column: 10

Seq primer: TCACACAGGAACAGCTATGAC.

## FEATURES

## source

1..492  
Location/Qualifiers  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF004A10PL"  
/tissue\_type="leaf"  
/dev\_stage="trifoliolate"  
/clone\_lib="phosphate starved leaf"  
/notes="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."

## ORIGIN

Alignment Scores:  
Pred. No.: 4,98e-18 Length: 492  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE323101 (1-492)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 75 ATGGCAGAGATTGGCTCTTCTACACAATGTGCGCAAGATCAAAAAATCTCTCCC 134  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40  
|||||  
DB 135 GTTGCAGCTTCCATCTCAATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 194  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||  
DB 195 GTGCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCACTCT 236

## RESULT 11

## BE316885

## LOCUS

## DEFINITION

BE316885 NF056F08LIF1063 Developing leaf Medicago truncatula cDNA clone

NP056F08LIF 5', mRNA sequence.

## ACCESSION

## BE316885

## VERSION

## BE316885.2

## GI:11960466

## KEYWORDS

## EST.

## SOURCE

## ORGANISM

## Medicago truncatula (barrel medic)

## Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 553)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

On Jul 14, 2000 this sequence version replaced gi:9190662.

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 224 6650

Fax: 580 224 6692

Email: gdmay@noble.org

Medicago Genome Initiative accession: MGI:S:21086

Insert Length: 697 Std Error: 0.00

Plate: 056 row: F column: 08

Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES

source

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Location/Qualifiers  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF056F08LIF"  
/tissue\_type="leaf"  
/dev\_stage="Pooled developmental"  
/clone\_lib="Developing leaf"  
/notes="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

ORIGIN

Alignment Scores:  
Pred. No.: 5,64e-18 Length: 541  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE316885 (1-541)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 135 ATGGCAGAGATTGGCTCTTCTACACAATGTGCGCAAGATCAAAAAATCTCTCCC 194  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40  
|||||  
DB 195 GTTGCAGCTTCCATCTCAATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 254  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||  
DB 255 GTGCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCACTCT 296

RESULT 12

BE319151

LOCUS

DEFINITION

BE319151 NF045C12LIF1087 Developing leaf Medicago truncatula cDNA clone

NP045C12LIF 5', mRNA sequence.

ACCESSION

BE319151

VERSION

BE319151.2

GI:11962557

KEYWORDS

EST.

SOURCE

ORGANISM

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 553)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

On Jul 14, 2000 this sequence version replaced gi:9190662.

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 224 6650

Fax: 580 224 6692

Email: gdmay@noble.org

Medicago Genome Initiative accession: MGI:S:21086

Insert Length: 697 Std Error: 0.00

Plate: 056 row: F column: 08

Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES

source

1..541  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF056F08LIF"  
/tissue\_type="leaf"  
/dev\_stage="Pooled developmental"  
/clone\_lib="Developing leaf"  
/notes="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

ORIGIN

Alignment Scores:  
Pred. No.: 5,64e-18 Length: 541  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE316885 (1-541)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 135 ATGGCAGAGATTGGCTCTTCTACACAATGTGCGCAAGATCAAAAAATCTCTCCC 194  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40  
|||||  
DB 195 GTTGCAGCTTCCATCTCAATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 254  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||  
DB 255 GTGCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCACTCT 296

RESULT 12

BE319151

LOCUS

DEFINITION

BE319151 NF045C12LIF1087 Developing leaf Medicago truncatula cDNA clone

NP045C12LIF 5', mRNA sequence.

ACCESSION

BE319151

VERSION

BE319151.2

GI:11962557

KEYWORDS

EST.

SOURCE

ORGANISM

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 553)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

On Jul 14, 2000 this sequence version replaced gi:9190662.

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

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Tel: 580 224 6650

Fax: 580 224 6692

Email: gdmay@noble.org

Medicago Genome Initiative accession: MGI:S:21086

Insert Length: 697 Std Error: 0.00

Plate: 056 row: F column: 08

Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES

source

1..541  
Location/Qualifiers  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF056F08LIF"  
/tissue\_type="leaf"  
/dev\_stage="Pooled developmental"  
/clone\_lib="Developing leaf"  
/notes="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

ORIGIN

Alignment Scores:  
Pred. No.: 5,64e-18 Length: 541  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE316885 (1-541)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 135 ATGGCAGAGATTGGCTCTTCTACACAATGTGCGCAAGATCAAAAAATCTCTCCC 194  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40  
|||||  
DB 195 GTTGCAGCTTCCATCTCAATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 254  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||  
DB 255 GTGCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCACTCT 296

RESULT 12

BE319151

LOCUS

DEFINITION

BE319151 NF045C12LIF1087 Developing leaf Medicago truncatula cDNA clone

NP045C12LIF 5', mRNA sequence.

ACCESSION

BE319151

VERSION

BE319151.2

GI:11962557

KEYWORDS

EST.

SOURCE

ORGANISM

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 553)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

On Jul 14, 2000 this sequence version replaced gi:9190662.

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

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Fax: 580 224 6692

Email: gdmay@noble.org

Medicago Genome Initiative accession: MGI:S:21086

Insert Length: 697 Std Error: 0.00

Plate: 056 row: F column: 08

Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES

source

1..541  
Location/Qualifiers  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF056F08LIF"  
/tissue\_type="leaf"  
/dev\_stage="Pooled developmental"  
/clone\_lib="Developing leaf"  
/notes="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

ORIGIN

Alignment Scores:  
Pred. No.: 5,64e-18 Length: 541  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE316885 (1-541)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 135 ATGGCAGAGATTGGCTCTTCTACACAATGTGCGCAAGATCAAAAAATCTCTCCC 194  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40  
|||||  
DB 195 GTTGCAGCTTCCATCTCAATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAA 254  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||  
DB 255 GTGCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCACTCT 296

RESULT 12

BE319151

LOCUS

DEFINITION

BE319151 NF045C12LIF1087 Developing leaf Medicago truncatula cDNA clone

NP045C12LIF 5', mRNA sequence.

ACCESSION

BE319151

VERSION

BE319151.2

GI:11962557

KEYWORDS

EST.

SOURCE

ORGANISM

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 553)

Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

On Jul 14, 2000 this sequence version replaced gi:9190662.

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

JOURNAL  
COMMENT

Medicago truncatula leaf library  
Unpublished (2000)  
On Jul 14, 2000 this sequence version replaced gi:9192928.  
Contact: May GD

Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 224 6650  
Fax: 580 224 6692  
Email: gdmay@noble.org

Medicago Genome Initiative accession: MGI:S:27435  
Insert Length: 719 Std Error: 0.00  
Plate: 045 row: C column: 12  
Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES  
source

1..553  
Location/Qualifiers  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF045C12LP"  
/tissue\_type="leaf"  
/dev\_stage="Pooled developmental"  
/clone\_lib="Developing leaf"  
/note="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."

## ORIGIN

Alignment Scores:  
Pred. No.: 5,81e-18 Length: 553  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE319151 (1-553)

QY 1 MetAlaGInileLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 38 ATGGCACAGATTTGGCTCTTACACAAATGTCAGGCAAGAAATCACAATAATCTCTCCC 97  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 98 GTTGCAACTCCAAATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAACAAAGAAA 157  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
Db 158 GTCGCACGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 199

RESULT 13  
BE321453  
LOCUS  
DEFINITION  
BE321453 562 bp mRNA linear EST 21-DEC-2000  
NF025E10IN1P1071 Insect herbivory Medicago truncatula cDNA clone  
VERSION  
BE321453  
KEYWORDS  
EST  
SOURCE  
Medicago truncatula (barrel medic)

ORGANISM  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 562)

REFERENCE  
AUTHORS  
Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.  
TITLE  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula insect herbivory library  
JOURNAL  
Unpublished (2000)  
COMMENT  
On Jul 14, 2000 this sequence version replaced gi:9195146.  
Contact: Korth K  
Dept. of Plant Pathology  
University of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA  
Tel: 501 575 5191  
Fax: 501 575 7601  
Email: kkortheomp@uark.edu

Medicago Genome Initiative accession: MGI:S:20109  
Insert Length: 680 Std Error: 0.00  
Plate: 025 row: E column: 10  
Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES  
source

1..562  
Location/Qualifiers  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone="NF025E10IN"  
/tissue\_type="local and systemic leaves"  
/dev\_stage="mature"  
/clone\_lib="Insect herbivory"  
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

## ORIGIN

Alignment Scores:  
Pred. No.: 5,94e-18 Length: 562  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE321453 (1-562)

QY 1 MetAlaGInileLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 40 ATGGCACAGATTTGGCTCTTACACAAATGTCAGGCAAGAAATCACAATAATCTCTCCC 99  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 100 GTTGCAACTCCAAATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAACAAAGAAA 159  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
Db 160 GTCGCACGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 201

RESULT 14  
BF638827  
LOCUS

DEFINITION  
BF638827 570 bp mRNA linear EST 19-DEC-2000  
NF079C04PL1P1024 Phosphate starved leaf Medicago truncatula cDNA  
VERSION  
BF638827.1 GI:11902985  
KEYWORDS  
EST  
SOURCE  
Medicago truncatula (barrel medic)

ORGANISM  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 570)

REFERENCE  
AUTHORS  
Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.  
TITLE  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula phosphate-starved leaf library  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Harrison MJ  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7325  
Fax: 580 221 7380  
Email: mjharrison@noble.org

Insert Length: 570 Std Error: 0.00  
 Plate: 079 row: C column: 04  
 Seq primer: TCACACGAGAAACAGCTATGAC.  
 Location/Qualifiers  
 1. .570  
 /organism="Medicago truncatula"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3880"  
 /clone="NF079C04PL"  
 /tissue\_type="leaf"  
 /dev\_stage="trifoliolate"  
 /clone\_lib="phosphate starved leaf"  
 /notes="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."

## FEATURES

source

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.05e-18 Length: 570  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BF638827 (1-570)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 |||||  
 Db 45 ATGGCACAGATTTGGCTCTCTTACACAATGTCAGGCAAGATCAAAAATCTCTCCC 104  
 |||||  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 105 GTTGCACCTCACTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAGAA 164  
 |||||  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
 |||||  
 Db 165 GTGGCAGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 206  
 |||||

## RESULT 15

CX526728  
 LOCUS s13DNF26A05AT037.513968 Aphid-Infected Shoots Medicago truncatula  
 DEFINITION cDNA, mRNA sequence.  
 ACCESSION CX526728  
 VERSION CX526728.1 GI:57495447  
 KEYWORDS EST.  
 SOURCE Medicago truncatula (barrel medic)  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

CX526728 s13DNF26A05AT037.513968 Aphid-Infected Shoots Medicago truncatula

580 bp mRNA linear EST 11-JAN-2005

cDNA, mRNA sequence.

CX526728

CX526728.1 GI:57495447

EST.

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 580)

Zhang, Y., Chekhovskiy, K., Scott, A.D., May, G.D. and Mian, M.A.R.

Medicago truncatula Aphid-Infected Shoot Expressed Sequence Tags

from the Samuel Roberts Noble Foundation - Center for Medicago

Genomics Research

Unpublished (2005)

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 224 6650

Fax: 580 224 6692

Email: gdmay@noble.org.

Location/Qualifiers

1. .580

/organism="Medicago truncatula"

/mol\_type="mRNA"

## FEATURES

source

/db\_xref="taxon:3880"  
 /tissue\_type="Aphid-infected shoots"  
 /dev\_stage="harvested after 12, 24, 48, 72 and 96 hours of infestation"  
 /clone\_lib="Aphid-Infected Shoots"  
 /notes="Vector: Lambda Zap; Medicago truncatula plants were infested with 300 spotted-aphids each. Tissue samples were collected by harvesting the entire shoots from 13 plants after 12, 24, 48, 72 and 96 hours of infestation. Total RNA was extracted from each sampling time and equal amounts of total RNA were pooled together for mRNA purification for cDNA library construction. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain Xli-Blue MRF<sup>+</sup> (Stratagene). Excised plasmids were plated using SOLR cells."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.19e-18 Length: 580  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 8 Gaps: 0

US-10-628-525A-35 (1-58) x CX526728 (1-580)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 |||||  
 Db 97 ATGGCACAGATTTGGCTCTCTTACACAATGTCAGGCAAGATCAAAAATCTCTCCC 156  
 |||||  
 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 |||||  
 Db 157 GTTGCACCTCAACTCTCATCAAGATGTGGAGTCTTTGGTTATGAACAAACAGAGAA 216  
 |||||  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
 |||||  
 Db 217 GTGGCAGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 258  
 |||||

## RESULT 16

CX526728

LOCUS AW688380

DEFINITION

NF006G01STIF1000 Developing stem Medicago truncatula cDNA clone

NF006G01ST 5', mRNA sequence.

ACCESSION AW688380

VERSION AW688380.1

GI:7563116

EST.

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;

Medicago.

1 (bases 1 to 582)

He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A.,

Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D. and

Dixon, R.A.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula stem library

Unpublished (2000)

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 582 Std Error: 0.00

Plate: 006 row: G column: 01

Seq primer: TCACACAGGAACACAGCTATGAC.

FEATURES  
source  
1..582 Location/Qualifiers  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"  
/clone\_lib="NF006G01ST"  
/tissue\_type="stem"  
/dev\_stage="Pooled developmental"  
/clone\_lib="Developing stem"  
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"

ORIGIN  
Alignment Scores:  
Pred. No.: 6,22e-18 Length: 582  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 1 Gaps: 0

US-10-628-525A-35 (1-58) x AM688380 (1-582)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 175 ATGGCACAGATTTGGCTCTTCTACCAATGTCAGGCAAGATCACAATAATCTCTCCC 234  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||||  
DB 235 GTTGCAACTCCAAATCTCATCAAGATGTGGAGTCTCTTTGGTTATGAAACAAACAGAA 294  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||  
DB 295 GTCCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 336

RESULT 17  
BE321399  
LOCUS  
DEFINITION NF024E10IN1F071 Insect herbivory Medicago truncatula cDNA clone  
ACCESSION NF024E10IN 5', mRNA sequence.  
VERSION BE321399  
KEYWORDS BE321399.2 GI:11963972  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula

REFERENCE 1 (bases 1 to 597)  
AUTHORS Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.  
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
JOURNAL Medicago truncatula insect herbivory library  
COMMENT On Jul 14, 2000 this sequence version replaced gi:9195092.  
Contact: Korth K  
Dept. of Plant Pathology  
University of Arkansas  
217 Plant Science Building, Fayetteville, AR 72701, USA  
Tel: 501 575 5191  
Fax: 501 575 7601  
Email: korth@comp.uark.edu  
Medicago Genome Initiative accession: MGI:S:19989  
Insert Length: 678 Std Error: 0.00  
Plate: 024 row: E column: 10  
Seq primer: TCACACAGGAACACAGCTATGAC.

FEATURES  
source  
1..597 Location/Qualifiers  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"

/clone="NF024E10IN"  
/tissue\_type="local and systemic leaves"  
/dev\_stage="mature"  
/clone\_lib="Insect herbivory"

/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

## ORIGIN

Alignment Scores:  
Pred. No.: 6,43e-18 Length: 597  
Score: 223.00 Matches: 47  
Percent Similarity: 88.9% Conservative: 1  
Best Local Similarity: 87.0% Mismatches: 6  
Query Match: 75.1% Indels: 0  
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BE321399 (1-597)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 40 ATGGCACAGATTTGGCTCTTCTACCAATGTCAGGCAAGATCACAATAATCTCTCCC 99  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||||  
DB 100 GTTGCAACTCCAAATCTCATCAAGATGTGGAGTCTCTTTGGTTATGAAACAAACAGAA 159  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||||  
DB 160 GTCCGACGTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 201

RESULT 18  
B1268095

LOCUS  
DEFINITION NF117F10IN1F091 Insect herbivory Medicago truncatula cDNA clone  
ACCESSION NF117F10IN 5', mRNA sequence.  
VERSION B1268095.1 GI:14873701  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula

REFERENCE 1 (bases 1 to 614)  
AUTHORS Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.  
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
JOURNAL Medicago truncatula insect herbivory library  
COMMENT Unpublished (2000)  
Dept. of Plant Pathology  
University of Arkansas  
217 Plant Science Building, Fayetteville, AR 72701, USA  
Tel: 501 575 5191  
Fax: 501 575 7601  
Email: korth@comp.uark.edu  
Insert Length: 614 Std Error: 0.00  
Plate: 117 row: F column: 10  
Seq primer: TCACACAGGAACACAGCTATGAC.

FEATURES  
source  
1..614 Location/Qualifiers  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/db\_xref="taxon:3880"

/clone="NF117F10IN"  
/tissue\_type="local and systemic leaves"  
/dev\_stage="mature"  
/clone\_lib="Insect herbivory"

/note="Vector: Lambda Zap; Library was produced from fully

expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

## ORIGIN

Alignment Scores:  
 Pred. No.: 6.67e-18 Length: 614  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x BI268095 (1-614)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 DB 88 ATGGCAGAGATTTGGCTCTTCTACACATGTGAGCAGAGATCAGAAAATCTCTCCC 147  
 QY 21 CyAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 DB 148 GTTGCACACTCCATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAACAAGAA 207  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
 DB 208 GTCGCAGCTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 249

## RESULT 19

AW696250 628 bp mRNA linear EST 21-DEC-2000  
 LOCUS NF104E11STP1086 Developing stem Medicago truncatula cDNA clone  
 DEFINITION NF104E11ST 5', mRNA sequence.

ACCESSION AW696250

VERSION AW696250.2 GI:11936207

KEYWORDS EST.

SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

REFERENCE 1 (bases 1 to 628)

AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A.,  
 Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and  
 Dixon,R.A.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
 Medicago truncatula stem library

JOURNAL Unpublished (2000)

COMMENT On Apr 14, 2000 this sequence version replaced gi:7571012.

Contact: Dixon RA

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 668 Std Error: 0.00

Plate: 104 row: E column: 11

Seq primer: TCACACAGGAAACAGCTATGAC.

## FEATURES

source  
 1..628  
 /organism="Medicago truncatula"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3880"  
 /clone="NF104E11ST"  
 /tissue\_type="stem"  
 /dev\_stage="Pooled developmental"  
 /clone\_lib="Developing stem"  
 /notes="Vector: Lambda Zap; Contains a mixture of  
 internodal stem segments"

## ORIGIN

## Alignment Scores:

Pred. No.: 6.88e-18 Length: 628  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6  
 Query Match: 75.1% Indels: 0  
 DB: 1 Gaps: 0

US-10-628-525A-35 (1-58) x AW696250 (1-628)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
 DB 121 ATGGCAGAGATTTGGCTCTTCTACACATGTGAGCAGAGATCAGAAAATCTCTCCC 180  
 QY 21 CyAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
 DB 181 GTTGCACACTCCATCTCATCAAGATGTGGAGTCTTTGGTTATGAACAACAAGAA 240  
 QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
 DB 241 GTCGCAGCTTCTGCTAAATTCAGAGTAATGGCAGTCAACTCT 282

## RESULT 20

BF642149 642 bp mRNA linear EST 19-DEC-2000  
 LOCUS NF058D06IN1057 Insect herbivory Medicago truncatula cDNA clone  
 DEFINITION NF058D06IN 5', mRNA sequence.

ACCESSION BF642149

VERSION BF642149.1 GI:11906307

KEYWORDS EST.

SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 Medicago.

REFERENCE 1 (bases 1 to 642)

AUTHORS Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation

JOURNAL Medicago truncatula insect herbivory library

COMMENT Unpublished (2000)

Contact: Korth K

Dept. of Plant Pathology

University of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA

Tel: 501 575 5191

Fax: 501 575 7601

Email: kkorthe@comp.uark.edu

Insert Length: 642 Std Error: 0.00

Plate: 058 row: D column: 06

Seq primer: TCACACAGGAAACAGCTATGAC.

## FEATURES

source  
 1..642  
 /organism="Medicago truncatula"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3880"  
 /clone="NF058D06IN"  
 /tissue\_type="local and systemic leaves"  
 /dev\_stage="mature"  
 /clone\_lib="Insect herbivory"  
 /note="Vector: Lambda Zap; Library was produced from fully  
 expanded M. truncatula leaves of plants fed upon by  
 Spodoptera exigua (beet armyworm) for 24 hours. Systemic  
 (undamaged leaves from injured plants) and wounded leaves  
 were harvested and pooled."

## ORIGIN

Alignment Scores:  
 Pred. No.: 7.08e-18 Length: 642  
 Score: 223.00 Matches: 47  
 Percent Similarity: 88.9% Conservative: 1  
 Best Local Similarity: 87.0% Mismatches: 6











JOURNAL  
COMMENT

truncatula  
Unpublished (2000)  
Contact: Carroll P. Vance  
Department of Agronomy and Plant Genetics  
University of Minnesota  
411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA  
Tel: 612 625 5715  
Fax: 651-649-5058  
Email: vance004@maroon.tc.umn.edu  
Minnesota EST name: M252574e  
TIGR sequence name: MTCAB61TK  
More information is available at: .  
'http://chrystie.tamu.edu/medicago',  
Seq primer: SKmod (CTA gAA CTA gTg gAT CC).  
Location/Qualifiers

## FEATURES

source

1..630  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/cultivar="genotype A17"  
/db\_xref="taxon:3880"  
/clone="pGVN-47L2"  
/tissue\_type="N2-fixing root nodules"  
/dev\_stage="effective root nodules harvested one month post inoculation with Sinorhizobium meliloti"  
/lab\_host="E. coli strain XL0LR"  
/clone\_lib="GVN"  
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Aassist helper phage and propagated in XL0LR cells."

## ORIGIN

## Alignment Scores:

Pred. No.: 2,23e-17 Length: 630  
Score: 219.00 Matches: 46  
Percent Similarity: 87.0% Conservative: 1  
Best Local Similarity: 85.2% Mismatches: 7  
Query Match: 73.7% Indels: 0  
DB: 1 Gaps: 0  
US-10-628-525A-35 (1-58) x AM573676 (1-630)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||  
DB 17 ATGGCACAGATTGTGCTCTCTACACAATGTCAGGCAAGAATCACAAAATCTCTCCC 76  
|||  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||  
DB 77 GTTGCAACTCCCAATCTCATCAAGATGTGGAGTCTTTGGTTATGAAACAAACAGAAA 136  
|||  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||  
DB 137 GTCGCACGTTCTGCTAATTCAGATTAATGGCAGTCACTCT 178  
|||

## RESULT 30

AL372792/c

LOCUS AL372792 457 bp mRNA linear EST 03-AUG-2000  
DEFINITION MtBA53F02R1 MtBA Medicago truncatula cDNA clone MtBA53F02 T7, mRNA sequence.

ACCESSION AL372792

VERSION AL372792.1 GI:9672545

KEYWORDS EST.

SOURCE Medicago truncatula (barrel medic)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

## REFERENCE

## AUTHORS

1 (bases 1 to 457)  
Journet E.P., Crespeau H., van-Tuinen D., Gouzy J., Jaillon O.,  
Niebel A., Carreau V., Chatagnier O., Kahn D.,  
Gianinazzi-Pearson V. and Gamas P.

## TITLE

## JOURNAL

## COMMENT

Medicago truncatula ESTs from nitrogen-starved roots  
Unpublished (2000)

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de

Biologie Moleculaire des Relations Plantes-Microorganismes,

CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :

Mt-est@toulouse.inra.fr Website :

http://sequence.toulouse.inra.fr/Mtruncatula.html).

## FEATURES

source

1..457  
/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/cultivar="Jemalong"  
/db\_xref="taxon:3880"  
/clone="MtBA53F02"  
/tissue\_type="root tips"  
/dev\_stage="harvested after 3 days of N-starvation"  
/clone\_lib="MtBA"  
/note="Vector: pBluescript PSK; Site 1: EcoRI; Site 2: XhoI; Plants were grown in an aeroponic chamber for 14 days on nitrogen-rich medium followed by 3 days on N-free medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zapXR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssist helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France)."

## ORIGIN

## Alignment Scores:

Pred. No.: 1.96e-17 Length: 457  
Score: 218.00 Matches: 46  
Percent Similarity: 87.0% Conservative: 1  
Best Local Similarity: 85.2% Mismatches: 7  
Query Match: 73.4% Indels: 0  
DB: 1 Gaps: 0  
US-10-628-525A-35 (1-58) x AL372792 (1-457)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
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DB 400 ATGGCACAGATTGTGCTCTCTACACAATGTCAGGCAAGAATCACAAAATCTCTCCC 341  
|||  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||  
DB 340 GTTGGCGCTCCCAATCTCATCAAGATGTGGAGTCTTTGGTTATGAAACAAACAGAAA 281  
|||  
QY 41 ValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54  
|||  
DB 280 GTCGCACGTTCTGCTAATTCAGATTAATGGCAGTCACTCT 239  
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Search completed: April 1, 2006, 19:23:30

Job time : 936.32 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: March 31, 2006, 22:47:42 ; Search time 77.568 Seconds  
(without alignments)  
1329.139 Million cell updates

**Title:** US-10-628-525A-35

**Perfect score: 297**

Sequence: 1 MAQILAPSTQWQMRTKTSP.....KKVAHSAKFRVMAVNSENGT 58

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5			
Fgapop 6.0 , Fgapext 7.0			
Delop 6.0 , Delext 7.0			

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length:	0
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### Post-processing: Minimum Match of

Processing: Minimum Match 0%  
Maximum Match 100%

Maximum Match 100%  
Listing first 150 summaries

**Command line parameters:**

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**Database :**

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9:	/cgn2.6/prodata1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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		Match	%			
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C 2	69.5	23.4	1137	4	US-09-605-703B-499	Sequence 499, App
C 3	69.5	23.4	1137	4	US-09-605-703B-501	Sequence 501, App
4	69.5	23.4	1539	3	US-09-602-777A-129	Sequence 129, App
5	69.5	23.4	1539	3	US-09-602-777A-131	Sequence 131, App
C 6	68	22.9	601	3	US-09-949-003-1185	Sequence 1185, Ap
C 7	68	22.9	601	3	US-09-949-003-1186	Sequence 1186, Ap
C 8	68	22.9	601	3	US-09-949-003-1187	Sequence 1187, Ap
C 9	68	22.9	601	3	US-09-949-003-9808	Sequence 9808, Ap

c 83	60	20.2	3210	3	US-09-710-279-3922	Sequence 3922, Ap
c 84	60	20.2	3368	3	US-09-710-279-4169	Sequence 4169, Ap
c 85	60	20.2	162025	3	US-09-834-700-13	Sequence 13, Appl
c 86	60	20.2	162025	3	US-09-834-700-14	Sequence 14, Appl
c 87	60	20.2	162025	3	US-09-834-700-17	Sequence 17, Appl
c 88	60	20.2	162025	3	US-09-834-700-18	Sequence 18, Appl
c 89	59.5	20.0	651	3	US-09-583-110-1895	Sequence 1895, Ap
c 90	59.5	20.0	699	3	US-09-107-433-936	Sequence 936, App
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c 104	59	19.9	1977	3	US-09-445-472-11	Sequence 11, Appl
c 105	59	19.9	1977	3	US-10-090-624-11	Sequence 11, Appl
c 106	59	19.9	1977	3	US-09-841-553-2	Sequence 2, Appl
c 107	59	19.9	1977	3	US-09-841-553-6	Sequence 6, Appl
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c 113	59	19.9	6608	3	US-08-994-570-4	Sequence 58, Appl
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c 136	58.5	19.7	2550	2	US-08-332-643-47	Sequence 47, Appl
c 137	58.5	19.7	2550	2	US-08-332-638-53	Sequence 53, Appl
c 138	58.5	19.7	5610	3	US-09-262-537-57	Sequence 57, Appl
c 139	58.5	19.7	12955	3	US-09-902-540-1068	Sequence 1068, Ap
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c 141	58.5	19.7	18343	3	US-09-949-016-16413	Sequence 16413, A
c 142	58.5	19.7	24791	3	US-09-902-540-1211	Sequence 1211, Ap
c 143	58.5	19.7	250352	3	US-09-949-016-14724	Sequence 14724, A
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c 145	58	19.5	444	3	US-09-397-787-152	Sequence 152, App
c 146	58	19.5	601	3	US-09-949-016-160183	Sequence 160183, A
c 147	58	19.5	601	3	US-09-949-016-201932	Sequence 201932, A
c 148	58	19.5	861	3	US-09-533-559-801	Sequence 801, App
c 149	58	19.5	931	2	US-08-203-905B-4	Sequence 4, Appl
c 150	58	19.5	1068	3	US-09-328-352-434	Sequence 434, App

ALIGNMENTS

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; Sequence 1, Application US/07715751B  
; Patent No. 5391725  
; GENERAL INFORMATION:  
; APPLICANT: CORUZZI, GLORIA M  
; APPLICANT: EDWARDS, JANICE W  
; APPLICANT: WALKER, ELSBETH L  
; APPLICANT: BREARS, TIMOTHY B  
; TITLE OF INVENTION: NOVEL ORGAN-SPECIFIC PLANT PROMOTER  
; NUMBER OF SEQUENCES: 3  
; TITLE OF INVENTION: SEQUENCES  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 AVENUE OF THE AMERICAS  
; CITY: NEW YORK  
; STATE: N.Y.  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07715,751B  
; FILING DATE: 19910613  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MISROCK, S. LESLIE  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 3288-017-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1601 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
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Query Match: 91.2% Indels: 0  
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Db 1503 TGTGCAACTCCCAATCACATCAAAAGATGTGGAGTTCTTTGGTTATGAAACAAACTAAGAAA 1562  
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Qy 41 ValAlaHisSerAlaIysPheArgValMetAlaValAen 53  
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Db 1563 GTTGGCATTTCGTAATAATTAGATTATGGCAGTCAAC 1601  
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RESULT 2  
US-09-605-703B-499/c  
; Sequence 499, Application US/09605703B  
; Patent No. 6962989  
; GENERAL INFORMATION:  
; APPLICANT: Pompejue, Markus  
; APPLICANT: Kroger, Burkhard

```
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; PRIOR FILING DATE: 2000-06-27, 764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 499
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1114)
; OTHER INFORMATION: RXN01128
US-09-605-703B-499

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Pred. No.: 5.07 Length: 1137
Score: 69.50 Matches: 17
Percent Similarity: 49.0% Conservative: 7
Best Local Similarity: 34.7% Mismatches: 16
Query Match: 23.4% Indels: 9
DB: 4 Gaps: 2

US-10-628-525A-35 (1-58) x US-09-605-703B-499 (1-1137)
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Db 306 TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAAATACCCCAAGCGCA 256

QY 41 ValAlaHisSerAlaLysPheArgVal 49
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Db 255 ACTGCTAATCCAGAGTTAGATTG 229

RESULT 3
US-09-605-703B-501/c
; Sequence 501, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 501
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1114)
; OTHER INFORMATION: FRXA01128
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US-09-605-703B-501
Alignment Scores:
Pred. No.: 5.07 Length: 1137
Score: 69.50 Matches: 17
Percent Similarity: 49.0% Conservative: 7
Best Local Similarity: 34.7% Mismatches: 16
Query Match: 23.4% Indels: 9
DB: 4 Gaps: 2

US-10-628-525A-35 (1-58) x US-09-605-703B-501 (1-1137)
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Db 348 ATGTCATCCTTTTGGAGCGATTCA-----ATGGACTCAACGCGCCT 307

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
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QY 41 ValAlaHisSerAlaLysPheArgVal 49
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Db 255 ACTGCTAATCCAGAGTTAGATTG 229

RESULT 4
US-09-602-777A-129
; Sequence 129, Application US/09602777A
; Patent No. 6831165
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberkauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128CP
; CURRENT APPLICATION NUMBER: US/09/602,777A
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932924.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932928.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932930.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
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/ PRIOR APPLICATION NUMBER: DE 19933003.4
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933005.0
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933006.9
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19941378.9
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941379.7
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941390.8
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941391.6
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19942088.2
/ PRIOR FILING DATE: 1999-09-03
/ NUMBER OF SEQ ID NOS: 442
/ SEQ ID NO 129
/ LENGTH: 1539
/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (101)..(1516)
/ OTHER INFORMATION: RXN00622
US-09-602-777A-129
Alignment Scores:
Pred. No.: 7.7 Length: 1539
Score: 69.50 Matches: 19
Percent Similarity: 50.8% Conservative: 14
Best Local Similarity: 29.2% Mismatches: 21
Query Match: 23.4% Indels: 11
DB: 3 Gaps: 3
US-10-628-525A-35 (1-58) x US-09-602-777A-129 (1-1539)
QY 3 GlnlleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla 22
Db 32 CAGATACTGTGGCGCCACAGGTGGGTACCCCGTTGAGAGACGCTGTGGTGATCC 91
QY 23 ThrProIleThrSerLysMet-----TrpSerSerLeuValMetLysGln----- 37
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US-09-602-777A-131
/ Sequence 131, Application US/09602777A
/ Patent No. 6831165
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Kroger, Burkhard
/ APPLICANT: Schroder, Hartwig
/ APPLICANT: Zelder, Oskar
/ APPLICANT: Haberhauer, Gregor
/ TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
/ TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
/ FILE REFERENCE: BGI-128CP
/ CURRENT APPLICATION NUMBER: US/09/602,777A
/ CURRENT FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 60/141031
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: DE 19931636.8
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19932125.6
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/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932126.4
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932127.2
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932128.0
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932129.9
/ PRIOR FILING DATE: 1999-07-19
/ PRIOR APPLICATION NUMBER: DE 19932226.0
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932920.6
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932922.2
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932924.9
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932928.1
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932930.3
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932933.8
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932935.4
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932973.7
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933002.6
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933003.4
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933005.0
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19933006.9
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19941378.9
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941379.7
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941390.8
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19941391.6
/ PRIOR FILING DATE: 1999-08-31
/ PRIOR APPLICATION NUMBER: DE 19942088.2
/ PRIOR FILING DATE: 1999-09-03
/ NUMBER OF SEQ ID NOS: 442
/ SEQ ID NO 131
/ LENGTH: 1539
/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (101)..(1516)
/ OTHER INFORMATION: FRXA00622
US-09-602-777A-131
Alignment Scores:
Pred. No.: 7.7 Length: 1539
Score: 69.50 Matches: 19
Percent Similarity: 50.8% Conservative: 14
Best Local Similarity: 29.2% Mismatches: 21
Query Match: 23.4% Indels: 11
DB: 3 Gaps: 3
US-10-628-525A-35 (1-58) x US-09-602-777A-131 (1-1539)
QY 3 GlnlleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla 22
Db 32 CAGATACTGTGGCGCCACAGGTGGGTACCCCGTTGAGAGACGCTGTGGTGATCC 91
QY 23 ThrProIleThrSerLysMet-----TrpSerSerLeuValMetLysGln----- 37
Db 92 ACCGAGCTGATGACGCTATTATCCACTGGGTGGGCACCACTCGTTCAGAAAAAGTTTCATC 151
QY 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAsn 53
Db 152 CTTTGTGGTGGCGCTCCAGATC-----ACCTCTGAAGTACGCGTGCTTCCTTCGAC 205
QY 54 SerGluAsnGlyThr 58
Db 206 CAGCCAGAGGGCACC 220
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QY 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAsn 53
Db 152 CTTTTTGGTTGGCGCTCCAGATC-----ACCTCTGAAGTACGGGTCTTCCTTCGAC 205
QY 54 SerGluAenGlyThr 58
Db 206 CAGCCAGAGGGCCACC 220

RESULT 6
US-09-949-002-1185/c
; Sequence 1185, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1185
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-1185

Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-1185 (1-601)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 573 GCCCGCGCACTCCACATGGTAGATGAATATACTGGAGACCCCTGTTCCAGCCTCAGAGATT 514
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 513 TGCCAGAGCCCATGGGGCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 454
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58
Db 453 AGATTTCAGCAGCTCAACGAGGAACCTGGAGAAAGGCACT 415

RESULT 7
US-09-949-002-1186/c
; Sequence 1186, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1186
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-1186

Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-1186 (1-601)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 573 GCCCGCGCACTCCACATGGTAGATGAATATACTGGAGACCCCTGTTCCAGCCTCAGAGATT 514
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 513 TGCCAGAGCCCATGGGGCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 454
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58
Db 453 AGATTTCAGCAGCTCAACGAGGAACCTGGAGAAAGGCACT 415

RESULT 8
US-09-949-002-1187/c
; Sequence 1187, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1187
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-1187

Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-1187 (1-601)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 290 GCCCGCGCACTCCACATGGTAGATGAATATACTGGAGACCCCTGTTCCAGCCTCAGAGATT 231
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 230 TGCCAGAGCCCATGGGGCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 171
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58
Db 170 AGATTTCAGCAGCTCAACGAGGAACCTGGAGAAAGGCACT 132

RESULT 9
US-09-949-002-9808/c
; Sequence 9808, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
```

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US-09-949-002-1186
Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0
```

```
US-10-628-525A-35 (1-58) x US-09-949-002-1186 (1-601)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 543 GCCCGCGCACTCCACATGGTAGATGAATATACTGGAGACCCCTGTTCCAGCCTCAGAGATT 484
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 483 TGCCAGAGCCCATGGGGCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 424
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58
Db 423 AGATTTCAGCAGCTCAACGAGGAACCTGGAGAAAGGCACT 385
```

```
RESULT 8
US-09-949-002-1187/c
; Sequence 1187, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1187
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-1187
```

```
Alignment Scores:
Pred. No.: 3.4 Length: 601
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 3 Gaps: 0
```

```
US-10-628-525A-35 (1-58) x US-09-949-002-1187 (1-601)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 290 GCCCGCGCACTCCACATGGTAGATGAATATACTGGAGACCCCTGTTCCAGCCTCAGAGATT 231
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 230 TGCCAGAGCCCATGGGGCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 171
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58
Db 170 AGATTTCAGCAGCTCAACGAGGAACCTGGAGAAAGGCACT 132
```

```
RESULT 9
US-09-949-002-9808/c
; Sequence 9808, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
```

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
FILE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: CL000790  
CURRENT APPLICATION NUMBER: US/09/949,002  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/231,401  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 10823  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9808  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-002-9808

Alignment Scores:  
Pred. No.: 3.4 Length: 601  
Score: 68.00 Matches: 17  
Percent Similarity: 45.3% Conservative: 7  
Best Local Similarity: 32.1% Mismatches: 29  
Query Match: 22.9% Indels: 0  
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-9808 (1-601)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
DB 573 GCGCCGCACTCACCATGGTAGATGAATATCTGGAGACCCCTGTTCCAGCCTCAGAGATT 514  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45  
DB 513 TGCCAGAGCCCATGGGCGAGAGTGGAGTGGGGGACAACTGGATGGTCCCTCAGGG 454  
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58  
DB 453 AGATTTCAGGCAGCTCAACAGGAGAACTGGGAGAAAGGCACT 415

RESULT 10  
US-09-949-002-9809/c  
Sequence 9809, Application US/09949002  
Patent No. 6900016  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
FILE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: CL000790  
CURRENT APPLICATION NUMBER: US/09/949,002  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/231,401  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 10823  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9809  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-002-9809

Alignment Scores:  
Pred. No.: 3.4 Length: 601  
Score: 68.00 Matches: 17  
Percent Similarity: 45.3% Conservative: 7  
Best Local Similarity: 32.1% Mismatches: 29  
Query Match: 22.9% Indels: 0  
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-9809 (1-601)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
DB 573 GCGCCGCACTCACCATGGTAGATGAATATCTGGAGACCCCTGTTCCAGCCTCAGAGATT 514  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45  
DB 513 TGCCAGAGCCCATGGGCGAGAGTGGAGTGGGGGACAACTGGATGGTCCCTCAGGG 454  
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58  
DB 453 AGATTTCAGGCAGCTCAACAGGAGAACTGGGAGAAAGGCACT 415

Db 543 GCGCCGCACTCACCATGGTAGATGAATATCTGGAGACCCCTGTTCCAGCCTCAGAGATT 484  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45  
Db 483 TGCCAGAGCCCATGGGCGAGAGTGGAGTGGGGGACAACTGGATGGTCCCTCAGGG 424  
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58  
Db 423 AGATTTCAGGCAGCTCAACAGGAGAACTGGGAGAAAGGCACT 385

RESULT 11  
US-09-949-002-9810/c  
Sequence 9810, Application US/09949002  
Patent No. 6900016  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
FILE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: CL000790  
CURRENT APPLICATION NUMBER: US/09/949,002  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/231,401  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 10823  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9810  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-002-9810

Alignment Scores:  
Pred. No.: 3.4 Length: 601  
Score: 68.00 Matches: 17  
Percent Similarity: 45.3% Conservative: 7  
Best Local Similarity: 32.1% Mismatches: 29  
Query Match: 22.9% Indels: 0  
DB: 3 Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-9810 (1-601)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
Db 290 GCGCCGCACTCACCATGGTAGATGAATATCTGGAGACCCCTGTTCCAGCCTCAGAGATT 231  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45  
Db 230 TGCCAGAGCCCATGGGCGAGAGTGGAGTGGGGGACAACTGGATGGTCCCTCAGGG 171  
QY 46 LysPheArgValMetAlaValAsnSerGluAenGlyThr 58  
Db 170 AGATTTCAGGCAGCTCAACAGGAGAACTGGGAGAAAGGCACT 132

RESULT 12  
US-09-949-002-836/c  
Sequence 836, Application US/09949002  
Patent No. 6900016  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
FILE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: CL000790  
CURRENT APPLICATION NUMBER: US/09/949,002  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/231,401  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 10823  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 836  
LENGTH: 34589  
TYPE: DNA



```
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(34589)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-836

Alignment Scores:
Pred. No.: 911          Length: 34589
Score: 68.00           Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9%      Indels: 0
DB: 3                   Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-836 (1-34589)

Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 9692 GCCCGGCACTACCACTGAGTAGAATATACCTGGAGACCCCTGTTCCAGCCTCAGAGATT 9633

Qy 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 9632 TGCAGAGCCCATGGGSCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 9573

Qy 46 LysPheArgValMetAlaValAlaSerGluAsnGlyThr 58
Db 9572 AGATTGAGGAGCTCAACGAGGAACCTGGAGAAAGGCACT 9534

RESULT 13
US-09-949-002-581/c
; Sequence 581, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 581
; LENGTH: 59258
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(59258)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-581

Alignment Scores:
Pred. No.: 1,92e+03      Length: 59258
Score: 68.00           Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9%      Indels: 0
DB: 3                   Gaps: 0

US-10-628-525A-35 (1-58) x US-09-949-002-581 (1-59258)

Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 27787 GCCCGGCACTACCACTGAGTAGAATATACCTGGAGACCCCTGTTCCAGCCTCAGAGATT 27728

Qy 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 27727 TGCAGAGCCCATGGGSCAGAGTGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 27668

Qy 46 LysPheArgValMetAlaValAlaSerGluAsnGlyThr 58
Db 27667 AGATTGAGGAGCTCAACGAGGAACCTGGAGAAAGGCACT 27629

RESULT 14
US-09-949-016-11976
; Sequence 11976, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11976
; LENGTH: 22874
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11976

Alignment Scores:
Pred. No.: 604          Length: 22874
Score: 67.50           Matches: 19
Percent Similarity: 54.5% Conservative: 11
Best Local Similarity: 34.5% Mismatches: 19
Query Match: 22.7%      Indels: 6
DB: 3                   Gaps: 2

US-10-628-525A-35 (1-58) x US-09-949-016-11976 (1-22874)

Qy 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSer-----ProCysAlaThr 23
Db 14553 CCCCCCTCCCTTGGCCCTTCTCTGACTTGGACTTCTGCTCCCTCCCTGTCCTCC 14612

Qy 23 rProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHi 43
Db 14613 ACCTTTACCACTGCTGGTGGTCTCTCTGAGGTTGAACAAGACTCTGAGGCGCACT 14672

Qy 43 sSerAlaLysPheArgValMetAlaValAlaSerGluAsnGly 57
Db 14673 GCAGGCCCTGCTGAGGTTGGTGGCC-----TCGGATGACGGG 14709

RESULT 15
US-09-949-016-16363
; Sequence 16363, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16363
; LENGTH: 22875
; TYPE: DNA
```

```
; ORGANISM: Human
US-09-949-016-16363

Alignment Scores:
Pred. No.: 604 Length: 22875
Score: 67.50 Matches: 19
Percent Similarity: 54.5% Conservative: 11
Best Local Similarity: 34.5% Mismatches: 19
Query Match: 22.7% Indels: 6
DB: 3 Gaps: 2

US-10-628-525A-35 (1-58) x US-09-949-016-16363 (1-22875)

QY 7 ProSerThrGlnTrpGlnMet-ArgfileThrLysThrSer-----ProCysAlaTh 23
Db 14553 CCCCCCTCCCTTGGCCCTCTCTGACTGGACTTCTCTCCCTCCCTGTCCTCC 14612

QY 23 rProleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHi 43
Db 14613 ACCTCTTACCACCTGGTGTCTCTCTGAGGTTGAACAGACTCTGAAGGCGACACT 14672

QY 43 sSerAlaLysPheArgValMetAlaValAsnSerGluAangly 57
Db 14673 GCAGGCCCTGCTGGAGGTGGTGCC-----TCGGATGACGG 14709

RESULT 16
US-09-761-534A-11/c
; Sequence 11, Application US/09761534A
; Patent No. 6875435
; GENERAL INFORMATION:
; APPLICANT: Huang, Qian
; APPLICANT: Richmond, Joan F.L.
; APPLICANT: Cho, Bryan K.
; APPLICANT: Palliser, Deborah
; APPLICANT: Chen, Jianzhu
; APPLICANT: Eisen, Herman N.
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
; FILE OF INVENTION: CD4+T Cell-Independent
; FILE REFERENCE: 0399.2006-003
; CURRENT APPLICATION NUMBER: US/09/761,534A
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US00/32831
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/176,143
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine hsp70
; NAME/KEY: CDS
; LOCATION: (1)...(1929)
; OTHER INFORMATION: Murine hsp70
US-09-761-534A-9

Alignment Scores:
Pred. No.: 23.4 Length: 1929
Score: 67.00 Matches: 19
Percent Similarity: 59.1% Conservative: 7
Best Local Similarity: 43.2% Mismatches: 12
Query Match: 22.6% Indels: 6
DB: 3 Gaps: 3

US-10-628-525A-35 (1-58) x US-09-761-534A-9 (1-1929)

QY 4 lleLeuAlaProSerThrGlnTrp---GlnMetArgIleThrLysThrSerPro----- 20
Db 740 CTCCTTGAACCTCCTCCACGAAGTGGCTCACCACCGGTTGTGCAAGTCTCTCCCTCCCGAG 681

QY 21 CysAlaThrPro-----IleThrSerLysMetTrpSerSerLeuValMetLysGln 37
Db 680 TCGGTGTGCGCGCGCGCTTCCCTTCACCTCGAAGATGCCGTCTCGATCGTCAGGATGGAC 621

QY 38 ThrLysLysVal 41
Db 620 ACGTCGAACGTG 609

RESULT 18
US-09-949-016-40647/c
; Sequence 40647, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40647
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-40647

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```
Best Local Similarity: 29.5% Mismatches: 24
Query Match: 22.2% Indels: 0
DB: 2 Gaps: 0

US-10-628-525A-35 (1-58) x US-08-824-707-1 (1-1459)
QY 1 MetAlaGlnIleuAlaProSerThrGlnMetArgIleThrLysThrSerPro 20
Db 822 GTGGCCAGGCGATCTGGTCGGCTTCTGGATGTCGGAGCGAACCTGCCGACACCCCT 881
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 882 GGCCTACCTCCGTCGATCGACATCATGAGAACGTCGGCAATGCGCCACGAGTCC 941
QY 41 ValAlaHisSer 44
Db 942 ACGGCACGGTCC 953

RESULT 21
US-10-012-231A-291
; Sequence 291, Application US/10012231A
; Patent No. 6924355
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC48
; CURRENT APPLICATION NUMBER: US/10/012,231A
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 291
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-231A-291

Alignment Scores:
Pred. No.: 24.2 Length: 1570
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 3 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-012-231A-291 (1-1570)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1209 TCACCATCCCCAAGCTGGAGCACCCACCAAGACATCGACCTGTACCAACCATGT 1268
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAG-----CACAGAGCC 1309
QY 46 LysPhe-----ArgValMetAlaValAsn 53
Db 1310 AAGTTCGGCCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 1348

RESULT 22
US-10-628-525A-35 (1-58) x US-10-012-231A-291 (1-1570)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1209 TCACCATCCCCAAGCTGGAGCACCCACCAAGACATCGACCTGTACCAACCATGT 1268
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAG-----CACAGAGCC 1309
QY 46 LysPhe-----ArgValMetAlaValAsn 53
Db 1310 AAGTTCGGCCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 1348

RESULT 23
US-10-006-768A-291
; Sequence 291, Application US/10006768A
; Patent No. 6936697
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
```

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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC10
; CURRENT APPLICATION NUMBER: US/10/006,768A
; CURRENT FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 291
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-768A-291

Alignment Scores:
Pred. No.: 24.2 Length: 1570
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 2 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-006-768A-291 (1-1570)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1209 TCACCATCCCAAGCTGGAGCACCACCCAGCAGACATCGACCTGTACCACCATGT 1268
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAG-----CACAGACC 1309
QY 46 LysPhe-----ArgValMetAlaValAsn 53
Db 1310 AAGTTGGGCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 1348
RESULT 25
US-10-015-393A-291
; Sequence 291, Application US/10015393A
; Patent No. 6951920
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 291
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-393A-291

Alignment Scores:
Pred. No.: 24.2 Length: 1570
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 2 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-015-393A-291 (1-1570)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1209 TCACCATCCCAAGCTGGAGCACCACCCAGCAGACATCGACCTGTACCACCATGT 1268
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAG-----CACAGACC 1309
QY 46 LysPhe-----ArgValMetAlaValAsn 53
Db 1310 AAGTTGGGCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 1348
RESULT 26
US-10-011-833A-291
; Sequence 291, Application US/10011833A
; Patent No. 6951920
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C22
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 291
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-011-833A-291

Alignment Scores:
Pred. No.: 24.2 Length: 1570
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 3 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-011-833A-291 (1-1570)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1209 TCACCATCCCAAGCTGGAGACCCCAACCCAGACACATCGACTGTACCAACCATGT 1268
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAG-----CACAGAGACC 1309
QY 46 LysPhe-----ArgValMetAlaValAsn 53
Db 1310 AAGTTCGGCCTCCCGAGAGACTGAGGTCTCTGGAGGTGAAC 1348

RESULT 27
US-10-006-041A-291
; Sequence 291, Application US/10006041A
; Patent No. 6951921
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C19
; CURRENT FILING DATE: 2002-07-15
; CURRENT APPLICATION NUMBER: US/10/012,064A
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; CURRENT FILING DATE: 1998-09-09

US-10-628-525A-35 (1-58) x US-10-011-833A-291 (1-1570)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1209 TCACCATCCCAAGCTGGAGACCCCAACCCAGACACATCGACTGTACCAACCATGT 1268
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAG-----CACAGAGACC 1309
QY 46 LysPhe-----ArgValMetAlaValAsn 53
Db 1310 AAGTTCGGCCTCCCGAGAGACTGAGGTCTCTGGAGGTGAAC 1348

RESULT 28
US-10-012-064A-291
; Sequence 291, Application US/10012064A
; Patent No. 6953841
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C19
; CURRENT FILING DATE: 2002-07-15
; CURRENT APPLICATION NUMBER: US/10/012,064A
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; CURRENT FILING DATE: 1998-09-09
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; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 291
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-064A-291

Alignment Scores:
Pred. No.: 24.2      Length: 1570
Score: 66.00        Matches: 19
Percent Similarity: 45.3%      Conservative: 5
Best Local Similarity: 35.8%   Mismatches: 18
Query Match: 22.2%           Indels: 12
DB: 3                  Gaps: 2

US-10-628-525A-35 (1-58) x US-10-012-064A-291 (1-1570)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
   :::::::::::::::::::::
Db 1209 TCACCATCCCAAGCTGGAGCACCACCAACCCAGCAGACATCGACCTGTACCACCATGT 1268
   :::::::::::::::::::::

QY 26 ThrSerLysMetTrpSerSerIleuValMetLysGlnThrLysLysValAlaHisSerAla 45
   :::::::::::::::::::::
Db 1269 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAAG-----CACAAAGACC 1309
   :::::::::::::::::::::

QY 46 LysPhe-----ArgValMetAlaValAsn 53
   :::::::::::::::::::::
Db 1310 AAGTTCGGCTCCCGGAGACTGAGTCTCGAGGTGAAC 1348
   :::::::::::::::::::::

RESULT 29
US-09-625-188-1
; Sequence 1, Application US/09625188
; Patent No. 6307037
; GENERAL INFORMATION:
; APPLICANT: No. 6307037artis AG
; TITLE OF INVENTION: Fungal Target Genes and Methods
; FILE REFERENCE: PB/5-31285P1
; CURRENT APPLICATION NUMBER: US/09/625,188
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Ashbya gossypii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1575)
US-09-625-188-1

Alignment Scores:
Pred. No.: 24.3      Length: 1575
Score: 66.00        Matches: 12
Percent Similarity: 63.3%      Conservative: 7
Best Local Similarity: 40.0%   Mismatches: 11
Query Match: 22.2%           Indels: 0
DB: 3                  Gaps: 0

US-10-628-525A-35 (1-58) x US-09-625-188-1 (1-1575)

QY 3 GlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla 22
   :::::::::::::::::::::
Db 1187 CGTTACTGGCACCTCGTACTACATGCGCGCGGAGCGATCCAGGCCAGCTTACAGCG 1246
   :::::::::::::::::::::

QY 23 ThrProIleThrSerLysMetTrpSerSer 32
   :::::::::::::::::::::
Db 1247 TCACCAAGCAGCGTCTGGTGGGCTCA 1276
   :::::::::::::::::::::

RESULT 30
US-09-949-016-2306/c

; Sequence 2306, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2306
; LENGTH: 2464
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2306

Alignment Scores:
Pred. No.: 45      Length: 2464
Score: 66.00      Matches: 21
Percent Similarity: 50.0%      Conservative: 7
Best Local Similarity: 37.5%   Mismatches: 12
Query Match: 22.2%           Indels: 16
DB: 3                  Gaps: 3

US-10-628-525A-35 (1-58) x US-09-949-016-2306 (1-2464)

QY 2 AlaGlnIleLeuAlaPro-----SerThrGlnTrp 11
   :::::::::::::::::::::
Db 861 GCGCGCTTGTGGGCCCAATGCTTCTTGTGCTTGAACCTCTCCGCCAGGTGG 802
   :::::::::::::::::::::

QY 12 ---GlnMetArgIleThrLysThrSerPro-----CysAlaThrProIle 25
   :::::::::::::::::::::
Db 801 CTCACCATGCGGTTGTGCGAAGTCCACCGCCCGGAGTGTGCGCGCGCGTGGACTTC 742
   :::::::::::::::::::::

QY 26 ThrSerLysMetTrpSerSerIleuValMetLysGlnThrLysLysVal 41
   :::::::::::::::::::::
Db 741 ACCTCGAAGATGCCATCCTCGATGTTGAGTGGACACGTCGAAAGTG 694
   :::::::::::::::::::::

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OM protein - nucleic search, using frame\_plus\_p2n model

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Title: US-10-628-525A-35

Perfect score: 297

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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-HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02h  
-USER=US10628525 @CEN 1 1 2715 @runat 31032006 095135 17190 -NCPU=6 -ICPU=3  
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-XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA Main:

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5: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/prodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	199	67.0	589	9	US-10-487-901-1682
2	199	67.0	1633	9	US-10-487-901-5829
3	197	66.3	2124	7	US-10-424-599-3238
4	174.5	58.8	1508	8	US-10-767-795-6095
5	155.5	52.4	3895	9	US-10-487-901-5832
6	137	46.1	382	7	US-10-424-599-465
7	115	38.7	487	3	US-09-770-961-774
					Sequence 1682, Ap
					Sequence 5829, Ap
					Sequence 3238, Ap
					Sequence 6095, Ap
					Sequence 5832, Ap
					Sequence 465, App
					Sequence 774, App

8	83	27.9	850	7	US-10-424-599-24764	Sequence 24764, A
9	74	24.9	770	8	US-10-425-115-53452	Sequence 53452, A
10	69.5	23.4	347	3	US-09-960-352-9991	Sequence 9991, Ap
11	69.5	23.4	1062	3	US-09-738-626-1418	Sequence 1418, Ap
12	69.5	23.4	1192	8	US-10-494-672-115	Sequence 115, App
13	69.5	23.4	1539	9	US-10-721-922A-137	Sequence 137, App
14	69.5	23.4	1539	9	US-10-721-922A-139	Sequence 139, App
15	69.5	23.4	3309400	3	US-09-738-626-1	Sequence 1, Appli
16	68	22.9	412	7	US-10-424-599-127800	Sequence 127800,
17	68	22.9	383432	9	US-10-737-082-34	Sequence 34, Appl
18	68	22.9	383432	9	US-10-765-790-34	Sequence 34, Appl
19	67.5	22.7	421	3	US-09-918-995-34956	Sequence 34956, A
20	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
21	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
22	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
23	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
24	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
25	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
26	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
27	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
28	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
29	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
30	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
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32	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
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34	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
35	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
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41	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
42	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
43	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
44	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
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46	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
47	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
48	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
49	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
50	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
51	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
52	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
53	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
54	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
55	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
56	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
57	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
58	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
59	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
60	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
61	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
62	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
63	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
64	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
65	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
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67	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
68	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
69	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
70	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
71	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
72	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
73	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
74	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
75	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
76	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
77	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
78	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
79	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl
80	67.5	22.7	939	3	US-09-764-881-61	Sequence 61, Appl

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82	66	22.2	1570	5	US-10-174-590-335	Sequence 335, App
83	66	22.2	1570	5	US-10-176-758-335	Sequence 335, App
84	66	22.2	1570	5	US-10-175-737-335	Sequence 335, App
85	66	22.2	1570	5	US-10-174-581-335	Sequence 335, App
86	66	22.2	1570	5	US-10-176-483-335	Sequence 335, App
87	66	22.2	1570	5	US-10-176-749-335	Sequence 335, App
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89	66	22.2	1570	5	US-10-176-915-335	Sequence 335, App
90	66	22.2	1570	5	US-10-173-708-335	Sequence 335, App
91	66	22.2	1570	5	US-10-175-738-335	Sequence 335, App
92	66	22.2	1570	5	US-10-175-752-335	Sequence 335, App
93	66	22.2	1570	5	US-10-176-482-335	Sequence 335, App
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100	66	22.2	1570	5	US-10-174-579-335	Sequence 335, App
101	66	22.2	1570	5	US-10-174-582-335	Sequence 335, App
102	66	22.2	1570	5	US-10-174-588-335	Sequence 335, App
103	66	22.2	1570	5	US-10-175-733-335	Sequence 335, App
104	66	22.2	1570	5	US-10-175-740-335	Sequence 335, App
105	66	22.2	1570	5	US-10-175-743-335	Sequence 335, App
106	66	22.2	1570	5	US-10-176-488-335	Sequence 335, App
107	66	22.2	1570	5	US-10-176-492-335	Sequence 335, App
108	66	22.2	1570	5	US-10-176-747-335	Sequence 335, App
109	66	22.2	1570	5	US-10-176-750-335	Sequence 335, App
110	66	22.2	1570	5	US-10-176-985-335	Sequence 335, App
111	66	22.2	1570	5	US-10-176-987-335	Sequence 335, App
112	66	22.2	1570	5	US-10-176-992-335	Sequence 335, App
113	66	22.2	1570	5	US-10-176-993-335	Sequence 335, App
114	66	22.2	1570	5	US-10-184-658-335	Sequence 335, App
115	66	22.2	1570	5	US-10-176-991-335	Sequence 335, App
116	66	22.2	1570	5	US-10-173-695-335	Sequence 335, App
117	66	22.2	1570	5	US-10-173-697-335	Sequence 335, App
118	66	22.2	1570	5	US-10-173-705-335	Sequence 335, App
119	66	22.2	1570	5	US-10-174-576-335	Sequence 335, App
120	66	22.2	1570	5	US-10-174-583-335	Sequence 335, App
121	66	22.2	1570	5	US-10-174-586-335	Sequence 335, App
122	66	22.2	1570	5	US-10-175-747-335	Sequence 335, App
123	66	22.2	1570	5	US-10-176-481-335	Sequence 335, App
124	66	22.2	1570	5	US-10-176-485-335	Sequence 335, App
125	66	22.2	1570	5	US-10-176-487-335	Sequence 335, App
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127	66	22.2	1570	5	US-10-176-756-335	Sequence 335, App
128	66	22.2	1570	5	US-10-176-911-335	Sequence 335, App
129	66	22.2	1570	5	US-10-176-919-335	Sequence 335, App
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131	66	22.2	1570	5	US-10-176-978-335	Sequence 335, App
132	66	22.2	1570	5	US-10-179-510-335	Sequence 335, App
133	66	22.2	1570	5	US-10-180-543-335	Sequence 335, App
134	66	22.2	1570	5	US-10-180-544-335	Sequence 335, App
135	66	22.2	1570	5	US-10-180-546-335	Sequence 335, App
136	66	22.2	1570	5	US-10-180-547-335	Sequence 335, App
137	66	22.2	1570	5	US-10-180-549-335	Sequence 335, App
138	66	22.2	1570	5	US-10-180-555-335	Sequence 335, App
139	66	22.2	1570	5	US-10-180-559-335	Sequence 335, App
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141	66	22.2	1570	5	US-10-183-010-335	Sequence 335, App
142	66	22.2	1570	5	US-10-183-012-335	Sequence 335, App
143	66	22.2	1570	5	US-10-184-614-335	Sequence 335, App
144	66	22.2	1570	5	US-10-184-623-335	Sequence 335, App
145	66	22.2	1570	5	US-10-184-635-335	Sequence 335, App
146	66	22.2	1570	5	US-10-184-637-335	Sequence 335, App
147	66	22.2	1570	5	US-10-184-646-335	Sequence 335, App
148	66	22.2	1570	5	US-10-184-647-335	Sequence 335, App
149	66	22.2	1570	5	US-10-184-652-335	Sequence 335, App
150	66	22.2	1570	5	US-10-187-594-335	Sequence 335, App

ALIGNMENTS

```

RESULT 1
US-10-487-901-1682
; Sequence 1682, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutula
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1682
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-1682

Alignment Scores:
Pred. No.: 2,2e-19 Length: 589
Score: 199.00 Matches: 40
Percent Similarity: 83.3% Conservative: 10
Best Local Similarity: 66.7% Mismatches: 8
Query Match: 67.0% Indels: 2
DB: 9 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-487-901-1682 (1-589)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
60 ATGGCTCAGATCTTGCTCCATCTCGCAATGGCAGATGAGATGACAAAGAGCTCAACA 119
21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
120 GATGCTAATCCCTTGACTTCAAGATGTGGAGTTCTGTGGTGTGGAAGCAGATAAAGA 179
41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
180 CTTCCTGTAAAGCTCTGCCAATTATAGTCTTTGCTCTCCAACTCTGATAGTGGCACT 239

RESULT 2
US-10-487-901-5829
; Sequence 5829, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCrery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Reddy, Avutula
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26

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; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5829
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-5829

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Alignment Scores:	
Pred. No.:	8.44e-19
Score:	199.00
Percent Similarity:	63.3%
Best Local Similarity:	86.7%
Query Match:	97.0%
DB:	9
Length:	1633
Matches:	40
Conservative:	10
Mismatches:	8
Indels:	2.0
Gaps:	1

US-10-628-525A-35 (1-58) x US-10-487-901-5829 (1-1633)

QY	1	MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro	20
DB	74	ATGGCTCAGATCTTGGCTCCATCTGCGCAATGCGCAGATGAGAATGACAAAGAGCTCAACA	133
QY	21	CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys	40
DB	134	GATGCTAATCCCTTGACTTCAAAGATGTGGAGTCTGTGGTGTGAAGCAGATAAAGA	193
QY	41	ValAla-----HisSerAlaIysPheArgValMetAlaValAenSerGluAenGlyThr	58
DB	194	CTGTGCTGTTAAAGAGCTGCGCAAAATTCGAGCTCTTGCTTCCAAATCTGTAAGTGGCACT	253

### RESULT 3

US-10-424-599-3238  
; Sequence 3238, Application US/10424599  
; Publication No. US20040031072A1

Alignment Scores:	
Pred. No.:	2,366-18
Score:	197.00
Percent Similarity:	84.7%
Best Local Similarity:	72.9%
Query Match:	66.3%
DB:	
Length:	2124
Matches:	43
Conservative:	6
Mismatches:	7
Indels:	3
Gaps:	1

US-10-628-525A-35 (1-58) x US-10-424-599-3238 (1-2124)

1	MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThr-LysThrSerPr	20	QY
480	ATGGCACAGNTTTTGGCTCCCTCTACGCAATGGCAGATGAGATCTTCAAAATCCTCTCC	539	DB
20	oCyeAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLy	40	QY
540	CAATCGCAATGCCATTACATCAAACTGTGGAGTTCTTTATCTGGAAACAAATATGAGA	599	DB

**Qy**    40 sValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56  
       |||:::  
**Dd**    600 AGTTTCACCCCAACAAGTCTCGCTAAATTTAGAGTGATGGCAATTAAAGTCTGCAAT 654

## RESULT 4

US-10-767-795-6095  
; Sequence 6095, Application US/10767795  
; Publication No. US20040181830A1

Alignment Scores:		
Pred. No.:	3.29e-15	1508
Score:	174.50	38
Percent Similarity:	76.7%	8
Best Local Similarity:	63.3%	11
Query Match:	58.8%	3
DB:	8	2
Length:		
Matches:		
Conservative:		
Mismatches:		
Indels:		
Gaps:		

US-10-628-525A-35 (1-58) x US-10-767-795-6095 (1-1508)

QY	1	MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro	20
		::::	
Db	135	ATGGCACAGCTTTTATGACACCCCTCAACTCAATGGCAATGACACTACCAAGACCTCAACC	194
		::::	
QY	21	CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys	40
		::::	
Db	195	TATGGAAGTCCTTATGCAACAAATAATGGAGTTCTCTGGTACTGAAACAGAACAGAAA	254
		::::	
QY	41	ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr	58
		::::	
Db	255	GGAGCTGCTAAAGCTCTGGCAAGTTTAAAGTGGTGGCTTG---TCTGAAACAGACACT	311
		::::	

## RESULT 5

US-10-487-901-5832  
; Sequence 5832, Application US/10487901  
; Publication No. US20050091708A1

; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-487-901-5832

## Alignment Scores:

Pred. No.: 7.59e-12 Length: 3895  
Score: 155.50 Matches: 34  
Percent Similarity: 72.1% Conservative: 10  
Best Local Similarity: 55.7% Mismatches: 14  
Query Match: 52.4% Indels: 3  
DB: 9 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-487-901-5832 (1-3895)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
Db 318 ATGGCACAGATTTTAGCCTTTCTACGCAATGTCAGATGAAGATAACAATACAACA 377  
QY 21 ---CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 39  
|||||  
Db 378 AATGCTGCAAGCCCAATTACTACAAGATGTGGGTTCTCTAATGTTTAAACCAAGAAAGA 437  
QY 40 Lys-----ValalaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGly 57  
|||||  
Db 438 AGTGGACTTACTAATAAACGCTTCTAATTCAAAGTTATGTTGTTTAAATCGGAACCGGT 497  
QY 58 Thr 58  
|||  
Db 498 ACC 500

## RESULT 6

US-10-424-599-465  
; Sequence 465, Application US/10424599  
; Publication No. US20040031072A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 465  
; LENGTH: 382  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_10041C.1

## US-10-424-599-465

Alignment Scores:  
Pred. No.: 1.98e-10 Length: 382  
Score: 137.00 Matches: 29  
Percent Similarity: 85.0% Conservative: 5  
Best Local Similarity: 72.5% Mismatches: 6  
Query Match: 46.1% Indels: 1  
DB: 7 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-424-599-465 (1-382)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
Db 263 ATGGCACAGATTTTGCTCCCTCTACGCAATGCGAGATGAGAATCTCAAAATCTCTCCC 322  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 40  
|||||  
Db 323 AATGCAATCCCATTCATCAACATGTGGGT-TCTTTATGTGGAAACAAATATAGAAAG 381

## RESULT 7

US-09-770-961-774  
; Sequence 774, Application US/09770961  
; Publication No. US20030115639A1  
; GENERAL INFORMATION:

; APPLICANT: Gorlach, Jorn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Kricker, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: 2026 (PARA-015PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,961  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR FILING DATE: 60/178,466  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 774  
; LENGTH: 487  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana

US-09-770-961-774

## Alignment Scores:

Pred. No.: 5.03e-07 Length: 487  
Score: 115.00 Matches: 28  
Percent Similarity: 66.1% Conservative: 11  
Best Local Similarity: 47.5% Mismatches: 18  
Query Match: 38.7% Indels: 2  
DB: 3 Gaps: 2

US-10-628-525A-35 (1-58) x US-09-770-961-774 (1-487)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
Db 48 ATGGCTCAGATCTTAGCAGCTTCTCCAACATGTCAGATGAGAGTGCTTAAACATCATCA 107  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLys 40  
|||||  
Db 108 GTCATTGTCATCA---TCATCCAAGTTATGGAGCTCTGTTGTTGAAACAGAGAAGCAG 164  
QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr 58  
|||||  
Db 165 AGCAACAACAAAGTCAGAGGCTTTAGAGTTCTTGCTCTCCAATCTGATAACAGTACT 221

## RESULT 8

US-10-424-599-24764  
; Sequence 24764, Application US/10424599  
; Publication No. US20040031072A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599



## Alignment Scores:

Pred. No.: 7.96 Length: 1062  
Score: 69.50 Matches: 17  
Percent Similarity: 49.0% Conservative: 7  
Best Local Similarity: 34.7% Mismatches: 16  
Query Match: 23.4% Indels: 9  
DB: 3 Gaps: 2

US-10-628-525A-35 (1-58) x US-09-738-626-1418 (1-1062)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db ATGTCATCTCTTTTGAGCGATTCA-----ATGACTCAACGGCGCCT 255

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAATATACCAAGCGCA 204

QY 41 ValAlaHisSerAlaLysPheArgVal 49  
Db ACTGCTAATTCACGAGTTTAGATTG 177

## RESULT 12

US-10-494-672-115/c  
; Sequence 115, Application US/10494672  
; Publication No. US20050003494A1  
; GENERAL INFORMATION:  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Klopprogge, Corinna  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: Genes coding for novel proteins  
; FILE REFERENCE: BGI-169US  
; CURRENT APPLICATION NUMBER: US/10/494,672  
; CURRENT FILING DATE: 2004-05-04  
; PRIOR FILING DATE: PCT/EP02/12134  
; PRIOR FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: DE 10154177  
; PRIOR FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 434  
; SEQ ID NO 115  
; LENGTH: 1192  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1162)  
; OTHER INFORMATION: RXA01128

## Alignment Scores:

Pred. No.: 9.27 Length: 1192  
Score: 69.50 Matches: 17  
Percent Similarity: 49.0% Conservative: 7  
Best Local Similarity: 34.7% Mismatches: 16  
Query Match: 23.4% Indels: 9  
DB: 8 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-494-672-115 (1-1192)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db ATGTCATCTCTTTTGAGCGATTCA-----ATGACTCAACGGCGCCT 355

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db TGTACAGATCCGACTACT-----TGGAGCTCAATGTTGTTCAATATACCAAGCGCA 304

QY 41 ValAlaHisSerAlaLysPheArgVal 49  
Db ACTGCTAATTCACGAGTTTAGATTG 277

## RESULT 13

US-10-721-922A-197  
; Sequence 197, Application US/10721922A  
; Publication No. US20050191732A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar  
; APPLICANT: Haberhauer, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION  
; FILE REFERENCE: BGI-132PCPN  
; CURRENT APPLICATION NUMBER: US/10/721,922A  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: 09/6027777  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 09/603124  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143694  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: US 60/151778  
; PRIOR FILING DATE: 1999-08-31  
; PRIOR APPLICATION NUMBER: DE 19931418.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.8  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932126.4  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932127.2  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19932133.7  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 480  
; SEQ ID NO 197  
; LENGTH: 1539  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (101)..(1516)  
; OTHER INFORMATION: RXN00622

## Alignment Scores:

Pred. No.: 13 Length: 1539  
Score: 69.50 Matches: 19  
Percent Similarity: 50.8% Conservative: 14  
Best Local Similarity: 29.2% Mismatches: 21  
Query Match: 23.4% Indels: 11  
DB: 9 Gaps: 3

US-10-628-525A-35 (1-58) x US-10-721-922A-197 (1-1539)

QY 3 GlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla 22  
Db CAGATACTGTGTGGCGCCACCAAGGTGGGTACCCCGTTGAAGAGACGTTGTTGGTGATCC 91

QY 23 ThrProIleThrSerLysMet-----TrpSerSerLeuValMetLysGln----- 37  
Db AGAGCCCTGATGAACGTTATTCCACTGGGTGGGCGCACCTCGTTTCAGAAAAGTTTCATC 151

QY 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAsn 53  
Db CTTTTTGGTGGCGCTCCAGATC-----ACCTCTGAAGTACGCGTGCTTCCTTCGAC 205

QY 54 SerGluAsnGlyThr 58  
Db CAGCCAGAGGGCACC 220







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Qy 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11
Db 261 ATGGGAGAGATCCCTTTCCCACTCTTAATGAACCGCCAGCGTGTGCCAAAGTTTTTGGTGG 320
Qy 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 321 AAAATGCAAGAACTTCCTTCAGTGTGTCTAGAAATCTCTGACCAGAAAGTGTGGAAAT 380
Qy 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 381 GGTATAC TGCTAAAGACTTCATTGTTGGGAAGTCACTCA 419

RESULT 20
US-09-764-881-61
; Sequence 61, Application US/09764881
; Publication No. US20020086821A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207
; CURRENT APPLICATION NUMBER: US/09/764,881
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (873)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (902)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (920)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (936)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-881-61

Alignment Scores:
Pred. No.: 13.4 Length: 939
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 3 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-764-881-61 (1-939)
Qy 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11
Db 159 ATGGGAGAGATCCCTTTCCCACTCTTAATGAACCGCCAGCGTGTGCCAAAGTTTTTGGTGG 218
Qy 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 219 AAAATGCAAGAACTTCCTTCAGTGTGTCTAGAAATCTCTGACCAGAAAGTGTGGAAAT 278
Qy 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 279 GGTATAC TGCTAAAGACTTCATTGTTGGGAAGTCACTCA 317

RESULT 21
US-09-764-881-61
; Sequence 61, Application US/09764881
; Publication No. US20030125246A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

```

```
; LOCATION: (920)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (936)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-875-496

Alignment Scores:
Pred. No.: 13.4 Length: 939
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 3 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-764-875-496 (1-939)

QY 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11
Db 159 ATGGGAGAGATCCTTTCCCACTCCTAATGAACCGCCAGCGTGTGCCAAAGTTTGGTGG 218
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 219 AAATGCAAGAACTCCCTCAGTGTGCTAGAAATCTCTGACCAAGAAAGTTTGGAAAT 278
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 279 GGTATCTACTAAGACTTCATTGTTGGGAAGTCACTCA 317

RESULT 23
US-10-242-747-61
; Sequence 61, Application US/10242747
; Publication No. US2004005577A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT207C1
; CURRENT APPLICATION NUMBER: US/10/242,747
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,881
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (873)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (902)
```

```
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (920)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (936)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-242-747-61

Alignment Scores:
Pred. No.: 13.4 Length: 939
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 6 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-242-747-61 (1-939)

QY 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11
Db 159 ATGGGAGAGATCCTTTCCCACTCCTAATGAACCGCCAGCGTGTGCCAAAGTTTGGTGG 218
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 219 AAATGCAAGAACTCCCTCAGTGTGCTAGAAATCTCTGACCAAGAAAGTTTGGAAAT 278
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 279 GGTATCTACTAAGACTTCATTGTTGGGAAGTCACTCA 317

RESULT 24
US-10-158-057-139
; Sequence 139, Application US/10158057
; Publication No. US20040014039A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ205C1
; CURRENT APPLICATION NUMBER: US/10/158,057
; CURRENT FILING DATE: 2002-06-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (873)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (902)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (920)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (936)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-158-057-139

Alignment Scores:
Pred. No.: 13.4 Length: 939
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
```

```
Query Match: 22.7% Indels: 9
DB: 7 Gaps: 1
US-10-628-525A-35 (1-58) x US-10-158-057-139 (1-939)
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTTP 11
Db 159 ATGGGAGAGATCTTTCCCACTCTTAATGAACCCGAGCGTGTGCCAAAGTTTGGTGG 218
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTTPSer 31
Db 219 AAAATGCAAGAACTTCCCTCAGTGTGTCTAGAAATCTCTGACCAAGAGTGTGGAAAT 278
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 279 GGTATACTGCTAAAGACTTCATTGTTGGGAAGTCACTCA 317
RESULT 25
US-09-764-875-202
; Sequence 202, Application US/09764875
; Publication No. US20040018969A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: RJ202
; CURRENT APPLICATION NUMBER: US/09/764,875
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1249
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 202
; LENGTH: 1339
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-875-202
Alignment Scores:
Pred. No.: 21.4 Length: 1339
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 3 Gaps: 1
US-10-628-525A-35 (1-58) x US-09-764-875-202 (1-1339)
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTTP 11
Db 102 ATGGGAGAGATCTTTCCCACTCTTAATGAACCCGAGCGTGTGCCAAAGTTTGGTGG 161
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTTPSer 31
Db 162 AAAATGCAAGAACTTCCCTCAGTGTGTCTAGAAATCTCTGACCAAGAGTGTGGAAAT 221
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 222 GGTATACTGCTAAAGACTTCATTGTTGGGAAGTCACTCA 260
RESULT 26
US-10-158-057-62
; Sequence 62, Application US/10158057
; Publication No. US20040014039A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: RJ205C1
; CURRENT APPLICATION NUMBER: US/10/158,057
; CURRENT FILING DATE: 2002-06-12
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-158-057-62
Alignment Scores:
Pred. No.: 21.5 Length: 1346
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 7 Gaps: 1
US-10-628-525A-35 (1-58) x US-10-158-057-62 (1-1346)
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTTP 11
Db 103 ATGGGAGAGATCTTTCCCACTCTTAATGAACCCGAGCGTGTGCCAAAGTTTGGTGG 162
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTTPSer 31
Db 163 AAAATGCAAGAACTTCCCTCAGTGTGTCTAGAAATCTCTGACCAAGAGTGTGGAAAT 222
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 223 GGTATACTGCTAAAGACTTCATTGTTGGGAAGTCACTCA 261
RESULT 27
US-10-232-484-3
; Sequence 3, Application US/10232484
; Publication No. US20030113847A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: No. US20030113847A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 79ICIP2BDIV
; CURRENT APPLICATION NUMBER: US/10/232,484
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/695,783
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/552,929
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (205)..(2124)
; OTHER INFORMATION:
US-10-232-484-3
Alignment Scores:
Pred. No.: 47.1 Length: 2438
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 5 Gaps: 1
US-10-628-525A-35 (1-58) x US-10-232-484-3 (1-2438)
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTTP 11
Db 1052 ATGGGAGAGATCTTTCCCACTCTTAATGAACCCGAGCGTGTGCCAAAGTTTGGTGG 1111
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTTPSer 31
Db 1112 AAAATGCAAGAACTTCCCTCAGTGTGTCTAGAAATCTCTGACCAAGAGTGTGGAAAT 1171
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
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Db 1172 GGTACTACTGTAAGACTTCATTGTTGGGAAGTCACTCA 1210  
:::|||||:::  
:::|||||:::

RESULT 28  
US-10-972-024-93  
; Sequence 93, Application US/10972024  
; Publication No. US20050221342A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 791CIP4  
; CURRENT APPLICATION NUMBER: US/10/972,024  
; CURRENT FILING DATE: 2004-10-22  
; PRIOR APPLICATION NUMBER: PCT/US01/08655  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 09/522,929  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 09/770,160  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/668,317  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/695,783  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 09/728,628  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/783,066  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 09/816,828  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 584  
; SOFTWARE: Custom  
; SEQ ID NO 93  
; LENGTH: 2438  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (205)..(2124)  
US-10-972-024-93

Alignment Scores:  
Pred. No.: 47.1 Length: 2438  
Score: 67.50 Matches: 15  
Percent Similarity: 49.1% Conservative: 11  
Best Local Similarity: 28.3% Mismatches: 18  
Query Match: 22.7% Indels: 9  
DB: 9 Gaps: 1  
US-10-628-525A-35 (1-58) x US-10-972-024-93 (1-2438)  
QY 1 MetAlaGlnIleuAla-----ProSerThrGlnTrp 11  
Db 1052 ATGGGAGAGATCTTCCCACTCTTAATGAACGCCAGGTGTGCCAAAGTTTGGTGG 1111  
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31  
Db 1112 AAAATGCAAGAACTTCCCTCAGTGTGCTAGAAATCTCTGACCAAGAGTGTGGAT 1171  
QY 32 SerLeuValMetCysGlnThrLysLysValAlaHisSer 44  
Db 1172 GGTACTACTGTAAGACTTCATTGTTGGGAAGTCACTCA 1210  
RESULT 29  
US-09-967-768A-314/c  
; Sequence 314, Application US/09967768A  
; Patent No. US20020150877A1  
; GENERAL INFORMATION:  
; APPLICANT: Augustus, Meena  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; FILE REFERENCE: Sets  
; NAME REFERENCE: 689290-72  
; CURRENT APPLICATION NUMBER: US/09/967,768A  
; CURRENT FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: US/60/236,109  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,034  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,111  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 325  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 314  
; LENGTH: 174424  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-967-768A-314  
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Pred. No.: 1.31e+04 Length: 174424  
Score: 67.50 Matches: 19  
Percent Similarity: 54.5% Conservative: 11  
Best Local Similarity: 34.5% Mismatches: 19  
Query Match: 22.7% Indels: 6  
DB: 3 Gaps: 2  
US-10-628-525A-35 (1-58) x US-09-967-768A-314 (1-174424)  
QY 7 ProSerThrGlnTrpGlnMet-ArgIleThrLysThrSer-----ProCysAlaTh 23  
Db 66631 CCCCCCTCCCTTGGCCCCCTCTCTGACTTGGACTTCTCTCCCTCTCTCTCCCTCC 66572  
QY 23 rProIleThrSerLysMetTrpSerSerIleuValMetLysGlnThrLysLysValAlaHi 43  
Db 66571 ACCTCTACCACTGGTGTGTCTCTCTGAGGTGAACAAGACTCTGAGAGCGGACACT 66512  
QY 43 sSerAlaLysPheArgValMetAlaValAsnSerGluangly 57  
Db 66511 GCAGGCCCTGTGGAGGTGGTGGCC-----TCGGATGACGGG 66475  
RESULT 30  
US-09-960-706-969/c  
; Sequence 969, Application US/09960706  
; Publication No. US20030134280A1  
; GENERAL INFORMATION:  
; APPLICANT: Munger, William E.  
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasi  
; FILE REFERENCE: 44921-5029-01US  
; CURRENT APPLICATION NUMBER: US/09/960,706  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/223,323  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 09/873,319  
; PRIOR FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 1124  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 969  
; LENGTH: 174424  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 U52112  
US-09-960-706-969  
Alignment Scores:  
Pred. No.: 1.31e+04 Length: 174424  
Score: 67.50 Matches: 19  
Percent Similarity: 54.5% Conservative: 11  
Best Local Similarity: 34.5% Mismatches: 19  
Query Match: 22.7% Indels: 6  
DB: 3 Gaps: 2  
US-10-628-525A-35 (1-58) x US-09-960-706-969 (1-174424)  
QY 7 ProSerThrGlnTrpGlnMet-ArgIleThrLysThrSer-----ProCysAlaTh 23  
|||:::||||:::|||||

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Db 66631 CCCCCCTCCCTTTGGCCCTTCCTTCGACTTGGACTTCCTGCTCCCTCCCTGTCCTCC 66572
Qy 23 rProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHi 43
Db 66571 ACCTTTACCACCCCTGGTGGTCTCCTCTGCAGGTGAACAAGACTCTGAAGGCGACACT 66512
Qy 43 sSerAlaLysPheArgValMetAlaValAsnSerGluAsnGly 57
Db 66511 GCAGGCCCTGCTGGAGGTGGTGGCC-----TCGGATGACGGG 66475

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OM protein - nucleic search, using frame_plus_p2n model

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Searched: 9263891 seqs, 1996499642 residues

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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result      *
No.         Query Match Length DB ID      Description
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1 115 38.7 1310 11 US-11-087-099-118      Sequence 118, App
2 70.5 23.7 1367 14 US-11-066-725-412      Sequence 412, App

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Sequence 111, App
Sequence 129, App
Sequence 131, App
Sequence 254, App
Sequence 84939,
Sequence 110, App
Sequence 4, Appli
Sequence 756, App
Sequence 18, Appl
Sequence 65106,
Sequence 8, Appli
Sequence 83, Appl
Sequence 2417, Ap
Sequence 261697,
Sequence 261698,
Sequence 33963,
Sequence 33964,
Sequence 95372,
Sequence 95373,
Sequence 309283,
Sequence 384895,
Sequence 998304,
Sequence 125, App
Sequence 127, App
Sequence 278266,
Sequence 35022, A
Sequence 136260,
Sequence 749669,
Sequence 66144, A
Sequence 66145, A
Sequence 66146, A
Sequence 167383,
Sequence 167384,
Sequence 167385,
Sequence 780792,
Sequence 780793,
Sequence 780794,
Sequence 27729, A
Sequence 27729, A
Sequence 430, App
Sequence 55, Appl
Sequence 587, App
Sequence 613996,
Sequence 20142, A
Sequence 121379,
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Sequence 1005260,
Sequence 316912,
Sequence 557775,
Sequence 1171184,
Sequence 22, Appl
Sequence 13230, A
Sequence 56066, A
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Sequence 36122, A
Sequence 36122, A
Sequence 51, Appl
Sequence 2518, Ap
Sequence 2720, Ap
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Sequence 23097, A
Sequence 23098, A
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Sequence 124335,
Sequence 737743,
Sequence 737743

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60	20.2	723	10	US-10-301-480-702883	Sequence 702883,
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60	20.2	997	10	US-10-301-480-589960	Sequence 589960,
60	20.2	997	10	US-10-301-480-1203369	Sequence 1203369,
60	20.2	1054	8	US-10-301-480-1203369	Sequence 1203369,
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60	20.2	2455	14	US-11-136-527-3862	Sequence 3862, Ap
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60	20.2	3368	8	US-10-793-626-4169	Sequence 4169, Ap
60	20.2	3614	8	US-10-689-742-37	Sequence 37, Appl
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59.5	20.0	509	6	US-09-925-065A-137014	Sequence 137014,
59.5	20.0	1239	8	US-10-750-185-38559	Sequence 38559, A
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59.5	20.0	4636	14	US-11-136-527-2060	Sequence 2060, Ap
59.5	20.0	90508	6	US-10-330-773-701	Sequence 701, App
59	19.9	732	6	US-09-925-065A-89204	Sequence 89204, A
59	19.9	732	9	US-10-301-480-190445	Sequence 190445,
59	19.9	732	10	US-10-301-480-803854	Sequence 803854,
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102	59	1472	6	US-09-925-065A-92401	Sequence 92401, A
103	59	1472	9	US-10-301-480-193642	Sequence 193642,
104	59	1472	9	US-10-301-480-193643	Sequence 193643,
105	59	1472	10	US-10-301-480-807051	Sequence 807051,
106	59	1472	10	US-10-301-480-807052	Sequence 807052,
107	59	1540	14	US-11-112-908-436	Sequence 436, App
108	59	3366	9	US-10-330-773-257	Sequence 257, App
109	59	3678	14	US-11-000-688-704	Sequence 704, App
110	59	177623	14	US-11-112-908-41	Sequence 41, Appl
111	58.5	416	6	US-09-925-065A-47761	Sequence 47761, A
112	58.5	416	6	US-09-925-065A-47762	Sequence 47762, A
113	58.5	416	9	US-10-301-480-148999	Sequence 148999,
114	58.5	416	9	US-10-301-480-149000	Sequence 149000,
115	58.5	416	10	US-10-301-480-762408	Sequence 762408,
116	58.5	416	10	US-10-301-480-762409	Sequence 762409,
117	58.5	492	6	US-09-925-065A-336258	Sequence 336258,
118	58.5	496	10	US-10-301-480-409578	Sequence 409578,
119	58.5	496	10	US-10-301-480-102297	Sequence 102297,
120	58.5	574	6	US-09-925-065A-31299	Sequence 31299, A
121	58.5	574	6	US-09-925-065A-31300	Sequence 31300, A
122	58.5	574	9	US-10-301-480-132537	Sequence 132537,
123	58.5	574	9	US-10-301-480-132538	Sequence 132538,
124	58.5	574	10	US-10-301-480-745946	Sequence 745946,
125	58.5	574	10	US-10-301-480-745947	Sequence 745947,
126	58.5	622	6	US-09-925-065A-28865	Sequence 28865, A
127	58.5	622	9	US-10-301-480-130103	Sequence 130103,
128	58.5	622	10	US-10-301-480-743512	Sequence 743512,
129	58.5	1330	14	US-11-066-725-273	Sequence 273, App
130	58.5	1767	8	US-10-750-185-51075	Sequence 51075, A
131	58.5	1767	8	US-10-750-623-51075	Sequence 51075, A
132	58.5	1809	9	US-10-301-480-98731	Sequence 98731, A
133	58.5	1809	10	US-10-301-480-712140	Sequence 712140,
134	58.5	2862	14	US-11-066-725-11	Sequence 11, Appl
135	58	481	6	US-09-925-065A-466693	Sequence 466693,
136	58	569	6	US-09-925-065A-884081	Sequence 884081,
137	58	569	6	US-09-925-065A-884082	Sequence 884082,
138	58	578	6	US-09-925-065A-331410	Sequence 331410,
139	58	581	10	US-10-301-480-405204	Sequence 405204,
140	58	581	10	US-10-301-480-1018613	Sequence 1018613,
141	58	597	6	US-09-925-065A-331412	Sequence 331412,
142	58	605	10	US-10-301-480-405206	Sequence 405206,
143	58	605	10	US-10-301-480-1018615	Sequence 1018615,
144	58	622	6	US-09-925-065A-27453	Sequence 27453, A
145	58	622	9	US-10-301-480-128690	Sequence 128690,
146	58	622	10	US-10-301-480-742099	Sequence 742099,
147	58	1058	8	US-10-750-185-63197	Sequence 63197, A
148	58	1058	8	US-10-750-623-63197	Sequence 63197, A

ALIGNMENTS

RESULT 1

US-11-087-099-118  
 ; Sequence 118, Application US/11087099  
 ; Publication NO. US20060041961A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abad, Mark S. et al.  
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
 ; FILE REFERENCE: 38-21(53450)B EP  
 ; CURRENT APPLICATION NUMBER: US/11/087,099  
 ; CURRENT FILING DATE: 2005-03-22  
 ; NUMBER OF SEQ ID NOS: 12464  
 ; SEQ ID NO 118  
 ; LENGTH: 1310  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-11-087-099-118

Alignment Scores:

Pred. No.: 8,77e-05 Length: 1310  
 Score: 115.00 Matches: 28  
 Percent Similarity: 65.1% Conservative: 11  
 Best Local Similarity: 47.5% Mismatches: 18  
 Query Match: 38.7% Indels: 2  
 DB: 11 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-087-099-118 (1-1310)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrIlyThrSerPro 20  
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 DB 10 ATGGCTCAGATTAGCAGCTTCTCCACATCTCAGATGAGAGTGCCTAAACACTCATCA 69  
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 QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrIlyLys 40  
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 DB 70 GTCATGTGCATCA---TCATCCAGTTATGAGACTCTGTGTGTTGAAACAGAGAGCAG 126  
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 QY 41 ValAlaHisSerAlaLys---PheArgValMetAlaValAsnSerGluAsnGlyThr 58  
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 DB 127 AGCAACAAACAAAGTCAGAGGCTTTAGAGTTCTTGCTCTCCAATCGGATAACAGTACT 183  
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RESULT 2

US-11-066-725-412  
 ; Sequence 412, Application US/11066725  
 ; Publication NO. US20050272680A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Isis Pharmaceuticals Inc.  
 ; APPLICANT: Sanjay Bhanot  
 ; APPLICANT: Kenneth W. Dobie  
 ; APPLICANT: King-Xian Yu  
 ; APPLICANT: Brett P. Monia  
 ; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION  
 ; FILE REFERENCE: RTS-0678US.C1  
 ; CURRENT APPLICATION NUMBER: US/11/066,725  
 ; CURRENT FILING DATE: 2003-02-24  
 ; PRIOR APPLICATION NUMBER: US/10/643,801  
 ; PRIOR FILING DATE: 2003-08-18  
 ; PRIOR APPLICATION NUMBER: PCT/US2004/024384  
 ; PRIOR FILING DATE: 2004-08-18  
 ; NUMBER OF SEQ ID NOS: 492  
 ; SEQ ID NO 412  
 ; LENGTH: 1367  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (201)...(1367)  
 US-11-066-725-412



Alignment Scores:	
Pred. No.:	53.6
Score:	70.50
Percent Similarity:	58.1%
Best Local Similarity:	48.4%
Query Match:	23.7%
DB:	14
	Gaps:
	Indels:
	Mismatches:
	Conservative:
	Matches:
	Length:

US-10-628-525A-35 (1-58) x US-11-066-725-412 (1-1367)

Qy	6	AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle	25
Db	1225	TCACCGTCCCTAAAGCTGGAGACCCGACCCAGAAAGACATCGACCTGTACCACCATGT	1284
Qy	26	ThrSerLysMetTrp---SerSerLeuValMet	35
Db	1285	ACATGAGGCGCCCTGGTGAAGCTCTTTGCACATC	1317

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RESULT 3
US-11-231-243-111
; Sequence 111, Application US/11231243
; Publication No. US20060063730A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Siwkowski, Andrew M.
; APPLICANT: Bhanot, Sanjay
; TITLE OF INVENTION: ENHANCED ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: CORE0051US
; CURRENT APPLICATION NUMBER: US/11/231,243
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: 60/611,100
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/663,442
; PRIOR FILING DATE: 2005-03-18
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 31737
; TYPE: DNA
; ORGANISM: R. norvegicus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (26994)..(27191)
; OTHER INFORMATION: n = A,T,C or G
US-11-231-243-111

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Score:	70.50	15
Percent Similarity:	58.1%	Conservative: 3
Best Local Similarity:	48.4%	Mismatches: 12
Query Match:	23.7%	Indels: 1
DB:	11	Gaps: 1

US-10-628-525A-35 (1-58) x US-11-231-243-111 (1-31737)

Oy		6 AlaProSerThrGlnTyrClnMetArgIleThrLysThrSerProCyAlaThrProIle 25
	:	:::::
Db	30208	TCCACGTCCCTAAGCTGGAGCACCCGCACCAGAAAGACATCGACTGTACCACCATGT 30267
Oy	26 ThrSerLysMetTrp---SerSerLeuValMet 35	
	:	:::::
Db	30268	ACATGGAGGCCCTCGTGAAGCTCTTTGACAATC 30300

RESULT 4  
US-10-454-437-129  
; Sequence 129, Application US/10454437  
; Publication No. US2005027115A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompejus, Markus  
; APPLICANT: Kroger, Burkhard  
; APPLICANT: Schroder, Hartwig  
; APPLICANT: Zelder, Oskar

```

; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 129
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1516)
; OTHER INFORMATION: RXN00622
US-10-454-437-129

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Alignment Scores:		
Pred. No.:	83	Length: 1539
Score:	69.50	Matches: 19
Percent Similarity:	50.8%	Conservative: 14
Best Local Similarity:	29.2%	Mismatches: 21
Query Match:	23.4%	Indels: 11
DB:	8	Gaps: 3

US-10-628-525A-35 (1-58) x US-10-454-437-129 (1-1539)

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Qy 3 GlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla 22
Db 32 CAGATACTGTGTGGGCCACAAAGGTGGGTATCCCGGTTGAAGAAGACGTGTGTGGTGATCC 91
Qy 23 ThrProIleThrSerLysMet-----TTrpSerSerLeuValMetLysGln----- 37
Db 92 ACGAGCCTGATGAACAGTTATTCCACCTGGGTGGGCACCACTCGTTTCAGAAAAAGTTTCATC 151
Qy 38 -----ThrLysLysValAlaAlaHisSerAlaLysPheArgValMetAlaValAsn 53
Db 152 CTTTGTGGTGGCCCTCCAGATC-----ACCTCTGAAGTACGCGGTCTCTCTTCGAC 205
Qy 54 SerGluAsnGlyThr 58
Db 206 CAGCCAGAGGGCACC 220

RESULT 5
US-10-454-437-131
; Sequence 131, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar

```

```
/ APPLICANT: Haberhauer, Gregor
/ TITLE OF INVENTION: CORNYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
/ FILE REFERENCE: BGI-128CFCN
/ CURRENT FILING DATE: 2003-06-13
/ CURRENT APPLICATION NUMBER: US/10/454,437
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: US 60/141031
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931636.8
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932125.6
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932126.4
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932127.2
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932128.0
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932129.9
/ PRIOR FILING DATE: 1999-07-19
/ PRIOR APPLICATION NUMBER: DE 19932226.0
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932920.6
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932922.2
/ PRIOR FILING DATE: 1999-07-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 442
/ SEQ ID NO 131
/ LENGTH: 1539
/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (101)..(1516)
/ OTHER INFORMATION: FRXA00622
US-10-454-437-131

Alignment Scores:
Pred. No.: 83 Length: 1539
Score: 69.50 Matches: 19
Percent Similarity: 50.8% Conservative: 14
Best Local Similarity: 29.2% Mismatches: 21
Query Match: 23.4% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-35 (1-58) x US-10-454-437-131 (1-1539)
QY 3 GlnilleLeuAlaProSerThrGlnTrpGlnMetArgileThrLysThrSerProCysAla 22
Db 32 CAGATACTGTGTGGCCACAGGTGGTACCCGGTTGAAGACGCGTTGGTGTACC 91
QY 23 ThrProilleThrSerLysMet-----TrpSerSerLeuValMetLysGln----- 37
Db 92 ACGAGCCTGATGAACGATTATTCCTCCCTGGTGGCCACCACTGTTTCAGAAAAAGTTTCATC 151
QY 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAla 53
Db 152 CTTTTTGGTGGCGCTCCAGATC-----ACCTCTGAAGTACGCGTGCTCTCTTCGAC 205
QY 54 SerGluAsnGlyThr 58
Db 206 CAGCCAGAGGGCACC 220

RESULT 6
US-10-330-773-254/c
/ Sequence 254, Application US/10330773
/ Publication No. US20060040262A1
/ GENERAL INFORMATION:
/ APPLICANT: David W. Morris
/ APPLICANT: Marc Malandro
/ TITLE OF INVENTION: Novel Compositions and Methods in Cancer
/ FILE REFERENCE: 529452001300

/ APPLICANT: Haberhauer, Gregor
/ TITLE OF INVENTION: CORNYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
/ FILE REFERENCE: BGI-128CFCN
/ CURRENT FILING DATE: 2003-06-13
/ CURRENT APPLICATION NUMBER: US/10/454,437
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: US 60/141031
/ PRIOR FILING DATE: 1999-07-08
/ PRIOR APPLICATION NUMBER: DE 19931636.8
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932125.6
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932126.4
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932127.2
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932128.0
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932129.9
/ PRIOR FILING DATE: 1999-07-19
/ PRIOR APPLICATION NUMBER: DE 19932226.0
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: DE 19932920.6
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: DE 19932922.2
/ PRIOR FILING DATE: 1999-07-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 442
/ SEQ ID NO 131
/ LENGTH: 1539
/ TYPE: DNA
/ ORGANISM: Corynebacterium glutamicum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (101)..(1516)
/ OTHER INFORMATION: FRXA00622
US-10-454-437-131

Alignment Scores:
Pred. No.: 83 Length: 1539
Score: 69.50 Matches: 19
Percent Similarity: 50.8% Conservative: 14
Best Local Similarity: 29.2% Mismatches: 21
Query Match: 23.4% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-35 (1-58) x US-10-454-437-131 (1-1539)
QY 3 GlnilleLeuAlaProSerThrGlnTrpGlnMetArgileThrLysThrSerProCysAla 22
Db 32 CAGATACTGTGTGGCCACAGGTGGTACCCGGTTGAAGACGCGTTGGTGTACC 91
QY 23 ThrProilleThrSerLysMet-----TrpSerSerLeuValMetLysGln----- 37
Db 92 ACGAGCCTGATGAACGATTATTCCTCCCTGGTGGCCACCACTGTTTCAGAAAAAGTTTCATC 151
QY 38 -----ThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAla 53
Db 152 CTTTTTGGTGGCGCTCCAGATC-----ACCTCTGAAGTACGCGTGCTCTCTTCGAC 205
QY 54 SerGluAsnGlyThr 58
Db 206 CAGCCAGAGGGCACC 220

RESULT 6
US-10-330-773-254/c
/ Sequence 254, Application US/10330773
/ Publication No. US20060040262A1
/ GENERAL INFORMATION:
/ APPLICANT: David W. Morris
/ APPLICANT: Marc Malandro
/ TITLE OF INVENTION: Novel Compositions and Methods in Cancer
/ FILE REFERENCE: 529452001300

/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 864939
/ LENGTH: 682
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-864939

Alignment Scores:
Pred. No.: 91.2 Length: 682
Score: 66.00 Matches: 12
Percent Similarity: 45.2% Conservative: 7
Best Local Similarity: 28.6% Mismatches: 23
Query Match: 22.2% Indels: 0
DB: 6 Gaps: 0

US-09-925-065A-864939/c
/ Sequence 864939, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 864939
/ LENGTH: 682
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-864939

Alignment Scores:
Pred. No.: 91.2 Length: 682
Score: 66.00 Matches: 12
Percent Similarity: 45.2% Conservative: 7
Best Local Similarity: 28.6% Mismatches: 23
Query Match: 22.2% Indels: 0
DB: 6 Gaps: 0

US-09-925-065A-864939
```

```
/ CURRENT APPLICATION NUMBER: US/10/330,773
/ CURRENT FILING DATE: 2002-12-27
/ NUMBER OF SEQ ID NOS: 981
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 254
/ LENGTH: 86149
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(86149)
/ OTHER INFORMATION: n = A,T,C or G
US-10-330-773-254

Alignment Scores:
Pred. No.: 1.42e+04 Length: 86149
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 9 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-330-773-254 (1-86149)
QY 6 AlaProSerThrGlnTrpGlnMetArgileThrLysThrSerProCysAlaThrProile 25
Db 46678 GCCCGCAGCTACCATGGTAGATGAATATCTGGAGACCCCTGTTCCAGCCCTCAGGATT 46619
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 46618 TGCCAGAGCCCATGGGCAGAGTGGAGATGGTGGGACAACTGGATGGGTCCCTCAGGG 46559
QY 46 LysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 46558 AGATTTCAGGCAGCTCAACGAGGAACTGGAGAAAGGCACT 46520

RESULT 7
US-09-925-065A-864939/c
/ Sequence 864939, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 864939
/ LENGTH: 682
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-864939

Alignment Scores:
Pred. No.: 91.2 Length: 682
Score: 66.00 Matches: 12
Percent Similarity: 45.2% Conservative: 7
Best Local Similarity: 28.6% Mismatches: 23
Query Match: 22.2% Indels: 0
DB: 6 Gaps: 0

US-09-925-065A-864939
```

```
US-10-628-525A-35 (1-58) x US-09-925-065A-864939 (1-682)
Qy 15 lleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSerSerLeuVal 34
Db 381 GTGGTTTCAACAGGCTCGGCTGCTGCCGCCAGCCCAAGCTTGTGGCAAGACCATC 322
Qy 35 MetLysGlnThrLysValAlaHisSerAlaLysPheArgValMetAlaValAsnSer 54
Db 321 ACCGACGAGGCCAGAGTGGGGGACCAAGCCAGAGAGGGCTACCTTCATGCTTTAGT 262
Qy 55 GluAsn 56
Db 261 TCCAAC 256

RESULT 8
US-11-231-243-110
; Sequence 110, Application US/11231243
; Publication No. US20060063730A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Siwkowski, Andrew M.
; APPLICANT: Bhanot, Sanjay
; TITLE OF INVENTION: ENHANCED ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: CORE0051US
; CURRENT APPLICATION NUMBER: US/11/231,243
; CURRENT FILING DATE: 2005-09-19
; PRIOR FILING DATE: 2004-09-17
; PRIOR FILING DATE: 2004-09-17
; PRIOR FILING DATE: 2005-03-18
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 2439
; TYPE: DNA
; ORGANISM: H. sapiens
US-11-231-243-110

Alignment Scores:
Pred. No.: 404 Length: 2439
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 11 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-231-243-110 (1-2439)
Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1255 TCACCATCCCAAGCTGGAGCCCAACCCAGCAAGACATCGACCTGTACCAACCATGT 1314
Qy 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1315 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAAG-----CACAAAGACC 1355
Qy 46 LysPhe-----ArgValMetAlaValAsn 53
Db 1356 AAGTTCGGCCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 1394

RESULT 9
US-11-066-725-4
; Sequence 4, Application US/11066725
; Publication No. US20050272680A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Doble
; APPLICANT: Xing-xian Yu
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-0678US.C1
; CURRENT APPLICATION NUMBER: US/11/066, 725
```

```
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: US/10/643,801
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: PCT/US2004/024384
; PRIOR FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 492
; SEQ ID NO 4
; LENGTH: 2439
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (231)...(1397)
US-11-066-725-4

Alignment Scores:
Pred. No.: 404 Length: 2439
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 14 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-066-725-4 (1-2439)
Qy 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 1255 TCACCATCCCAAGCTGGAGCCCAACCCAGCAAGACATCGACCTGTACCAACCATGT 1314
Qy 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 1315 ACATGGAGGCCCTGGTG-AAGCTCTTCGACAAAG-----CACAAAGACC 1355
Qy 46 LysPhe-----ArgValMetAlaValAsn 53
Db 1356 AAGTTCGGCCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 1394

RESULT 10
US-11-072-512-756
; Sequence 756, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 756
; LENGTH: 2678
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-756

Alignment Scores:
Pred. No.: 450 Length: 2678
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservatives: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 11 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-072-512-756 (1-2678)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
   ::::::::::::::::::::
Db 2412 TCACCATCCCCAAGCTGGAGACCCCAACCCAGACATCGACCTGTACCAACACCATGT 2471
   ::::::::::::::::::::

QY 26 ThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLysValAlaHisSerAla 45
   ::::::::::::::::::::
Db 2472 ACATGGAGGCCCTGGTG-AGGCTCTTCGACAG-----CACAGACC 2512
   ::::::::::::::::::::

QY 46 LysPhe-----ArgValMetAlaValAen 53
   ::::::::::::::::::::
Db 2513 AAGTTGGGCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 2551
   ::::::::::::::::::::

RESULT 11
US-11-066-725-18
; Sequence 18, Application US/11066725
; Publication No. US20050272680A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals Inc.
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Dobie
; APPLICANT: King-Xian Yu
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
; FILE REFERENCE: RTS-0678US.C1
; CURRENT APPLICATION NUMBER: US/11/066,725
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: US/10/643,801
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: PCT/US2004/024384
; PRIOR FILING DATE: 2004-08-18
; NUMBER OF SEQ ID NOS: 492
; SEQ ID NO 18
; LENGTH: 42823
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-11-066-725-18

Alignment Scores:
Pred. No.: 1,14e+04 Length: 42823
Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservatives: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 14 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-066-725-18 (1-42823)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
   ::::::::::::::::::::
Db 41255 TCACCATCCCCAAGCTGGAGACCCCAACCCAGACATCGACCTGTACCAACACCATGT 41314
   ::::::::::::::::::::

QY 26 ThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLysValAlaHisSerAla 45
   ::::::::::::::::::::
Db 41315 ACATGGAGGCCCTGGTG-AGGCTCTTCGACAG-----CACAGACC 41355
   ::::::::::::::::::::

QY 46 LysPhe-----ArgValMetAlaValAen 53
   ::::::::::::::::::::
Db 41356 AAGTTGGGCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 41394
   ::::::::::::::::::::
```

```
RESULT 12
US-09-925-065A-651006/c
; Sequence 651006, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 651006
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-651006

Alignment Scores:
Pred. No.: 76.8 Length: 518
Score: 65.50 Matches: 17
Percent Similarity: 66.7% Conservatives: 9
Best Local Similarity: 43.6% Mismatches: 12
Query Match: 22.1% Indels: 2
DB: 6 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-925-065A-651006 (1-518)

QY 17 LysThrSerProCysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLys 36
   ::::::::::::::::::::
Db 466 AAATCTCTACCATGTGCCAA-----CTCTGTGCCAAGGGCTGGGATACTCTGGGAATAAAA 411
   ::::::::::::::::::::

QY 37 GlnThrLysLysValAlaHisSerAlaLysPheArgValMetAlaValAenSerGlu 55
   ::::::::::::::::::::
Db 410 AGATRGAGAAAGATCTCTTCTTCTGTGAGTTTCAGGGTCAGTGGGGTGTCAAGTGAG 354
   ::::::::::::::::::::

RESULT 13
US-11-177-506-8/c
; Sequence 8, Application US/11177506
; Publication No. US20060029956A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Venetta, Thomas M.
; APPLICANT: Groelke, John W.
; APPLICANT: Blaesius, Rainer H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE
; FILE REFERENCE: 46143/294851
; CURRENT APPLICATION NUMBER: US/11/177,506
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: 60/586,856
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 5067
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)...(5052)
```

## US-11-177-506-8

Alignment Scores:  
Pred. No.: 1.28e+03 Length: 5067  
Score: 65.00 Matches: 13  
Percent Similarity: 63.0% Conservative: 4  
Best Local Similarity: 48.1% Mismatches: 10  
Query Match: 21.9% Indels: 0  
DB: 11 Gaps: 0

## US-10-628-525A-35 (1-58) x US-11-177-506-8 (1-5067)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26  
Db 251 CCTGGGAGTCGTGGACAGTAACAGTGGACATCCCTTCGCGGTGCGGCGCTCC 192  
QY 27 SerLysMetTrpSerSerLeu 33  
Db 191 AGCACCATGGTCTCTCTCGCTC 171

## RESULT 14

US-11-000-688-83/c  
; Sequence 83, Application US/11000688  
; Publication No. US20050287544A1  
; GENERAL INFORMATION:  
; APPLICANT: BERTUCCI, Francois  
; APPLICANT: HOULGATTE, Remi  
; APPLICANT: BIRNBAUM, Daniel  
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS  
; FILE REFERENCES: 1423-R-03  
; CURRENT APPLICATION NUMBER: US/11/000,688  
; CURRENT FILING DATE: 2004-12-01  
; PRIOR APPLICATION NUMBER: US 60/525,987  
; PRIOR FILING DATE: 2003-12-01  
; NUMBER OF SEQ ID NOS: 1596  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 83  
; LENGTH: 5067  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial sequences: primer  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(5067)  
; OTHER INFORMATION: complement component 3 (C3) gene.  
US-11-000-688-83

Alignment Scores:  
Pred. No.: 1.28e+03 Length: 5067  
Score: 65.00 Matches: 13  
Percent Similarity: 63.0% Conservative: 4  
Best Local Similarity: 48.1% Mismatches: 10  
Query Match: 21.9% Indels: 0  
DB: 14 Gaps: 0

## US-10-628-525A-35 (1-58) x US-11-000-688-83 (1-5067)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26  
Db 251 CCTGGGAGTCGTGGACAGTAACAGTGGACATCCCTTCGCGGTGCGGCGCTCC 192  
QY 27 SerLysMetTrpSerSerLeu 33  
Db 191 AGCACCATGGTCTCTCTCGCTC 171

## RESULT 15

US-10-467-657-2417  
; Sequence 2417, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 2417  
; LENGTH: 1569  
; TYPE: DNA  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2417

Alignment Scores:  
Pred. No.: 377 Length: 1569  
Score: 64.50 Matches: 18  
Percent Similarity: 50.0% Conservative: 2  
Best Local Similarity: 45.0% Mismatches: 13  
Query Match: 21.7% Indels: 7  
DB: 8 Gaps: 2

## US-10-628-525A-35 (1-58) x US-10-467-657-2417 (1-1569)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 25  
Db 221 CGTCAACCTCTTGGACACCGCGGACACCAAGACTTCTCCG---AAGACACCTACCGCG 277  
QY 26 -----ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 278 TTTTAAACCGCAGTGGACAGCGCTTGCATCGACGCGCAAAAGGCGTGGAGCGC 337

## RESULT 16

US-09-925-065A-261697  
; Sequence 261697, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2004-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 261697  
; LENGTH: 562  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-261697

Alignment Scores:  
Pred. No.: 132 Length: 562  
Score: 64.00 Matches: 11  
Percent Similarity: 50.0% Conservative: 8  
Best Local Similarity: 28.9% Mismatches: 19  
Query Match: 21.5% Indels: 0  
DB: 6 Gaps: 0

## US-10-628-525A-35 (1-58) x US-09-925-065A-261697 (1-562)

```
QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 440 CCCACAGTCAGTGGCACTGAGAGTGAAGATAGCTTGCCTTGGAAATCCAACTGAA 499

QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 500 GGGAAATATGGGTTAAAGAAATAGAGGGGGATTGTACACTTAGCACATACT 553

RESULT 17
US-09-925-065A-261698
; Sequence 261698, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261698
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-261698

Alignment Scores:
Pred. No.: 132 Length: 562
Score: 64.00 Matches: 11
Percent Similarity: 50.0% Conservative: 8
Best Local Similarity: 28.9% Mismatches: 19
Query Match: 21.5% Indels: 0
DB: 6 Gaps: 0

US-10-628-525A-35 (1-59) x US-09-925-065A-261698 (1-562)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 440 CCCACAGTCAGTGGCACTGAGAGTGAAGATAGCTTGCCTTGGAAATCCAACTGAA 499

QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 500 GGGAAATATGGGTTAAAGAAATAGAGGGGGATTGTACACTTAGCACATACT 553

RESULT 18
US-10-301-480-339963
; Sequence 339963, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 339963
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-339963

Alignment Scores:
Pred. No.: 133 Length: 565
Score: 64.00 Matches: 11
Percent Similarity: 50.0% Conservative: 8
Best Local Similarity: 28.9% Mismatches: 19
Query Match: 21.5% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-301-480-339963 (1-565)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 440 CCCACAGTCAGTGGCACTGAGAGTGAAGATAGCTTGCCTTGGAAATCCAACTGAA 499

QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 500 GGGAAATATGGGTTAAAGAAATAGAGGGGGATTGTACACTTAGCACATACT 553

RESULT 19
US-10-301-480-339964
; Sequence 339964, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339964
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-339964

Alignment Scores:
Pred. No.: 133 Length: 565
Score: 64.00 Matches: 11
Percent Similarity: 50.0% Conservative: 8
Best Local Similarity: 28.9% Mismatches: 19
Query Match: 21.5% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-301-480-339964 (1-565)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 440 CCCACAGTCAGTGGCACTGAGAGTGAAGATAGCTTGCCTTGGAAATCCAACTGAA 499

QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 500 GGGAAATATGGGTTAAAGAAATAGAGGGGGATTGTACACTTAGCACATACT 553

RESULT 20
US-10-301-480-953372
; Sequence 953372, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; in the Human Genome
```

```

; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 953372
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-953372

Alignment Scores:
Pred. No.: 133 Length: 565
Score: 64.00 Matches: 11
Percent Similarity: 50.0% Conservative: 8
Best Local Similarity: 28.9% Mismatches: 19
Query Match: 21.5% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-301-480-953372 (1-565)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
Db 440 CCCACAGTCAGTGGCAACTGAGAGTGAAGATAGCTTGCCAAATGGAAATCCCACTGAA 499
QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValalaHisSer 44
Db 500 GGGAAATATGGGTTAAAGAAATAGAGGGGGGATTTGTACACTTAGCACATACT 553

RESULT 21
US-10-301-480-953373
; Sequence 953373, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 953373
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-953373

Alignment Scores:
Pred. No.: 133 Length: 565
Score: 64.00 Matches: 11
Percent Similarity: 50.0% Conservative: 8
Best Local Similarity: 28.9% Mismatches: 19
Query Match: 21.5% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-301-480-953373 (1-565)

QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
Db 440 CCCACAGTCAGTGGCAACTGAGAGTGAAGATAGCTTGCCAAATGGAAATCCCACTGAA 499
QY 27 SerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValalaHisSer 44
Db 500 GGGAAATATGGGTTAAAGAAATAGAGGGGGGATTTGTACACTTAGCACATACT 553

RESULT 22
US-09-925-065A-309283/c
; Sequence 309283, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 309283
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-309283

Alignment Scores:
Pred. No.: 149 Length: 549
Score: 63.50 Matches: 13
Percent Similarity: 63.6% Conservative: 8
Best Local Similarity: 39.4% Mismatches: 11
Query Match: 21.4% Indels: 1
DB: 6 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-925-065A-309283 (1-549)

QY 10 GlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMet 29
Db 416 CAGTGGGAGATG---ATCAAAATTGACATCACCTGTTCTAAACCATTAATCTGGTGAGACA 360
QY 30 TrpSerSerLeuValMetLysGlnThrLysLysValala 42
Db 359 TAATATAGCCTCTGTATTAGGGACACAAATTTCTTATCT 321

RESULT 23
US-10-301-480-384895/c
; Sequence 384895, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 384895
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-384895

Alignment Scores:
Pred. No.: 152 Length: 558
```









GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 20:18:18 ; Search time 1585.5 Seconds  
(without alignments)  
2022.653 Million cell updates/sec

Title: US-10-628-525A-35

Perfect score: 297

Sequence: 1 MAQILAPSTQWQRITKTP.....KKVAHSAKFRMAVNSNGT 58

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-Q=/abs/ABSSWEB.spool/US10628525/runat\_31032006\_095128\_16978/app\_query.fasta\_1  
-DB=Pending Patents NA.Main -OPMT=fastap -SUFFIX=p2n.rndm -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=150 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=abes06h  
-USER=US10628525 @CGN 1.1 19447 @runat\_31032006\_095128\_16978 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DISPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending Patents NA.Main:  
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69: /cgn2\_6/ptodata/1/pna/US110D\_COMB.seq.\*  
70: /cgn2\_6/ptodata/1/pna/US111A\_COMB.seq.\*  
71: /cgn2\_6/ptodata/1/pna/US111B\_COMB.seq.\*  
72: /cgn2\_6/ptodata/1/pna/US112\_COMB.seq.\*  
73: /cgn2\_6/ptodata/1/pna/US117\_COMB.seq.\*  
74: /cgn2\_6/ptodata/1/pna/US600\_COMB.seq.\*  
75: /cgn2\_6/ptodata/1/pna/US601\_COMB.seq.\*  
76: /cgn2\_6/ptodata/1/pna/US602A\_COMB.seq.\*  
77: /cgn2\_6/ptodata/1/pna/US602B\_COMB.seq.\*  
78: /cgn2\_6/ptodata/1/pna/US603\_COMB.seq.\*  
79: /cgn2\_6/ptodata/1/pna/US604A\_COMB.seq.\*  
80: /cgn2\_6/ptodata/1/pna/US604B\_COMB.seq.\*  
81: /cgn2\_6/ptodata/1/pna/US605\_COMB.seq.\*  
82: /cgn2\_6/ptodata/1/pna/US606\_COMB.seq.\*  
83: /cgn2\_6/ptodata/1/pna/US607\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	216	72.7	262	23	Sequence 184930,
2	216	72.7	262	23	Sequence 184930,
3	216	72.7	262	39	Sequence 184930,
4	216	72.7	278	23	Sequence 106380,
5	216	72.7	278	23	Sequence 106380,
6	216	72.7	278	39	Sequence 106380,
7	216	72.7	282	22	Sequence 9660, Ap



```
RESULT 1
US-09-304-517A-184930
; Sequence 184930, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 184930
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-184930

Alignment Scores:
Pred. No.: 8,2e-23 Length: 262
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-304-517A-184930 (1-262)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 70 ATGGCACAGATTTGGCTCCCTTACGCAATGCGAGATGAGATCTCAAAATCTCTCCC 129
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40
Db 130 AATGCAACTCCCATATACATCAACATGTCGAGTCTCTTATTGTGGAAACAAATAAGAAA 189
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 190 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTCTGCGCAATTAAGTCTGCAATAGCACT 249

RESULT 2
US-09-371-146A-184930
; Sequence 184930, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 184930
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-146A-184930

Alignment Scores:
Pred. No.: 8,2e-23 Length: 262
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-371-146A-184930 (1-262)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 70 ATGGCACAGATTTGGCTCCCTTACGCAATGCGAGATGAGATCTCAAAATCTCTCCC 129
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40
Db 130 AATGCAACTCCCATATACATCAACATGTCGAGTCTCTTATTGTGGAAACAAATAAGAAA 189
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 190 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTCTGCGCAATTAAGTCTGCAATAGCACT 249

RESULT 3
US-09-985-678-184930
; Sequence 184930, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 184930
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-184930

Alignment Scores:
Pred. No.: 8,2e-23 Length: 262
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 39 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-985-678-184930 (1-262)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 70 ATGGCACAGATTTGGCTCCCTTACGCAATGCGAGATGAGATCTCAAAATCTCTCCC 129
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40
Db 130 AATGCAACTCCCATATACATCAACATGTCGAGTCTCTTATTGTGGAAACAAATAAGAAA 189
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 190 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTCTGCGCAATTAAGTCTGCAATAGCACT 249

RESULT 4
US-09-304-517A-106380
; Sequence 106380, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 106380
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-106380

Alignment Scores:
Pred. No.: 9e-23 Length: 278
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 23 Gaps: 1
```

```
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40
Db 130 AATGCAACTCCCATATACATCAACATGTCGAGTCTCTTATTGTGGAAACAAATAAGAAA 189
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 190 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTCTGCGCAATTAAGTCTGCAATAGCACT 249

RESULT 3
US-09-985-678-184930
; Sequence 184930, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 184930
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-184930

Alignment Scores:
Pred. No.: 8,2e-23 Length: 262
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 39 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-985-678-184930 (1-262)
QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 70 ATGGCACAGATTTGGCTCCCTTACGCAATGCGAGATGAGATCTCAAAATCTCTCCC 129
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLysValMetLysGlnThrLysLys 40
Db 130 AATGCAACTCCCATATACATCAACATGTCGAGTCTCTTATTGTGGAAACAAATAAGAAA 189
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 190 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTCTGCGCAATTAAGTCTGCAATAGCACT 249

RESULT 4
US-09-304-517A-106380
; Sequence 106380, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 106380
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-106380

Alignment Scores:
Pred. No.: 9e-23 Length: 278
Score: 216.00 Matches: 44
Percent Similarity: 85.0% Conservative: 7
Best Local Similarity: 73.3% Mismatches: 7
Query Match: 72.7% Indels: 2
DB: 23 Gaps: 1
```

US-10-628-525A-35 (1-58) x US-09-304-517A-106380 (1-278)

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 92 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 151
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 152 AATGCAACTCCCATTCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 211
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 212 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGGCAATTAAGTCTGACAATAGCACC 271
```

## RESULT 5

```
US-09-371-146A-106380
; Sequence 106380, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 106380
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-146A-106380
```

Alignment Scores:  
Pred. No.: 9e-23 Length: 278  
Score: 216.00 Matches: 44  
Percent Similarity: 85.0% Conservative: 7  
Best Local Similarity: 73.3% Mismatches: 7  
Query Match: 72.7% Indels: 2  
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-371-146A-106380 (1-278)

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 92 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 151
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 152 AATGCAACTCCCATTCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 211
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 212 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGGCAATTAAGTCTGACAATAGCACC 271
```

## RESULT 6

```
US-09-985-678-106380
; Sequence 106380, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 106380
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
```

US-09-985-678-106380

Alignment Scores:  
Pred. No.: 9e-23 Length: 278  
Score: 216.00 Matches: 44  
Percent Similarity: 85.0% Conservative: 7  
Best Local Similarity: 73.3% Mismatches: 7  
Query Match: 72.7% Indels: 2  
DB: 39 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-985-678-106380 (1-278)

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 92 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 151
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 152 AATGCAACTCCCATTCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 211
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 212 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGGCAATTAAGTCTGACAATAGCACC 271
```

## RESULT 7

```
US-09-244-000A-9660
; Sequence 9660, Application US/09244000A
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15305)B
; CURRENT APPLICATION NUMBER: US/09/244,000A
; CURRENT FILING DATE: 1999-02-08
; PRIOR APPLICATION DATA removed - refer to PALM or File Wrapper
; NUMBER OF SEQ ID NOS: 101193
; SEQ ID NO 9660
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(282)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 700682115H1
US-09-244-000A-9660
```

Alignment Scores:  
Pred. No.: 9.2e-23 Length: 282  
Score: 216.00 Matches: 44  
Percent Similarity: 85.0% Conservative: 7  
Best Local Similarity: 73.3% Mismatches: 7  
Query Match: 72.7% Indels: 2  
DB: 22 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-244-000A-9660 (1-282)

```
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 92 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 151
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 152 AATGCAACTCCCATTCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 211
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 212 GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGGCAATTAAGTCTGACAATAGCACC 271
```

## RESULT 8

US-09-978-703-9660

; Sequence 9660, Application US/09978703  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Thompson, Michael D.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15305)B  
; CURRENT APPLICATION NUMBER: US/09/978,703  
; CURRENT FILING DATE: 2001-10-18  
; PRIOR APPLICATION NUMBER: US 09/244,000  
; PRIOR FILING DATE: 1999-02-08  
; PRIOR APPLICATION NUMBER: US 60/074201  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074282  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074280  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074281  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074566  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/074567  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/074565  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/074562  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/074789  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075459  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075461  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075464  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075460  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075463  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/086183  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: US 60/086188  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: US 09/198779  
; PRIOR FILING DATE: 1998-11-24  
; PRIOR APPLICATION NUMBER: US 60/110108  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: US 60/110109  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: US 60/111033  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: US 60/111742  
; PRIOR FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 101193  
; SEQ ID NO 9660  
; LENGTH: 282  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURES:  
; NAME/KEY: unsure  
; LOCATION: (1)..(282)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 700682115H1  
US-09-978-703-9660

Alignment Scores:  
Pred. No.: 9,2e-23  
Score: 216.00  
Percent Similarity: 85.0%  
Best Local Similarity: 73.3%  
Query Match: 72.7%  
DB: 36  
Length: 282  
Matches: 44  
Conservative: 7  
Mismatch: 7  
Indels: 2  
Gaps: 1

US-10-628-525A-35 (1-58) x US-09-978-703-9660 (1-282)  
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db ATGGCACAGATTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCTCTCCC 151  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db AATGCAACTCCCATTTACATCAACATGTGCGAGTTCTTTATTGTGGAAACAAATAAGAA 211  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaSerGluAsnGlyThr 58  
Db GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGCGCAATTAAAGTCTGACATAGCACC 271

## RESULT 9

US-60-723-596-48951  
; Sequence 48951, Application US/60723596  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark et. al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53708)B  
; CURRENT APPLICATION NUMBER: US/60/723,596  
; CURRENT FILING DATE: 2005-10-04  
; NUMBER OF SEQ ID NOS: 58588  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 48951  
; LENGTH: 1299  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-60-723-596-48951

Alignment Scores:  
Pred. No.: 1,01e-21  
Score: 216.00  
Percent Similarity: 85.0%  
Best Local Similarity: 73.3%  
Query Match: 72.7%  
DB: 83  
Length: 1299  
Matches: 44  
Conservative: 7  
Mismatch: 7  
Indels: 2  
Gaps: 1

US-10-628-525A-35 (1-58) x US-60-723-596-48951 (1-1299)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db ATGGCACAGATTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCTCTCCC 60  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db AATGCAACTCCCATTTACATCAACATGTGCGAGTTCTTTATTGTGGAAACAAATAAGAA 120  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAlaSerGluAsnGlyThr 58  
Db GTTTCACCTACCAGTTCTGCTAAATTTAGAGTGTGCGCAATTAAAGTCTGACATAGCACC 180

## RESULT 10

US-11-216-545-8521  
; Sequence 8521, Application US/11216545  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO Technology, LLC  
; APPLICANT: McLeod, Paul L  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping  
; TITLE OF INVENTION: Soybeans  
; FILE REFERENCE: 38-21(53659)B  
; CURRENT APPLICATION NUMBER: US/11/216,545  
; CURRENT FILING DATE: 2005-08-31  
; PRIOR APPLICATION NUMBER: US 60/606,062  
; PRIOR FILING DATE: 2004-08-31  
; NUMBER OF SEQ ID NOS: 8783  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8521  
; LENGTH: 1808







```
Alignment Scores:
Pred. No.: 5.56e-21 Length: 1217
Score: 211.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 71.0% Indels: 2
DB: 29 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-654-617-15751 (1-1217)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 265 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 324
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 325 AATGCACTCCCATTTACATCAACATGTGGAGTTCTTTATTGTGGAAACAAATAAGAA 384
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 385 GTTTCACCTACCAAGTTCTGCTAAATTAGAGTGTGGCAATTAAAGTCTGACAA 438

RESULT 18
US-09-684-016-15751
; Sequence 15751, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; NUMBER OF SEQ ID NOS: 2000-09-05
; SEQ ID NO 15751
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Glycine max
US-09-684-016-15751

Alignment Scores:
Pred. No.: 5.56e-21 Length: 1217
Score: 211.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 71.0% Indels: 2
DB: 29 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-684-016-15751 (1-1217)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 265 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGAATCTCAAAATCCTCTCCC 324
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 325 AATGCACTCCCATTTACATCAACATGTGGAGTTCTTTATTGTGGAAACAAATAAGAA 384
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 385 GTTTCACCTACCAAGTTCTGCTAAATTAGAGTGTGGCAATTAAAGTCTGACAA 438

RESULT 19
US-09-304-517A-120859
; Sequence 120859, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; PRIOR FILING DATE: 1999-05-06
```

```
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 120859
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-120859

Alignment Scores:
Pred. No.: 7.57e-22 Length: 272
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-304-517A-120859 (1-272)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 87 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGCGAATCTCAAAATCCTCTCCC 146
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 147 AATGCAAGTCCCATTTACATCAACATGTGGAGTTCTTTATTGTGGAAACAAATAAGAA 206
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 207 GTTTCACCCACAAGTTCTGCTAAATTAGAGTGTGGCAATTAAAGTCTGACAA 260

RESULT 20
US-09-371-146A-120859
; Sequence 120859, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 120859
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-146A-120859

Alignment Scores:
Pred. No.: 7.57e-22 Length: 272
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-371-146A-120859 (1-272)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 87 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGCGAATCTCAAAATCCTCTCCC 146
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 147 AATGCAAGTCCCATTTACATCAACATGTGGAGTTCTTTATTGTGGAAACAAATAAGAA 206
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 207 GTTTCACCCACAAGTTCTGCTAAATTAGAGTGTGGCAATTAAAGTCTGACAA 260

RESULT 21
US-09-985-678-120859
; Sequence 120859, Application US/09985678
```

```

; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 120859
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-120859

Alignment Scores:
Pred. No.: 7,84e-22 Length: 272
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 39 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-985-678-120859 (1-272)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 87 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 146
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 147 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 206
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAaenSerGluAaen 56
DB 207 GTTTCACCCACAGTTCTGCTAAATTTAGAGTGTGATGCAATTAAGTCTGCAAT 260

RESULT 22
US-09-199-129A-1763
; Sequence 1763, Application US/09199129A
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15075)B
; CURRENT APPLICATION NUMBER: US/09/199,129A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 5521
; SEQ ID NO 1763
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700555550H1
US-09-199-129A-1763

Alignment Scores:
Pred. No.: 7,84e-22 Length: 278
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 21 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-199-129A-1763 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 93 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152

US-10-628-525A-35 (1-58) x US-09-985-678-120859 (1-272)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 147 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 206
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAaenSerGluAaen 56
DB 207 GTTTCACCCACAGTTCTGCTAAATTTAGAGTGTGATGCAATTAAGTCTGCAAT 260

RESULT 22
US-09-371-146A-276680
; Sequence 276680, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 276680
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-146A-276680

Alignment Scores:
Pred. No.: 7,84e-22 Length: 278
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-371-146A-276680 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 147 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 206
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAaenSerGluAaen 56
DB 213 GTTTCACCCACAGTTCTGCTAAATTTAGAGTGTGATGCAATTAAGTCTGCAAT 266

RESULT 24
US-09-371-146A-276680
; Sequence 276680, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 276680
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-146A-276680

Alignment Scores:
Pred. No.: 7,84e-22 Length: 278
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-371-146A-276680 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 147 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 206
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAaenSerGluAaen 56
DB 213 GTTTCACCCACAGTTCTGCTAAATTTAGAGTGTGATGCAATTAAGTCTGCAAT 266
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Db 153 AATGCAAGTCCCATCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAaenSerGluAaen 56
DB 213 GTTTCACCCACAGTTCTGCTAAATTTAGAGTGTGATGCAATTAAGTCTGCAAT 266

RESULT 23
US-09-304-517A-277899
; Sequence 277899, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 277899
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-277899

Alignment Scores:
Pred. No.: 7,84e-22 Length: 278
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-304-517A-277899 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAaenSerGluAaen 56
DB 213 GTTTCACCCACAGTTCTGCTAAATTTAGAGTGTGATGCAATTAAGTCTGCAAT 266

RESULT 24
US-09-371-146A-276680
; Sequence 276680, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 276680
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Glycine max
US-09-371-146A-276680

Alignment Scores:
Pred. No.: 7,84e-22 Length: 278
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 70.7% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-371-146A-276680 (1-278)

QY 1 MetAlaGlnLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 93 ATGGCACAGATTTTGGCTCCCTCTACGCAATGGCAGATGCAATCTCAAAATCCTCTCCC 152
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 153 AATGCAAGTCCCATCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 212
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAaenSerGluAaen 56
DB 213 GTTTCACCCACAGTTCTGCTAAATTTAGAGTGTGATGCAATTAAGTCTGCAAT 266
```

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 93 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 152  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 153 AATGCAAGTCCCATACATCAACATGTGGAGTTCCTTTATTGTGGAAACAAATAAGAAA 212  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56  
Db 213 GTTCCACCACCAAGTTCGTCTAAATTTAGAGTGTGCAATTAAGTCTGCAAT 266

## RESULT 25

US-09-985-678-277899

; Sequence 277899, Application US/09985678

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; TITLE OF INVENTION: Annotated Plant Genes

; FILE REFERENCE: 16517.255/38-21(15097)F

; CURRENT APPLICATION NUMBER: US/09/985,678

; CURRENT FILING DATE: 2001-11-05

; PRIOR APPLICATION NUMBER: US 09/304,517

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 295529

; SEQ ID NO 277899

; LENGTH: 278

; TYPE: DNA

; ORGANISM: Glycine max

US-09-985-678-277899

Alignment Scores:  
Pred. No.: 7,84e-22 Length: 278  
Score: 210.00 Matches: 43  
Percent Similarity: 86.2% Conservative: 7  
Best Local Similarity: 74.1% Mismatches: 6  
Query Match: 70.7% Indels: 2  
DB: 39 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-985-678-277899 (1-278)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 93 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 152  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 153 AATGCAAGTCCCATACATCAACATGTGGAGTTCCTTTATTGTGGAAACAAATAAGAAA 212  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56  
Db 213 GTTCCACCACCAAGTTCGTCTAAATTTAGAGTGTGCAATTAAGTCTGCAAT 266

## RESULT 26

US-09-199-129A-1352

; Sequence 1352, Application US/09199129A

; GENERAL INFORMATION:

; APPLICANT: Byrum, Joseph R.

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 38-21(15075)B

; CURRENT APPLICATION NUMBER: US/09/199,129A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 5521

; SEQ ID NO 1352

; LENGTH: 289

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(289)

; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 700555034H1  
US-09-199-129A-1352

Alignment Scores:  
Pred. No.: 8,33e-22 Length: 289  
Score: 210.00 Matches: 43  
Percent Similarity: 86.2% Conservative: 7  
Best Local Similarity: 74.1% Mismatches: 6  
Query Match: 70.7% Indels: 2  
DB: 21 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-199-129A-1352 (1-289)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 28 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 87  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 88 AATGCAAGTCCCATACATCAACATGTGGAGTTCCTTTATTGTGGAAACAAATAAGAAA 147  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56  
Db 148 GTTCCACCACCAAGTTCGTCTAAATTTAGAGTGTGCAATTAAGTCTGCAAT 201

## RESULT 27

US-09-304-517A-277751

; Sequence 277751, Application US/09304517A

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; TITLE OF INVENTION: Annotated Plant Genes

; FILE REFERENCE: 38-21(15097)B

; CURRENT APPLICATION NUMBER: US/09/304,517A

; CURRENT FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 295529

; SEQ ID NO 277751

; LENGTH: 289

; TYPE: DNA

; ORGANISM: Glycine max

; OTHER INFORMATION: unsure at all n locations

US-09-304-517A-277751

Alignment Scores:  
Pred. No.: 8,33e-22 Length: 289  
Score: 210.00 Matches: 43  
Percent Similarity: 86.2% Conservative: 7  
Best Local Similarity: 74.1% Mismatches: 6  
Query Match: 70.7% Indels: 2  
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-304-517A-277751 (1-289)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 28 ATGGCACAGATTTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 87  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
Db 88 AATGCAAGTCCCATACATCAACATGTGGAGTTCCTTTATTGTGGAAACAAATAAGAAA 147  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56  
Db 148 GTTCCACCACCAAGTTCGTCTAAATTTAGAGTGTGCAATTAAGTCTGCAAT 201

## RESULT 28

US-09-371-146A-276532

; Sequence 276532, Application US/09371146A

; GENERAL INFORMATION:

; APPLICANT: Cheikh, Nordine

; APPLICANT: Liu, Jingdong

; TITLE OF INVENTION: ANNOTATED PLANT GENES

FILE REFERENCE: 38-21(15097)C  
CURRENT APPLICATION NUMBER: US/09/371,146A  
CURRENT FILING DATE: 1999-08-09  
PRIOR APPLICATION NUMBER: US 09/304,517  
PRIOR FILING DATE: 1999-05-06  
NUMBER OF SEQ ID NOS: 294310  
SEQ ID NO 276532  
LENGTH: 289  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(289)  
OTHER INFORMATION: unsure at all n locations  
US-09-371-146A-276532

Alignment Scores:  
Pred. No.: 8.33e-22 Length: 289  
Score: 210.00 Matches: 43  
Percent Similarity: 86.2% Conservative: 7  
Best Local Similarity: 74.1% Mismatches: 6  
Query Match: 70.7% Indels: 2  
DB: 23 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-371-146A-276532 (1-289)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 28 ATGGCAGATTTTGGCTCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 87  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||||  
DB 88 AATGCAAGTCCCATACATCAACATGTGGAGTTCTTTATTTGGAAACAAATAAGAAA 147  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAAsnSerGluAAsn 56  
|||||  
DB 148 GTTTCACCCACAGATTCGCTAAATTTAGAGTGTAGGCAATTAAGTCTGCAAT 201

## RESULT 29

US-09-985-678-277751  
Sequence 277751, Application US/09985678  
GENERAL INFORMATION:  
APPLICANT: Cheikh, Nordine  
APPLICANT: Liu, Jingdong  
TITLE OF INVENTION: Annotated Plant Genes  
FILE REFERENCE: 16517.255/38-21(15097)F  
CURRENT APPLICATION NUMBER: US/09/985,678  
CURRENT FILING DATE: 2001-11-05  
PRIOR APPLICATION NUMBER: US 09/304,517  
PRIOR FILING DATE: 1999-05-06  
NUMBER OF SEQ ID NOS: 295529  
SEQ ID NO 277751  
LENGTH: 289  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(289)  
OTHER INFORMATION: unsure at all n locations  
US-09-985-678-277751

Alignment Scores:  
Pred. No.: 8.33e-22 Length: 289  
Score: 210.00 Matches: 43  
Percent Similarity: 86.2% Conservative: 7  
Best Local Similarity: 74.1% Mismatches: 6  
Query Match: 70.7% Indels: 2  
DB: 39 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-985-678-277751 (1-289)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||

DB 28 ATGGCAGATTTTGGCTCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 87  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||||  
DB 88 AATGCAAGTCCCATACATCAACATGTGGAGTTCTTTATTTGGAAACAAATAAGAAA 147  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAAsnSerGluAAsn 56  
|||||  
DB 148 GTTTCACCCACAGATTCGCTAAATTTAGAGTGTAGGCAATTAAGTCTGCAAT 201

## RESULT 30

US-09-244-000A-60903  
Sequence 60903, Application US/09244000A  
GENERAL INFORMATION:  
APPLICANT: Byrum, Joseph R.  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Thompson, Michael D.  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
FILE OF INVENTION: Plants  
FILE REFERENCE: 38-21(15305)B  
CURRENT APPLICATION NUMBER: US/09/244,000A  
CURRENT FILING DATE: 1999-02-08  
PRIOR APPLICATION DATA removed - refer to PALM or File Wrapper  
NUMBER OF SEQ ID NOS: 101193  
SEQ ID NO 60903  
LENGTH: 293  
TYPE: DNA  
ORGANISM: Glycine max  
OTHER INFORMATION: Clone ID: 700996496H1  
US-09-244-000A-60903

Alignment Scores:  
Pred. No.: 8.51e-22 Length: 293  
Score: 210.00 Matches: 43  
Percent Similarity: 86.2% Conservative: 7  
Best Local Similarity: 74.1% Mismatches: 6  
Query Match: 70.7% Indels: 2  
DB: 22 Gaps: 1

US-10-628-525A-35 (1-58) x US-09-244-000A-60903 (1-293)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
|||||  
DB 92 ATGGCAGATTTTGGCTCCTCTACGCAATGGCAGATGAGATCTCAAAATCCTCTCCC 151  
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40  
|||||  
DB 152 AATGCAAGTCCCATACATCAACATGTGGAGTTCTTTATTTGGAAACAAATAAGAAA 211  
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAAsnSerGluAAsn 56  
|||||  
DB 212 GTTTCACCCACAGATTCGCTAAATTTAGAGTGTAGGCAATTAAGTCTGCAAT 265

Search completed: April 2, 2006, 03:27:36  
Job time : 1590.5 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 21:21:57 ; Search time 108.468 Seconds  
(without alignments)  
1603.719 Million cell updates/sec

Title: US-10-628-525A-35

Perfect score: 297

Sequence: 1 MAQILAPSTQWQRIKTSPTSP.....KKVAHSAKFRVMAVNSNGT 58

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 6698573 seqs, 1499593917 residues

Total number of hits satisfying chosen parameters: 13397146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abes/ABSWEB\_spool/US10628525/runat\_31032006\_095132\_17106/app.query.fasta\_1  
-DB=Pending Patents NA New -QFMT=fastcap -SUPFIX=p2n.inpn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62  
-TRANS=human40 cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abes06h  
-USER=US10628525 @CGN 1 1 1552 @runat\_31032006\_095132\_17106 -NCFU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending Patents NA New: \*  
1: /SIDSS/ptodata/2/pna/PTC\_NEW\_COMB.seq: \*  
2: /SIDSS/ptodata/2/pna/US06\_NEW\_COMB.seq: \*  
3: /SIDSS/ptodata/2/pna/US07\_NEW\_COMB.seq: \*  
4: /SIDSS/ptodata/2/pna/US08\_NEW\_COMB.seq: \*  
5: /SIDSS/ptodata/2/pna/US09\_NEW\_COMB.seq: \*  
6: /SIDSS/ptodata/2/pna/US10\_NEW\_COMB.seq: \*  
7: /SIDSS/ptodata/2/pna/US11\_NEW\_COMB.seq: \*  
8: /SIDSS/ptodata/2/pna/US12\_NEW\_COMB.seq: \*  
9: /SIDSS/ptodata/2/pna/US13\_NEW\_COMB.seq: \*  
10: /SIDSS/ptodata/2/pna/US14\_NEW\_COMB.seq: \*  
11: /SIDSS/ptodata/2/pna/US15\_NEW\_COMB.seq: \*  
12: /SIDSS/ptodata/2/pna/US16\_NEW\_COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215	72.4	391	8	US-11-239-610A-11025 Sequence 11025, A
2	210	70.7	293	8	US-11-330-082-1395 Sequence 1395, Ap
3	210	70.7	372	8	US-11-239-610A-16542 Sequence 16542, A
4	210	70.7	401	8	US-11-239-610A-30892 Sequence 30892, A
5	199	67.0	248	8	US-11-330-082-20029 Sequence 20029, A

Sequence 9120, Ap	360	58.8	174.5	6	US-11-331-019-9120
Sequence 3684, A	380	58.8	174.5	7	US-11-331-019-3684
Sequence 40055, A	401	58.8	174.5	8	US-11-331-019-40055
Sequence 36769, A	723	58.8	174.5	9	US-11-331-019-36769
Sequence 40579, A	730	57.7	171.5	10	US-11-331-019-40579
Sequence 7837, Ap	441	56.4	167.5	11	US-11-331-019-7837
Sequence 6654, Ap	453	56.2	167	12	US-11-331-019-6654
Sequence 8967, Ap	376	54.7	162.5	13	US-11-331-019-8967
Sequence 8122, Ap	203	37.7	112	14	US-11-331-019-8122
Sequence 15715, A	314	35.0	104	15	US-11-331-019-15715
Sequence 8922, A	401	24.9	74	16	US-11-329-388-15715
Sequence 189520, A	1830	24.4	72.5	17	US-11-056-358-82922
Sequence 243182, A	1594	23.7	70.5	18	US-11-266-748A-189520
Sequence 45019, A	1594	23.7	70.5	19	US-11-266-748A-243182
Sequence 345, App	958	23.4	69.5	20	US-11-360-355-45019
Sequence 162817, A	1950	23.1	69	21	US-10-533-232A-345
Sequence 11005, A	1053	23.1	68.5	22	US-11-266-748A-162817
Sequence 254, App	412	22.9	68	23	US-11-239-610A-11005
Sequence 11416, A	86149	22.9	68	24	US-10-540-898-254
Sequence 3689, Ap	2103	22.7	67.5	25	US-10-917-503B-11416
Sequence 1611, Ap	2103	22.7	67.5	26	US-60-751-455-3689
Sequence 249122, A	1366	22.6	67	27	US-10-515-325-1611
Sequence 434, App	1412	22.6	66.5	28	US-11-266-748A-249122
Sequence 51591, A	224716	22.4	66.5	29	US-10-018-470B-1
Sequence 219252, A	503	22.2	66	30	US-10-501-187-434
Sequence 418580, A	776	22.2	66	31	US-11-266-748A-51591
Sequence 54928, A	789	22.2	66	32	US-11-266-748A-219252
Sequence 184821, A	887	22.2	66	33	US-11-266-748A-418580
Sequence 192322, A	900	22.2	66	34	US-11-266-748A-54928
Sequence 1655, Ap	924	22.2	66	35	US-11-266-748A-184821
Sequence 91047, A	924	22.2	66	36	US-11-266-748A-192322
Sequence 143958, A	1075	22.2	66	37	US-11-266-748A-480462
Sequence 335, App	1510	22.2	66	38	US-60-751-455-1655
Sequence 7039, App	1517	22.2	66	39	US-11-266-748A-91047
Sequence 9, App11	1517	22.2	66	40	US-11-266-748A-143958
Sequence 918, App	2269	22.2	66	41	US-10-206-921A-335
Sequence 94, App1	2428	22.2	66	42	US-10-347-870-9
Sequence 30574, A	2496	22.2	66	43	US-10-539-228-631
Sequence 25, App1	2496	22.2	66	44	US-10-529-348-918
Sequence 1541, Ap	2496	22.2	66	45	US-11-295-188-94
Sequence 2786, A	2713	22.2	66	46	US-11-266-748A-2786
Sequence 27565, A	3795	22.2	66	47	US-11-266-748A-27565
Sequence 1730, Ap	3914	22.2	66	48	US-10-567-867-1730
Sequence 3910, App	4858	22.2	66	49	US-60-751-455-3910
Sequence 630, App	52799	22.2	66	50	US-10-539-228-630
Sequence 42, App1	977	22.1	65.5	51	US-11-378-920-42
Sequence 77004, A	1199	22.1	65.5	52	US-11-360-355-77004
Sequence 2675, Ap	1359	22.1	65.5	53	US-10-276-817B-2675
Sequence 81680, A	1523	22.1	65.5	54	US-11-360-355-81680
Sequence 17214, A	1452	22.1	65.5	55	US-11-360-355-17214
Sequence 1954, Ap	6031	22.1	65.5	56	US-11-360-355-1954
Sequence 7194, Ap	410	21.9	65	57	US-11-227-183A-7194
Sequence 2229, Ap	418	21.9	65	58	US-11-353-150-2229
Sequence 187151, A	962	21.9	65	59	US-11-266-748A-187151
Sequence 258017, A	1044	21.9	65	60	US-11-266-748A-258017
Sequence 278363, A	1044	21.9	65	61	US-11-266-748A-278363
Sequence 318534, A	1044	21.9	65	62	US-11-266-748A-318534
Sequence 258016, A	1536	21.9	65	63	US-11-266-748A-258016
Sequence 278362, A	1536	21.9	65	64	US-11-266-748A-278362
Sequence 318533, A	1536	21.9	65	65	US-11-266-748A-318533
Sequence 29769, A	2300	21.9	65	66	US-60-762-056-29769
Sequence 832, App	5067	21.9	65	67	US-10-531-147-832
Sequence 1173, App	5067	21.9	65	68	US-10-529-348-1173
Sequence 28805, A	5067	21.9	65	69	US-11-266-748A-28805
Sequence 29054, A	5067	21.9	65	70	US-11-266-748A-29054
Sequence 1667, Ap	5070	21.9	65	71	US-60-742-219-1667
Sequence 2477, Ap	5070	21.9	65	72	US-10-276-817B-2477
Sequence 408170, A	933	21.5	64	73	US-11-266-748A-408170
Sequence 479216, A	933	21.5	64	74	US-11-266-748A-479216

79	64	21.5	1509	10	US-11-266-748A-256041,	Sequence 256041,
80	64	21.5	1509	10	US-11-266-748A-316558,	Sequence 316558,
81	64	21.5	2891	7	US-10-917-503B-18116	Sequence 18116, A
82	64	21.5	3720	7	US-10-515-325-1523	Sequence 1523, Ap
83	64	21.5	138837	6	US-10-539-228-146	Sequence 146, App
84	63.5	21.4	441	10	US-11-292-078-3277	Sequence 3277, Ap
85	63.5	21.4	445	10	US-11-266-748A-178801	Sequence 178801,
86	63	21.2	270	8	US-11-239-610A-20443	Sequence 20443, A
87	63	21.2	422	8	US-11-353-150-37237	Sequence 37237, A
88	63	21.2	439	8	US-11-239-591A-24111	Sequence 24111, A
89	63	21.2	445	8	US-11-353-150-37316	Sequence 37316, A
90	63	21.2	2152	7	US-10-953-349-38921	Sequence 38921, A
91	63	21.2	2152	8	US-11-056-355B-1264	Sequence 1264, Ap
92	63	21.2	2168	8	US-11-174-307B-4949	Sequence 4949, Ap
93	63	21.2	2300	12	US-60-762-056-40717	Sequence 40717, A
94	63	21.2	4233	10	US-11-266-748A-57283	Sequence 57283, A
95	62.5	21.0	450	10	US-11-266-748A-15982	Sequence 15982, A
96	62.5	21.0	450	10	US-11-266-748A-21632	Sequence 21632, A
97	62.5	21.0	1000	10	US-11-266-748A-117181	Sequence 117181,
98	62.5	21.0	1000	10	US-11-266-748A-159345	Sequence 159345,
99	62.5	21.0	1000	10	US-11-266-748A-288683	Sequence 288683,
100	62.5	21.0	1000	10	US-11-266-748A-340112	Sequence 340112,
101	62.5	21.0	1000	10	US-11-266-748A-399591	Sequence 399591,
102	62.5	21.0	1000	10	US-11-266-748A-470637	Sequence 470637,
103	62.5	21.0	1109	10	US-11-266-748A-74428	Sequence 74428, A
104	62.5	21.0	1193	10	US-11-266-748A-127239	Sequence 127239,
105	62.5	21.0	1493	10	US-11-266-748A-187292	Sequence 187292,
106	62.5	21.0	1611	10	US-11-266-748A-350349	Sequence 350349,
107	62.5	21.0	1611	10	US-11-266-748A-382873	Sequence 382873,
108	62.5	21.0	1611	10	US-11-266-748A-433728	Sequence 433728,
109	62.5	21.0	2300	12	US-60-762-056-25883	Sequence 25883, A
110	62.5	21.0	3944	12	US-60-763-366-800	Sequence 800, App
111	62.5	21.0	3944	12	US-60-763-366-801	Sequence 801, App
112	62.5	21.0	3974	12	US-60-763-366-802	Sequence 802, App
113	62.5	21.0	3974	12	US-60-763-366-803	Sequence 803, App
114	62.5	21.0	4190	1	PC7-US06-05584-102	Sequence 102, App
115	62.5	21.0	4190	1	PC7-US06-05584-786	Sequence 786, App
116	62.5	21.0	4190	7	US-10-917-503B-14679	Sequence 14679, A
117	62.5	21.0	89807	10	US-11-266-748A-61887	Sequence 61887, A
118	62	20.9	360	8	US-11-352-295-6868	Sequence 6868, Ap
119	62	20.9	384	10	US-11-313-816-660	Sequence 660, App
120	62	20.9	419	10	US-11-313-816-1501	Sequence 1501, Ap
121	62	20.9	802	8	US-11-360-355-50381	Sequence 50381, A
122	62	20.9	1000	10	US-11-266-748A-195439	Sequence 195439,
123	62	20.9	1000	10	US-11-266-748A-282873	Sequence 282873,
124	62	20.9	1000	10	US-11-266-748A-309513	Sequence 309513,
125	62	20.9	1000	10	US-11-266-748A-392449	Sequence 392449,
126	62	20.9	1000	10	US-11-266-748A-483167	Sequence 483167,
127	62	20.9	1510	7	US-10-953-349-14286	Sequence 14286, A
128	62	20.9	1947	12	US-60-772-265-638	Sequence 638, App
129	62	20.9	1947	12	US-60-772-265-960	Sequence 960, App
130	62	20.9	1950	12	US-60-772-265-812	Sequence 812, App
131	62	20.9	1953	12	US-60-772-265-1512	Sequence 1512, Ap
132	62	20.9	2029	8	US-11-360-355-47647	Sequence 47647, A
133	62	20.9	2036	12	US-60-772-265-554	Sequence 554, App
134	62	20.9	2092	8	US-11-360-355-48763	Sequence 48763, A
135	62	20.9	2094	8	US-11-360-355-50003	Sequence 50003, A
136	62	20.9	2097	12	US-60-772-265-1288	Sequence 1288, Ap
137	62	20.9	2682	10	US-11-266-446-7	Sequence 7, Appl
138	61.5	20.7	248	8	US-11-360-355-59810	Sequence 59810, A
139	61.5	20.7	510	8	US-11-360-355-96506	Sequence 96506, A
140	61.5	20.7	693	8	US-11-360-355-73204	Sequence 73204, A
141	61.5	20.7	721	8	US-11-360-355-95226	Sequence 95226, A
142	61.5	20.7	773	8	US-11-360-355-89016	Sequence 89016, A
143	61.5	20.7	950	10	US-11-266-748A-381222	Sequence 381222,
144	61.5	20.7	950	10	US-11-266-748A-430978	Sequence 430978,
145	61.5	20.7	1004	10	US-11-266-748A-70999	Sequence 70999, A
146	61.5	20.7	1004	10	US-11-266-748A-106371	Sequence 106371,
147	61.5	20.7	1004	10	US-11-266-748A-123810	Sequence 123810,
148	61.5	20.7	1080	10	US-11-266-748A-258185	Sequence 258185,
149	61.5	20.7	1080	10	US-11-266-748A-278448	Sequence 278448,
150	61.5	20.7	1080	10	US-11-266-748A-318702	Sequence 318702,

ALIGNMENTS

RESULT 1

US-11-239-610A-11025  
; Sequence 11025, Application US/11239610A  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 16517.341 - 38-21(15793)C/US  
; CURRENT APPLICATION NUMBER: US/11/239,610A  
; CURRENT FILING DATE: 2005-09-30  
; PRIOR APPLICATION NUMBER: US 09/565,240  
; PRIOR FILING DATE: 2000-05-08  
; NUMBER OF SEQ ID NOS: 54005  
; SEQ ID NO 11025  
; LENGTH: 391  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3092-013-Q1-K1-C1  
US-11-239-610A-11025

Alignment Scores:

Pred. No.: 76-21 Length: 391  
Score: 215.00 Matches: 44  
Percent Similarity: 83.3% Conservative: 6  
Best local Similarity: 73.3% Mismatches: 8  
Query Match: 72.4% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-239-610A-11025 (1-391)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20

Db 10 ATGGCACAGATTGGCTCCCTACGCATGCGAGATGAGAAATCTCAAGGCCCTCTCCC 69

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40

Db 70 AATGCACTCCCATTTACATCAACATGTGGAGTTCTTTATTGTGGAACAAATAAGAAA 129

QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58

Db 130 GTTCCCTACCACTTCGTAAATTAGTGTGGCAATTAGTCTGACCAATAGCACCC 189

RESULT 2

US-11-330-082-1395  
; Sequence 1395, Application US/113300082  
; GENERAL INFORMATION:  
; APPLICANT: Buehler, Robert E.  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Coombs, Brian E.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 16517.356 - 38-21(15760)C/US  
; CURRENT APPLICATION NUMBER: US/11/330,082  
; CURRENT FILING DATE: 2006-01-12  
; PRIOR APPLICATION NUMBER: US 09/552,086  
; PRIOR FILING DATE: 2000-04-19  
; NUMBER OF SEQ ID NOS: 27278  
; SEQ ID NO 1395  
; LENGTH: 293  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700996496H1  
US-11-330-082-1395

Alignment Scores:

Pred. No.: 2.42e-20 Length: 293



```

Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 80.7% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-330-082-1395 (1-293)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 92 ATGGCACAGATTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCTCTCCC 151
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 152 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 211
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 212 GTTTCACCCACAGATTCTGCTAAATTAGATGATGCAATTAAAGTCTGACAAAT 265

RESULT 3
US-11-239-610A-16542
; Sequence 16542, Application US/11239610A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.341 - 38-21(15793)C/US
; CURRENT APPLICATION NUMBER: US/11/239,610A
; PRIOR FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US 09/565,240
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 54005
; SEQ ID NO 16542
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3106-116-Q1-K1-C5
US-11-239-610A-16542

Alignment Scores:
Pred. No.: 3,38e-20 Length: 372
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 80.7% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-239-610A-16542 (1-372)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 80 ATGGCACAGATTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCTCTCCC 139
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 140 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 199
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 200 GTTTCACCCACAGATTCTGCTAAATTAGATGATGCAATTAAAGTCTGACAAAT 253

RESULT 4
US-11-239-610A-30892
; Sequence 30892, Application US/11239610A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.341 - 38-21(15793)C/US
; CURRENT APPLICATION NUMBER: US/11/239,610A
; PRIOR FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US 09/565,240
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 54005
; SEQ ID NO 16542
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3106-116-Q1-K1-C5
US-11-239-610A-16542

Alignment Scores:
Pred. No.: 3,38e-20 Length: 372
Score: 210.00 Matches: 43
Percent Similarity: 86.2% Conservative: 7
Best Local Similarity: 74.1% Mismatches: 6
Query Match: 80.7% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-239-610A-16542 (1-372)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 80 ATGGCACAGATTGGCTCCCTCTACGCAATGGCAGATGAGATCTCAAAATCTCTCCC 148
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 149 AATGCAAGTCCCATCATCAACATGTGGAGTCTTTATTGTGGAAACAAATAAGAAA 208
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 209 GTTTCACCCACAGATTCTGCTAAATTAGATGATGCAATTAAAGTCTGACAAAT 262

RESULT 5
US-11-330-082-20029
; Sequence 20029, Application US/11330082
; GENERAL INFORMATION:
; APPLICANT: Buehler, Robert E.
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Coombs, Brian E.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.356 - 38-21(15760)C/US
; CURRENT APPLICATION NUMBER: US/11/330,082
; PRIOR FILING DATE: 2006-01-12
; PRIOR APPLICATION NUMBER: US 09/552,086
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 27278
; SEQ ID NO 20029
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700872751H1
US-11-330-082-20029

Alignment Scores:
Pred. No.: 7,13e-19 Length: 248
Score: 199.00 Matches: 41
Percent Similarity: 87.0% Conservative: 6
Best Local Similarity: 75.9% Mismatches: 5
Query Match: 67.0% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-330-082-20029 (1-248)

QY 1 MetAlaGlnIleuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20

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Db      84  ATGGCAGAGATTTGGCTCCCTCAGCAATGGCAGATGCGAATCTCAAAATCCTCTCC 143
QY      21  CysAlaThrProIleThrSerIysMetTTPSerSerLeuValMetIysGlnThrIysIys 40
Db      144  ATGCAACTCCCATATACATCAACATGTGGAGTCTCTTATTGTGGAACACAAATTAAGAAA 203
QY      41  ValAla-----HisSerAlaIysPheArgValMetAlaVal 52
Db      204  GTTCACTACCAAGTCTCTGTAATTTAGATGCTGGCAATT 245

RESULT 6
US-11-331-019-9120
; Sequence 9120, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 9120
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-053-P1-K1-C3
US-11-331-019-9120

Alignment Scores:
Pred. No.:      3-75e-15      Length:      360
Score:          174.50      Matches:      38
Percent Similarity: 76.7%      Conservatives: 8
Best Local Similarity: 63.3%      Mismatches: 11
Query Match:    58.8%      Indels:      3
DB:             8          Gaps:      2

US-10-628-525A-35 (1-58) x US-11-331-019-9120 (1-360)
QY      1  MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db      104  ATGGCACAGCTTTTAGCACCTCAACTCAATGGCAATGACACTACCAAGACCTCAACC 163
QY      21  CysAlaThrProIleThrSerIysMetTTPSerSerLeuValMetIysGlnThrIysIys 40
Db      164  TATGGAAGTCCCATTCGCAACAAATGTGGAGTCTCTGGTACTGAAACAGAACAGAAA 223
QY      41  ValAla-----HisSerAlaIysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db      224  GGAGCTGTAAAGCTCTGGCAAGTTAAAGTGTGCTTG---TCTGAAAACAGCACT 280

RESULT 7
US-11-331-019-36684
; Sequence 36684, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
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; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 36684
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-006-P1-K3-A11
US-11-331-019-36684

Alignment Scores:
Pred. No.:      4-05e-15      Length:      380
Score:          174.50      Matches:      38
Percent Similarity: 76.7%      Conservatives: 8
Best Local Similarity: 63.3%      Mismatches: 11
Query Match:    58.8%      Indels:      3
DB:             8          Gaps:      2

US-10-628-525A-35 (1-58) x US-11-331-019-36684 (1-380)
QY      1  MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db      119  ATGGCACAGCTTTTAGCACCTCAACTCAATGGCAATGACACTACCAAGACCTCAACC 178
QY      21  CysAlaThrProIleThrSerIysMetTTPSerSerLeuValMetIysGlnThrIysIys 40
Db      179  TATGGAAGTCCCATTCGCAACAAATGTGGAGTCTCTGGTACTGAAACAGAACAGAAA 238
QY      41  ValAla-----HisSerAlaIysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db      239  GGAGCTGTAAAGCTCTGGCAAGTTAAAGTGTGCTTG---TCTGAAAACAGCACT 295

RESULT 8
US-11-331-019-40055
; Sequence 40055, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; PRIOR FILING DATE: 2006-01-13
; PRIOR APPLICATION NUMBER: US 09/637,086
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 40055
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-048-Q1-K1-C1
US-11-331-019-40055

Alignment Scores:
Pred. No.:      4-36e-15      Length:      401
Score:          174.50      Matches:      38
Percent Similarity: 76.7%      Conservatives: 8
Best Local Similarity: 63.3%      Mismatches: 11
Query Match:    58.8%      Indels:      3
DB:             8          Gaps:      2

US-10-628-525A-35 (1-58) x US-11-331-019-40055 (1-401)
QY      1  MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrIysThrSerPro 20
Db      122  ATGGCACAGCTTTTAGCACCTCAACTCAATGGCAATGACACTACCAAGACCTCAACC 181
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Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 182 TATGGAAGTCCATTCACAAATAATGTGGAGTTCTCTGGTACTGAAACACAGCAAGAAA 241
Qy 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAAsnSerGluAAsnGlyThr 58
Db 242 GGAGCTGCTAAAGCTCTGGCAAGCTTTAAAGTGGTGGCTTG---TCTGAAACAGCACT 298

RESULT 9
US-11-331-019-36769
; Sequence 36769, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 36769
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-006-P1-K4-A9
US-11-331-019-36769

Alignment Scores:
Pred. No.: 9.9e-15 Length: 723
Score: 174.50 Matches: 38
Percent Similarity: 76.7% Conservatives: 8
Best Local Similarity: 63.3% Mismatches: 11
Query Match: 58.8% Indels: 3
DB: 2 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-331-019-36769 (1-723)

Qy 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 116 ATGGCACAGCTTTTAGCACCTCACTCAATGGCAATGACACTACCAAGACCTCAACC 175
Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 176 TATGGAAGTCCCATTCGCAAAATAATGTGGAGTTCTCTGGTACTGAAACACAGCAAGAAA 235
Qy 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAAsnSerGluAAsnGlyThr 58
Db 236 GGAGCTGCTAAAGCTCTGGCAAGCTTTAAAGTGGTGGCTTG---TCTGAAACAGCACT 292

RESULT 10
US-11-331-019-40579
; Sequence 40579, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 40579
; LENGTH: 340
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-056-P1-K1-D10
US-11-331-019-40579

Alignment Scores:
Pred. No.: 9.29e-15 Length: 340
Score: 171.50 Matches: 37
Percent Similarity: 76.7% Conservatives: 9
Best Local Similarity: 61.7% Mismatches: 11
Query Match: 57.7% Indels: 3
DB: 2 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-331-019-40579 (1-340)

Qy 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 135 ATGGCACAGCTTTTATCACCTCACTCAATGGCAATGACACTACCAAGACCTCAACC 194
Qy 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
Db 195 TATGGAAGTCCCATTCGCAAAATAATGTGGAGTTCTCTGGTACTGAAACACAGCAAGAAA 254
Qy 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAAsnSerGluAAsnGlyThr 58
Db 255 GGAGCTGCTAAAGCTCTGGCAAGCTTTAAAGTGGTGGCTTG---TCTGAAACAGCACT 311

RESULT 11
US-11-331-019-7837
; Sequence 7837, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 2000-08-11
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 7837
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-024-Q1-K1-F11
US-11-331-019-7837

Alignment Scores:
Pred. No.: 4.96e-14 Length: 441
Score: 167.50 Matches: 37
Percent Similarity: 75.0% Conservatives: 8
Best Local Similarity: 61.7% Mismatches: 12
Query Match: 56.4% Indels: 3
DB: 2 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-331-019-7837 (1-441)

Qy 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 82 ATGGCACAGCTTTTAGCACCTCACTCAATGGCAATGACACTACCAAGACCTCAACC 141
```

```
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 142 TATGGAAGTCCCATTCACAAAGATGTGGAGTTCTCTGGTACTGAAACAGACAGAA 201
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
DB 202 GGAGCTGCTAAAGACTCTGCAGAGTTAAAGTGTTCCTTG---TCTGAAACAGCACT 258

RESULT 12
US-11-331-019-6654
; Sequence 6654, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 6654
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-010-Q1-K1-B1
US-11-331-019-6654

Alignment Scores:
Pred. No.: 6,07e-14 Length: 167.00 Matches: 453
Score: 167.00
Percent Similarity: 73.3% Conservative: 10
Best Local Similarity: 56.7% Mismatches: 14
Query Match: 56.2% Indels: 2
DB: 8 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-331-019-6654 (1-453)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 110 ATGGCAGATTTCTGGCCTTCACTCAATGCGGATGAGAGTACCAAGAGCTGGACC 169
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 170 TTGGAGGCCCATTCGCAAGATGTGGAGTCTCTGATCTTGAACAGACCATGAA 229
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
DB 230 GGAGCAGCAAAAGTCTGCAGAGTTAAAGTGTTCCTTGCTTCTGAGAACAGCACT 289

RESULT 13
US-11-331-019-36617
; Sequence 36617, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
```

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; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 36617
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3165-006-P1-K2-A9
US-11-331-019-36617

Alignment Scores:
Pred. No.: 2,06e-13 Length: 162.50 Matches: 376
Score: 162.50
Percent Similarity: 71.7% Conservative: 7
Best Local Similarity: 60.0% Mismatches: 14
Query Match: 54.7% Indels: 3
DB: 8 Gaps: 2

US-10-628-525A-35 (1-58) x US-11-331-019-36617 (1-376)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 116 ATGGCAGAGCTTTTAAACACCTCTCAACTCAATGCGCAATGACACTACCAAGACCTCAACC 175
QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLys 40
DB 176 TATGGAAGTCCCATTCGCAAGATGTGGAGTCTCTGGTACTGAAACAGACAGAA 235
QY 41 ValAla-----HisSerAlaLysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
DB 236 GGAGCTGTAAAGCTCTGCAGAGTTAAAGTGTTCCTTG---TCTGAAACAGCACT 292

RESULT 14
US-11-331-019-8967
; Sequence 8967, Application US/11331019
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: McCarter, David W.
; APPLICANT: Pear, Julie R.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US
; CURRENT APPLICATION NUMBER: US/11/331,019
; CURRENT FILING DATE: 2006-01-13
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/149,881
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 52949
; SEQ ID NO 8967
; LENGTH: 203
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3120-046-P1-K1-C10
US-11-331-019-8967

Alignment Scores:
Pred. No.: 1,4e-06 Length: 112.00 Matches: 203
Score: 112.00
Percent Similarity: 73.0% Conservative: 6
Best Local Similarity: 56.8% Mismatches: 10
Query Match: 37.7% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-35 (1-58) x US-11-331-019-8967 (1-203)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
DB 7 CTGGCAGAGCTTTTAGCACCTCTCAACTCAATGCGCAATGACACTACCAAGACCTTGTC 66
```

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLysGln 37  
Db 67 TGTGAAGTCCATTGCGCAATAATGTGGAGTCTCTGGTACTGATACAG 117

## RESULT 15

US-11-331-019-8122  
; Sequence 8122, Application US/11331019  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: McCarter, David W.  
; APPLICANT: Pear, Julie R.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.359 - 38-21(51375)C/US  
; CURRENT APPLICATION NUMBER: US/11/331,019  
; PRIOR FILING DATE: 2006-01-13  
; PRIOR APPLICATION NUMBER: US 09/637,086  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: US 60/149,881  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 52949  
; SEQ ID NO 8122  
; LENGTH: 314  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3120-028-Q1-K1-B3  
US-11-331-019-8122

Alignment Scores:  
Pred. No.: 3,56e-05 Length: 314  
Score: 104.00 Matches: 20  
Percent Similarity: 75.0% Conservative: 7  
Best Local Similarity: 55.6% Mismatches: 9  
Query Match: 35.0% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-35 (1-58) x US-11-331-019-8122 (1-314)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 115 ATGGCAAACTTTTAAACCGTCTACTTAACGGCAATGACACTACCAAGGACCTCATCC 174

QY 21 CysAlaThrProIleThrSerLysMetTrpSerSerLeuValMetLys 36

Db 175 TATGAAGTCCATTGCGCAATAATGTGGAGTCTCTGGTACTGATA 222

## RESULT 16

US-11-329-388-15715  
; Sequence 15715, Application US/11329388  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US  
; CURRENT APPLICATION NUMBER: US/11/329,388  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: 09/553,094  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18831  
; SEQ ID NO 15715  
; LENGTH: 401  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB83-002-Q1-E1-E8  
US-11-329-388-15715

Alignment Scores:  
Pred. No.: 0.956 Length: 401  
Score: 74.00 Matches: 16

Percent Similarity: 43.6% Conservative: 1  
Best Local Similarity: 41.0% Mismatches: 22  
Query Match: 24.9% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-35 (1-58) x US-11-329-388-15715 (1-401)

QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25  
Db 93 GCACCCCATCAGCGTGGCTCTTCGGCGAGCGCGCATCACCATGCGCAAGCCGTGG 152  
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysLysValAlaHisSer 44  
Db 153 GCAAGCCCAATGTGGCGGTCTCTGGCAGCGCGTGTACGCGCCCGCGGTCAAGT 209

## RESULT 17

US-11-056-355B-82922  
; Sequence 82922, Application US/11056355B  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nickolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; PRIOR FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 82922  
; LENGTH: 1830  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1830)  
; OTHER INFORMATION: Ceres Seq. ID no. 12667901  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1830)  
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 12613725  
; OTHER INFORMATION: as cited in SEQ ID NO 68196  
US-11-056-355B-82922

Alignment Scores:  
Pred. No.: 12.9 Length: 1830  
Score: 72.50 Matches: 21  
Percent Similarity: 38.2% Conservative: 13  
Best Local Similarity: 23.6% Mismatches: 20  
Query Match: 24.4% Indels: 35  
DB: 8 Gaps: 4

US-10-628-525A-35 (1-58) x US-11-056-355B-82922 (1-1830)

QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20  
Db 775 TTGGTGGCTTTTTCGCCCCCAACAAGCAATATCGTTAT-----GTCAGCCG 822  
QY 21 CysAlaThrProIle-----ThrSerLysMetTrpSer 31  
Db 823 TGTGTAACCCGTTGCTGCTGCTGCGCAAGTATTGTTGCGCCACTGCTCGTAAGTGAGT 882  
QY 32 SerLeu-----ValMet 35  
Db 883 GTTGTTCGACGAGAGATCCGATGAGTGTAGCAACTTGAAGGCTCTGAATCCGCATT 942  
QY 36 LysGlnThrLysLysValAlaHisSerAlaLysPhe-----ArgVal 49  
Db 943 AAAGGAAGTCGAAGATATTTCATAGTACCAAAATTTCTTCTTGTGATAGCAGCAGTG 1002  
QY 50 MetAlaValAsnSerGluAsnGlyThr 58  
Db 1003 ATTACAGGAATGATAGGAATGGACA 1029

```
RESULT 18
US-11-266-748A-189520/c
; Sequence 189520, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189520
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-189520

Alignment Scores:
Pred. No.: 20.6 Length: 1594
Score: 70.50 Matches: 15
Percent Similarity: 57.1% Conservative: 5
Best Local Similarity: 42.9% Mismatches: 14
Query Match: 23.7% Indels: 1
DB: 10 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-266-748A-189520 (1-1594)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 852 TCACCATCCCAAGCTGGAGACCCCAACCCAGCAGACATCGACCTGTATACCAACCATGT 793
QY 26 ThrSerLysMetTrp---SerSerLeuValMetLysGlnThrLys 39
Db 792 ACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCAACAAAGACCAAG 748

RESULT 19
US-11-266-748A-243182
; Sequence 243182, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
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; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 243182
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-243182

Alignment Scores:
Pred. No.: 20.6 Length: 1594
Score: 70.50 Matches: 15
Percent Similarity: 57.1% Conservative: 5
Best Local Similarity: 42.9% Mismatches: 14
Query Match: 23.7% Indels: 1
DB: 10 Gaps: 1

US-10-628-525A-35 (1-58) x US-11-266-748A-243182 (1-1594)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 743 TCACCATCCCAAGCTGGAGACCCCAACCCAGCAGACATCGACCTGTATACCAACCATGT 802
QY 26 ThrSerLysMetTrp---SerSerLeuValMetLysGlnThrLys 39
Db 803 ACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCAACAAAGACCAAG 847

RESULT 20
US-11-360-355-45019/c
; Sequence 45019, Application US/11360355
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey
; APPLICANT: Du, Zijiang
; APPLICANT: Guo, Liang
; APPLICANT: Kovalic, David
; APPLICANT: Lu, Maolong
; APPLICANT: McCarter, James
; APPLICANT: Miller, Nancy
; APPLICANT: Williams, Deryck
; APPLICANT: Vaudin, Mark
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
; FILE REFERENCE: 38-21(53885)
; CURRENT APPLICATION NUMBER: US/11/360,355
; CURRENT FILING DATE: 2006-02-24
; NUMBER OF SEQ ID NOS: 171306
; SEQ ID NO 45019
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Heterodera glycines
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (941)..(941)
; OTHER INFORMATION: n is a, c, g, or t
US-11-360-355-45019

Alignment Scores:
Pred. No.: 14.1 Length: 958
Score: 69.50 Matches: 16
Percent Similarity: 56.1% Conservative: 16
Best Local Similarity: 28.1% Mismatches: 10
Query Match: 23.4% Indels: 15
DB: 8 Gaps: 3
```

```
US-10-628-525A-35 (1-58) x US-11-360-355-45019 (1-958)
Qy 3 GlnLeuAlaProSerThrGlnMetArgIleThrLysThrSerProCysAla 22
Db 446 AAGATGATGGCAGCAGCGATTTGGCGATGGCGTCACTTGGACAGCAATTTGTCTC 387
Qy 23 -----ThrProIleThrSerLysMet---TriSer 31
Db 386 GACGAGCGCAACATCATCGGTACGAGCTGCGGATGGTCTCCAAATTTGCCCTGGACA 327
Qy 32 SerLeuValMetLys-----GlnThrLysLysValAlaHisSer 44
Db 326 AACATTGGTGAAGCGGCTCAATAGCAGCAACCAACAGCGGCGCAAAATCG 276
RESULT 21
US-10-533-232A-345/c
; Sequence 345, Application US/10533232A
; GENERAL INFORMATION:
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: CELL PROLIFERATION-RELATED POLYPEPTIDES AND USES THEREFOR
; FILE REFERENCE: 1392-10-19-2
; CURRENT APPLICATION NUMBER: US/10/533,232A
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/436,565
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 345
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1950)
US-10-533-232A-345
Alignment Scores:
Pred. No.: 44.6 Length: 1950
Score: 69.00 Matches: 18
Percent Similarity: 63.6% Conservative: 10
Best Local Similarity: 40.9% Mismatches: 10
Query Match: 23.2% Indels: 6
DB: 7 Gaps: 2
US-10-628-525A-35 (1-58) x US-10-533-232A-345 (1-1950)
Qy 4 IleLeuAlaProSerThrGlnTrp---GlnMetArgIleThrLysThrSerPro----- 20
Db 758 CTTTGAATTTTGCACAAAGTGGTGGACCATCGGTGTGCAAAATCTTCACCAACCAAGA 699
Qy 21 -----CysAlaThrProIleThrSerLysMetTriSerSerLeuValMetLysGln 37
Db 698 TGGGTGTCCACCACTGTGGCTTGACTCAAGATACCTCTCTCAATGTGAAGAGGGA 639
Qy 38 ThrLysLysVal 41
Db 638 ACATCAAGGTA 627
RESULT 22
US-11-266-748A-162817
; Sequence 162817, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
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; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162817
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-162817
Alignment Scores:
Pred. No.: 22.3 Length: 1053
Score: 68.50 Matches: 18
Percent Similarity: 52.3% Conservative: 5
Best Local Similarity: 40.9% Mismatches: 16
Query Match: 23.1% Indels: 5
DB: 10 Gaps: 2
US-10-628-525A-35 (1-58) x US-11-266-748A-162817 (1-1053)
Qy 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIleThr 26
Db 483 CCATCACCAGGTGGGTGAGACGCTGACTCGCAGATCAAGTTGT-----CCA 530
Qy 27 SerLeuMetTriSer---SerLeuValMetLysGlnThrLysLysValAlaHisSerAla 45
Db 531 TCAAGCGCTGGTCCACCAAGCGGTGCTCTCAAGCAGACCAAGGGGTGGGGGCTCGGG 590
Qy 46 LysPheArgVal 49
Db 591 TCCTTCGGGCTA 602
RESULT 23
US-11-239-610A-11005
; Sequence 11005, Application US/11239610A
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.341 - 38-21(15793)C/US
; CURRENT APPLICATION NUMBER: US/11/239,610A
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US 09/565,240
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 54005
; SEQ ID NO 11005
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3092-013-Q1-K1-E1
US-11-239-610A-11005
Alignment Scores:
Pred. No.: 7.13 Length: 412
Score: 68.00 Matches: 22
Percent Similarity: 55.9% Conservative: 11
Best Local Similarity: 37.3% Mismatches: 23
Query Match: 22.9% Indels: 3
DB: 8 Gaps: 1
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US-10-628-525A-35 (1-58) x US-11-239-610A-11005 (1-412)
QY 1 MetAlaGlnIleLeuAlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerPro 20
Db 10 ATGGATCAAAATTTGGCGCTCGCTTTACGCAACGGCTTATTAGAATGTCAAGGTGCTATTCA 69
QY 21 CysAlaThrProIleThrSerLysMet-TrpSerSerLeuValMetLysGlnThrLys 40
Db 70 TATGGCATCTTATTACATCAACATTTTGCATTCCTTATTGTGGAAACAAAATGAAGAA 129
QY 40 sVal-----AlaHisSerAlaLysPheArgValMetAlaValAsnSerGluAsn 56
Db 130 CGCTTAACCTACCAGTATTGCTAAATTTACAGTGTCTGATTAATTCAGCAAT 184

RESULT 24
US-10-540-898-254/c
; Sequence 254, Application US/10540898
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0056-101 (PP023367.0003)
; CURRENT APPLICATION NUMBER: US/10/540,898
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 10/330,773
; PRIOR FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; TYPE: DNA
; LENGTH: 86149
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(86149)
; OTHER INFORMATION: n = A,T,C or G
US-10-540-898-254

Alignment Scores:
Pred. No.: 1.21e+04 Length: 86149
Score: 68.00 Matches: 17
Percent Similarity: 45.3% Conservative: 7
Best Local Similarity: 32.1% Mismatches: 29
Query Match: 22.9% Indels: 0
DB: 7 Gaps: 0

US-10-628-525A-35 (1-58) x US-10-540-898-254 (1-86149)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 46678 GCCCGCGCACTCACCATGGTAGATGATATCTGGAGACCCCTGTCCAGCCCTCAGAGATT 46619
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45
Db 46618 TGCCAGAGCCCATGGGCGAGATGGAGATGGTGGGACAACTGGATGGTCCCTCAGGG 46559
QY 46 LysPheArgValMetAlaValAsnSerGluAsnGlyThr 58
Db 46558 AGATTTCAGCAGCTCAACAGGAACTGGAGAGAAAGGCACT 46520

RESULT 25
US-10-917-503B-11416
; Sequence 11416, Application US/10917503B
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503B
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11416
; LENGTH: 2103
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (102)..(2021)
US-10-917-503B-11416

Alignment Scores:
Pred. No.: 81.2 Length: 2103
Score: 67.50 Matches: 15
Percent Similarity: 49.1% Conservative: 11
Best Local Similarity: 28.3% Mismatches: 18
Query Match: 22.7% Indels: 9
DB: 7 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-917-503B-11416 (1-2103)
QY 1 MetAlaGlnIleLeuAla-----ProSerThrGlnTrp 11
Db 949 ATGGGAGAGATCTTTCCCACTCTTAATGAACCGCAGCGTGTGCCCAAAGTTTGGTGG 1008
QY 12 GlnMetArgIleThrLysThrSerProCysAlaThrProIleThrSerLysMetTrpSer 31
Db 1009 AAAATGCAAGAAGAACTTCCTCAGTGTGTGCTAGAAATCTCTGACCAAGAGTGTGGAT 1068
QY 32 SerLeuValMetLysGlnThrLysLysValAlaHisSer 44
Db 1069 GGTATACTGCTAAAGACTTCATTGTTGGAGAGTCACTCA 1107

RESULT 26
US-60-751-455-3689
; Sequence 3689, Application US/60751455
; GENERAL INFORMATION:
; APPLICANT: Radich, Jerald P.
; APPLICANT: Dai, Hongyue
; APPLICANT: Mao, Mao
; APPLICANT: Schelter, Janell
; APPLICANT: Linsley, Peter S.
; TITLE OF INVENTION: GENES ASSOCIATED WITH PROGRESSION AND RESPONSE IN
; FILE REFERENCE: 9301-253-888
; CURRENT APPLICATION NUMBER: US/60/751,455
; CURRENT FILING DATE: 2005-12-15
; NUMBER OF SEQ ID NOS: 7936
; SOFTWARE: FastSeq 4.01
; SEQ ID NO 3689

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; APPLICANT: MASIGNANI, Vega
; APPLICANT: GALEOTTI, Cesira
; APPLICANT: MORA, Marirosa
; APPLICANT: RATTI, Giulio
; APPLICANT: SCARSELLI, Maria
; APPLICANT: SCARLATO, Vincenzo
; APPLICANT: RAPPUOLI, Rino
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: GRANDI, Guido
; TITLE OF INVENTION: NEISSERIA GENOMIC SEQUENCES AND METHODS OF THEIR USE
; FILE REFERENCE: 223002100400
; CURRENT APPLICATION NUMBER: US/10/018,470B
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/US00/05928
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: US 60/132,068
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: GB 0004695.3
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT/US99/23573
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Seqwin99, version 1.0.4
; SEQ ID NO 1
; LENGTH: 2242716
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
US-10-018-470B-1

Alignment Scores:
Pred. No.: 1.72e+06 Length: 2242716
Score: 66.50 Matches: 18
Percent Similarity: 47.7% Conservative: 3
Best Local Similarity: 40.9% Mismatches: 18
Query Match: 22.4% Indels: 5
DB: 7 Gaps: 1

US-10-628-525A-35 (1-58) x US-10-018-470B-1 (1-2242716)
QY 7 ProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAla----- 22
Db 660554 CGGTCAACCTCTTGGACACGCGCGGACACCAAGACTTCTCCGAGACACCTACCGCGTTT 660495
QY 23 ---ThrProIleThrSerLysMetTrpSerLeuValMetLysGlnThrLysVal 41
Db 660494 TAACGCGGTGGACAGCGATTATGGTCATUCGACGCGGCAAGGCGTGGAGCGCAA 660435
QY 42 AlaHisSerAla 45
Db 660434 CCATCAAGCTCT 660423

RESULT 30
US-10-187-187-434
; Sequence 434, Application US/10501187
; GENERAL INFORMATION:
; APPLICANT: Hansen, Rhonda
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 2300-17767
; CURRENT APPLICATION NUMBER: US/10/501,187
; CURRENT FILING DATE: 2004-07-08
; PRIOR FILING DATE: 2004-03-15, 637
; PRIOR APPLICATION NUMBER: 60/345,637
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 434
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-501-187-434

Alignment Scores:
Pred. No.: 18.1 Length: 503

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Score: 66.00 Matches: 19
Percent Similarity: 45.3% Conservative: 5
Best Local Similarity: 35.8% Mismatches: 18
Query Match: 22.2% Indels: 12
DB: 7 Gaps: 2

US-10-628-525A-35 (1-58) x US-10-501-187-434 (1-503)
QY 6 AlaProSerThrGlnTrpGlnMetArgIleThrLysThrSerProCysAlaThrProIle 25
Db 277 TCACCATCCCAAGCTGGAGCACCCACCAAGACATCGACCTGTACCACCATGT 336
QY 26 ThrSerLysMetTrpSerSerLeuValMetLysGlnThrLysValAlaHisSerAla 45
Db 337 ACATGGAGGCGCTGGTG-AAGCTCTTCCGACAG-----CACAGACC 377
QY 46 LysPhe-----ArgValMetAlaValAsn 53
Db 378 AAGTTCGGGCTCCCGGAGACTGAGGTCTCTGGAGGTGAAC 416

```

Search completed: April 2, 2006, 04:09:35  
Job time : 276.468 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search using ~~us-10-628-525a-36.p2n.model~~

Run on: April 1, 2006, 04:29:01 ; Search time 1473.89 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525A-36

Perfect score: 368

Sequence: 1 MAALATSQLVATAGHGVPD.....RHQQARRGRRPFPSLVVC 74

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abes/ABSSWEB spool/US10628525/runat\_31032006\_095113\_16622/app\_query.fasta\_1  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -IOOPCL=0 -IOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes06h  
-USER=US10628525 @CGN 1.1 4375 @runat\_31032006\_095113\_16622 -NCPU=6 -ICPU=3  
-NO\_WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.sts.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pa.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	90.5	1018	6	AR427888 Sequence
2	333	90.5	4274	15	AF544096
3	333	90.5	4287	15	AF544092

4	333	90.5	4449	15	AF544094
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13	336	88.6	4433	15	AF544099
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15	332	87.5	4395	15	AF544089
16	316.5	86.0	3533	15	AF544077
17	316.5	86.0	4210	15	AF544078
18	316.5	86.0	4230	15	AF544075
19	316.5	86.0	4436	15	AF544085
20	316.5	86.0	4436	15	AF544087
21	316.5	86.0	4436	15	AF544090
22	316.5	86.0	4438	15	AF544095
23	316.5	86.0	4463	15	AF544069
24	316.5	86.0	4463	15	AF544097
25	316.5	86.0	4475	15	AF544081
26	307	83.4	4246	15	AF544086
27	298	81.0	4420	15	AF544072
28	293	79.6	143300	15	AF488416
29	289	78.5	2267	6	AR195560
30	286	77.7	4449	15	AF544093
31	282.5	76.8	4428	15	AF544080
32	279	75.8	1915	6	BD071184
33	279	75.8	4433	15	AF544084
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35	237.5	64.5	130987	15	AF488412
36	219	59.5	2115	15	AB089141
37	205.5	55.8	4416	15	AF544076
38	183	49.7	121	6	AX325915
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40	175	47.6	121	6	AX325911
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42	172.5	46.9	123096	15	AF488414
43	159	43.2	121	6	AX325919
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49	128.5	34.9	1642	15	AF092443
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63	128.5	34.9	4100	15	OSWAXYL
64	128.5	34.9	4252	15	RICWAXYA
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66	128.5	34.9	5317	15	OSWAXYG
67	128.5	34.9	5356	15	AF141954
68	128.5	34.9	5379	15	AF031162
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75	113	30.7	121	6	AX325907
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AF544094 Zea mays  
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AF544088 Zea mays  
AF544091 Zea mays  
AF544074 Zea mays  
AR106490 Sequence  
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AF544079 Zea mays  
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AF488412 Sorghum b  
AB089141 Setaria i  
AF544076 Zea mays  
AX325915 Sequence  
AX325916 Sequence  
AX325911 Sequence  
AX325912 Sequence  
AF488414 Pennisetu  
AX325919 Sequence  
AX325920 Sequence  
AX325923 Sequence  
AX325924 Sequence  
AF544082 Zea mays  
AF092444 Oryza sat  
AF092443 Oryza sat  
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BD185621 Low-amylo  
AB066093 Oryza sat  
AB066094 Oryza sat  
AF515480 Oryza sat  
AF515481 Oryza sat  
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AF515483 Oryza sat  
AK070431 Oryza sat  
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X62134 O.sativa Wa  
AX755432 Sequence  
X68228 O.sativa wa  
D10472 Oryza glabe  
X64108 O.sativa wa  
X65183 O.sativa wa  
AF141954 Oryza sat  
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X53694 Rice waxy g  
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AF488413 Oryza sat  
AF607102 Oryza sat  
AP002542 Oryza sat  
AX325907 Sequence  
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TITLE      Direct Submission
JOURNAL    Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
           Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES   Location/Qualifiers
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Best Local Similarity: 95.9%      Mismatches: 1
Query Match:    90.5%      Indels:      2
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US-10-628-525A-36 (1-74) x AF544092 (1-4287)

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Qy      21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db      886 GCCTCCACGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 945
Qy      41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60
Db      946 GCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1005
Qy      61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db      1006 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1041

RESULT 4
AF544094
LOCUS    AF544094
DEFINITION Zea mays subsp. mays cultivar Oh43 granule-bound starch synthase (waxy1) gene, partial sequence.
ACCESSION AF544094
VERSION   AF544094.1 GI:23395315
KEYWORDS
SOURCE    Zea mays
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             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
             clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 4449)
AUTHORS   Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
           IV.
TITLE      Genetic diversity and selection in the maize starch pathway
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED    12244216
REFERENCE 2 (bases 1 to 4449)
AUTHORS   Whitt,S.R. and Buckler,E.S. IV.
TITLE      Direct Submission
JOURNAL   Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
           Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES   Location/Qualifiers
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Best Local Similarity: 95.9%      Mismatches: 1
Query Match:    90.5%      Indels:      2
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US-10-628-525A-36 (1-74) x AF544094 (1-4449)

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 Db 1047 GCGTCCACGTTCCGCGCGCGCGCGCGAGGCGCTGAGGGGGCGCGCGCGTCCGGCGG 1106  
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 Db 1107 GCGGACACGCTCAGCATGGGACCGACGCGCGCGCGCGCGCCCGGCGCCAGGCGACCGAGCAGCGG 1166  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 1167 CGCCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 1202  
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 LOCUS  
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 ACCESSION AF544071  
 VERSION AF544071.1 GI:23395292  
 KEYWORDS  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoidae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 4467)  
 AUTHORS Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.  
 IV.  
 TITLE Genetic diversity and selection in the maize starch pathway  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2002) In press  
 PUBMED 12244216  
 REFERENCE 2 (bases 1 to 4467)  
 AUTHORS Whitt,S.R. and Buckler,E.S. IV.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State  
 Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA  
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 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 1064 GCGTCCACGTTCCGCGCGCGCGCGAGGCGCTGAGGGGGCGCGCGCGTCCGGCGG 1123  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 1124 GCGGACACGCTCAGCATGGGACCGACGCGCGCGCGCGCCCGGCGCCAGGCGACCGAGCAGCGG 1183

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 1184 CGCCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 1219  
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 AF544088  
 LOCUS  
 DEFINITION Zea mays subsp. mays cultivar Ky21 granule-bound starch synthase  
 ACCESSION AF544088  
 VERSION AF544088.1 GI:23395309  
 KEYWORDS  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoidae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 4470)  
 AUTHORS Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.  
 IV.  
 TITLE Genetic diversity and selection in the maize starch pathway  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2002) In press  
 PUBMED 12244216  
 REFERENCE 2 (bases 1 to 4470)  
 AUTHORS Whitt,S.R. and Buckler,E.S. IV.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State  
 Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA  
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 Db 1063 GCGTCCACGTTCCGCGCGCGCGCGAGGCGCTGAGGGGGCGCGCGCGTCCGGCGG 1122  
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 Db 1123 GCGGACACGCTCAGCATGGGACCGACGCGCGCGCGCGCCCGGCGCCAGGCGACCGAGCAGCGG 1182  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 1183 CGCCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 1218  
 RESULT 7  
 AF544091  
 LOCUS  
 DEFINITION Zea mays subsp. mays cultivar N28ht granule-bound starch synthase  
 ACCESSION AF544091  
 VERSION AF544091.1 GI:23395312  
 KEYWORDS

SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 4477)  
AUTHORS Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S. IV.  
TITLE Genetic diversity and selection in the maize starch pathway  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2002) In press  
PUBMED 12244216  
REFERENCE 2 (bases 1 to 4477)  
AUTHORS Whitt,S.R. and Buckler,E.S. IV.  
TITLE Direct Submission  
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA  
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Query Match: 90.5% Indels: 2  
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US-10-628-525A-36 (1-74) x AF544091 (1-4477)  
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Db 1014 ATGGCGGCTCTGGCCACGTCGCGAGCTGTCGCAACGGCGCGCGCTGGCGGCG 1073  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 1074 GCGTCCACGTCCTCCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCG 1133  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 1134 GCGGACACGCTCAGCAGTCGCGACGCGCGCGCGCGCGCGCGCCAGGCACGAGCGG 1193  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 1194 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTC 1229  
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AP544074  
LOCUS Zea mays subsp. mays cultivar B97 granule-bound starch synthase (waxy1) gene, partial sequence. 4484 bp DNA linear PLN 27-APR-2004  
DEFINITION  
ACCESSION AP544074  
VERSION AP544074.1 GI:23395295  
KEYWORDS  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 4484)  
AUTHORS Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S. IV.  
TITLE Genetic diversity and selection in the maize starch pathway  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2002) In press  
PUBMED 12244216  
REFERENCE 2 (bases 1 to 4484)

AUTHORS Whitt,S.R. and Buckler,E.S. IV.  
TITLE Direct Submission  
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA  
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Percent Similarity: 95.9% Conservatives: 0  
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Query Match: 90.5% Indels: 2  
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Db 1015 ATGGCGGCTCTGGCCACGTCGCGAGCTGTCGCAACGGCGCGCGCTGGCGGCG 1074  
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Db 1075 GCGTCCACGTCCTCCCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCG 1134  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 1135 GCGGACACGCTCAGCAGTCGCGACGCGCGCGCGCGCGCGCCAGGCACGAGCGG 1194  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 1195 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTC 1230  
RESULT 9  
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LOCUS Zea mays subsp. mays cultivar B97 granule-bound starch synthase (waxy1) gene, partial sequence. 4800 bp DNA linear PAT 14-FEB-2001  
DEFINITION  
ACCESSION AR106490  
VERSION AR106490.1 GI:12821020  
KEYWORDS  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 4800)  
AUTHORS Keeling,P. and Guan,H.  
TITLE Starch encapsulation  
JOURNAL Patent: US 6107060-A 4 22-AUG-2000;  
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Pred. No.: 1.62e-13 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservatives: 0  
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Query Match: 90.5% Indels: 2  
DB: 6 Gaps: 1  
US-10-628-525A-36 (1-74) x AR106490 (1-4800)  
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polya_site      4625
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      21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
      1293 GCGTCACAGTTCCGCCCGCGCGCCGCGCAGGCTCTGAGGGGGGGCCCGGGCGTGGCGGCG 1352
      41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
      1353 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCCAGGACACGACGAGCGGCG 1412
      61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
      1413 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 1448

RESULT 11
AF544079
LOCUS
DEFINITION
Zea mays subsp. mays cultivar D940Y granule-bound starch synthase
ACCESSION
AF544079.1 GI:23395300
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 4090)
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
AUTHORS
Genetic diversity and selection in the maize starch pathway
PROC. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED
12244216
TITLE
Direct Submission
AUTHORS
Whitt,S.R. and Buckler,E.S. IV.
JOURNAL
Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
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Score:          327.00      Matches:      70
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Best Local Similarity: 94.6%      Mismatches: 2
Query Match:    88.9%      Indels:      2
DB:             15      Gaps:        1

US-10-628-525A-36 (1-74) x AF544079 (1-4090)

QY      1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
      972 ATGGCGGCTCTGGCCACGTCGCGAGCTGTCGCAACGCGCGCGGCTGGGGCGTCCCGGAC 1031
      21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
      1032 GCGTCACAGTTCCGCCCGCGCGCCGCGCAGGCTCTGAGGGGGGGCCCGGGCGTGGCGGCG 1091
      41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
      1092 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCCAGGACACGACGAGCGGCG 1151

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QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
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Db 1152 CGCCGCGGGGCGAGG-----TTCCCGTGGCTGGTGTGTC 1187

RESULT 13
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LOCUS
DEFINITION Zea mays subsp. mays cultivar W153R granule-bound starch synthase
(waxy1) gene, partial sequence.
ACCESSION AF544099
VERSION AF544099.1 GI:23395320
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. (2002) In press
12244216
PUBMED
TITLE Zea mays
JOURNAL Zea mays
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
Direct Submission
JOURNAL Zea mays
SUBMITTED (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
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/feature="granule-bound starch synthase; wx1"

gene
US-10-628-525A-36 (1-74) x AF544099 (1-4433)

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Alignment Scores:
Pred. No.: 4,478-13 Length: 4433
Score: 326.00 Matches: 70
Percent Similarity: 94.6% Conservative: 0
Best Local Similarity: 94.6% Mismatches: 2
Query Match: 88.6% Indels: 2
DB: 15 Gaps: 1

US-10-628-525A-36 (1-74) x AF544099 (1-4433)

QY 1 MetaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
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Db 972 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTGCACGCCCGCGGCTGGCGCTCCCGGAC 1031

QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 40
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Db 1032 GCGTCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1091

QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
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QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
|||||
Db 1152 CGCCGCGGGGCGAGG-----TTCCCGTGGCTGGTGTGTC 1187

RESULT 14
AF544083
LOCUS
DEFINITION Zea mays subsp. mays cultivar I205 granule-bound starch synthase
(waxy1) gene, partial sequence.
ACCESSION AF544083
VERSION AF544083.1 GI:23395304
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. (2002) In press
12244216
PUBMED
TITLE Zea mays
JOURNAL Zea mays
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
Direct Submission
JOURNAL Zea mays
SUBMITTED (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
source
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US-10-628-525A-36 (1-74) x AF544083 (1-4444)

ORIGIN
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Percent Similarity: 94.6% Conservative: 0
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Query Match: 88.6% Indels: 2
DB: 15 Gaps: 1

US-10-628-525A-36 (1-74) x AF544083 (1-4444)

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Db 972 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTGCACGCCCGCGGCTGGCGCTCCCGGAC 1031

QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 40
|||||
Db 1032 GCGTCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1091

QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
|||||
Db 1092 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1151

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
|||||
Db 1152 CGCCGCGGGGCGAGG-----TTCCCGTGGCTGGTGTGTC 1187

RESULT 15
AF544089
LOCUS
DEFINITION Zea mays subsp. mays cultivar M162W granule-bound starch synthase
(waxy1) gene, partial sequence.
ACCESSION AF544089
VERSION AF544089.1 GI:23395310
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
Genetic diversity and selection in the maize starch pathway
Proc. Natl. Acad. Sci. U.S.A. (2002) In press
12244216
PUBMED
TITLE Zea mays
JOURNAL Zea mays
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
Direct Submission
JOURNAL Zea mays
SUBMITTED (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
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REFERENCE 2 (bases 1 to 4395)
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA

FEATURES
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Best Local Similarity: 93.2% Mismatches: 3
Query Match: 87.5% Indels: 2
DB: 15 Gaps: 1

US-10-628-525A-36 (1-74) x AF544089 (1-4395)

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Db 972 ATGGCGGCTCTGGCCACGTCGAGCTCGTGCACCGCCCGCGCTGGGCGTCCCGGAC 1031
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 1032 GCGTCACAGTTCGCGCGCGCGCCGACGAGGCTGAGGGGGCGCCGCGCGCG 1091
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaProArgHisGlnGlnAla 60
Db 1092 GCGGACACGCTCAGTCAGTCCGACGCGCGCGCGCGCGCGCGCCAGGACCGAGCGG 1151
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 1152 CGCGCGGGGGCAGG-----TTCCGTCGCTCGTGTGTGC 1187

RESULT 16
AF544077
LOCUS AF544077
DEFINITION Zea mays subsp. mays cultivar CML258 granule-bound starch synthase (waxy1) gene, partial sequence.
ACCESSION AF544077
VERSION AF544077.1 GI:23395298
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 3533)
AUTHORS Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S. IV.
TITLE Genetic diversity and selection in the maize starch pathway
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED 12244216
REFERENCE 2 (bases 1 to 4210)
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
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source
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Percent Similarity: 93.3% Conservative: 0
Best Local Similarity: 93.3% Mismatches: 2
Query Match: 86.0% Indels: 3
DB: 15 Gaps: 2

US-10-628-525A-36 (1-74) x AF544077 (1-3533)

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QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 499 GCGTCACAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaProArgHisGlnGln 59
Db 559 GCGGACACGCTCAGTCAGTCCGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 618
QY 60 AlaArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 619 GCGCGCGGGGGCAGG-----TTCCGTCGCTCGTGTGTGC 657

RESULT 17
AF544078
LOCUS AF544078
DEFINITION Zea mays subsp. mays cultivar CML333 granule-bound starch synthase (waxy1) gene, partial sequence.
ACCESSION AF544078
VERSION AF544078.1 GI:23395299
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 4210)
AUTHORS Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S. IV.
TITLE Genetic diversity and selection in the maize starch pathway
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED 12244216
REFERENCE 2 (bases 1 to 4210)
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
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Percent Similarity: 93.3% Conservative: 0
Best Local Similarity: 93.3% Mismatches: 2
Query Match: 86.0% Indels: 3
DB: 15 Gaps: 2

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VERSION AF544087.1 GI:23395308
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ORGANISM Zea mays
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AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
FEATURES
1 (bases 1 to 4436)
LOCATION/Qualifiers
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
Genetic diversity and selection in the maize starch pathway
PROC. Natl. Acad. Sci. U.S.A. (2002) In press
12244216
PUBLISHED
TITLE Direct Submission
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
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/notes="granule-bound starch synthase; wx1"
ORIGIN
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Pred. No.: 1.95e-12 Length: 4436
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Percent Similarity: 93.3% Conservative: 0
Best Local Similarity: 93.3% Mismatches: 2
Query Match: 86.0% Indels: 3
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US-10-628-525A-36 (1-74) x AF544087 (1-4436)
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Db 1009 ATGGCGGCTCTGGCCACGTCGCGAGCTGTCGCACACGGCGCGGCTGGCGGTCCCGGAC 1068
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40
Db 1069 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1128
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGln---GlnGln 59
Db 1129 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1188
QY 60 AlaArgArgGlyGlyValPheProPheProSerLeuValValCys 74
Db 1189 GCGCGCGCGCGGCGCCAGG-----TTCCGTCGCTGCTGTGTGC 1227
RESULT 21
AF544090
LOCUS Zea mays subsp. mays cultivar Mol7 granule-bound starch synthase
DEFINITION (waxy1) gene, partial sequence.
ACCESSION AF544090
VERSION AF544090.1 GI:23395311
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 4436)
LOCATION/Qualifiers
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
Genetic diversity and selection in the maize starch pathway
PROC. Natl. Acad. Sci. U.S.A. (2002) In press
12244216
PUBLISHED
TITLE Direct Submission
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
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Best Local Similarity: 93.3% Mismatches: 2
Query Match: 86.0% Indels: 3
DB: 15 Gaps: 2
US-10-628-525A-36 (1-74) x AF544087 (1-4436)
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QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40
Db 1069 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1128
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGln---GlnGln 59
Db 1129 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1188
QY 60 AlaArgArgGlyGlyValPheProPheProSerLeuValValCys 74
Db 1189 GCGCGCGCGCGGCGCCAGG-----TTCCGTCGCTGCTGTGTGC 1227
RESULT 21
AF544090
LOCUS Zea mays subsp. mays cultivar Mol7 granule-bound starch synthase
DEFINITION (waxy1) gene, partial sequence.
ACCESSION AF544090
VERSION AF544090.1 GI:23395311
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 4436)
LOCATION/Qualifiers
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
Genetic diversity and selection in the maize starch pathway
PROC. Natl. Acad. Sci. U.S.A. (2002) In press
12244216
PUBLISHED
TITLE Direct Submission
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES
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Query Match: 86.0% Indels: 3
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US-10-628-525A-36 (1-74) x AF544090 (1-4436)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAsp 20
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QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40
Db 1069 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1128
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGln---GlnGln 59
Db 1129 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1188
QY 60 AlaArgArgGlyGlyValPheProPheProSerLeuValValCys 74
Db 1189 GCGCGCGCGCGGCGCCAGG-----TTCCGTCGCTGCTGTGTGC 1227
RESULT 22
AF544095
LOCUS Zea mays subsp. mays cultivar P39 granule-bound starch synthase
DEFINITION (waxy1) gene, partial sequence.
ACCESSION AF544095
VERSION AF544095.1 GI:23395316
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 4438)
LOCATION/Qualifiers
Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
Genetic diversity and selection in the maize starch pathway
PROC. Natl. Acad. Sci. U.S.A. (2002) In press
12244216
PUBLISHED
TITLE Direct Submission
AUTHORS Whitt,S.R. and Buckler,E.S. IV.
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State
Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
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US-10-628-525A-36 (1-74) x AF544069 (1-4463)	
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QY	21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db	1063 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGCCCGGGCGTCCGGCGG 1122
QY	41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln---GlnGln 59
Db	1123 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCCCGCCAGCACCAGCAGCAG 1182
QY	60 AlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db	1183 GCGCGCGCGGGGCCAGG-----TTCCGTCGCTCGTGTGTGC 1221
RESULT 24	
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LOCUS	
DEFINITION	Zea mays subsp. mays cultivar T232 granule-bound starch synthase (waxy1) gene, partial sequence.
ACCESSION	AF544097
VERSION	AF544097.1 GI:23395318
KEYWORDS	
SOURCE	Zea mays
ORGANISM	Zea mays
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 4463)
AUTHORS	Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S. IV.
TITLE	Genetic diversity and selection in the maize starch pathway
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED	12244216
REFERENCE	2 (bases 1 to 4463)
AUTHORS	Whitt,S.R. and Buckler,E.S. IV.
TITLE	Direct Submission
JOURNAL	Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
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ORIGIN	
Alignment Scores:	
Pred. No.:	1.96e-12 Length: 4463
Score:	316.50 Matches: 70
Percent Similarity:	93.3% Conservative: 0
Best Local Similarity:	93.3% Mismatches: 2
Query Match:	86.0% Indels: 3
DB:	15 Gaps: 2
US-10-628-525A-36 (1-74) x AF544097 (1-4463)	
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QY	21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db	1062 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGCCCGGGCGTCCGGCGG 1121
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Query Match:	86.0% Indels: 3
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QY	41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln---GlnGln 59
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QY	60 AlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
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AF544069	
LOCUS	
DEFINITION	Zea mays subsp. mays cultivar A6 granule-bound starch synthase (waxy1) gene, partial sequence.
ACCESSION	AF544069
VERSION	AF544069.1 GI:23395290
KEYWORDS	
SOURCE	Zea mays
ORGANISM	Zea mays
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 4463)
AUTHORS	Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S. IV.
TITLE	Genetic diversity and selection in the maize starch pathway
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED	12244216
REFERENCE	2 (bases 1 to 4463)
AUTHORS	Whitt,S.R. and Buckler,E.S. IV.
TITLE	Direct Submission
JOURNAL	Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
FEATURES	Location/Qualifiers
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	/note="granule-bound starch synthase; wxl"
ORIGIN	
Alignment Scores:	
Pred. No.:	1.96e-12 Length: 4463
Score:	316.50 Matches: 70
Percent Similarity:	93.3% Conservative: 0
Best Local Similarity:	93.3% Mismatches: 2
Query Match:	86.0% Indels: 3
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QY	41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln---GlnGln 59



JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (2002) In press
PUBMED	12244216
REFERENCE	2 (bases 1 to 4420)
AUTHORS	Whitt,S.R. and Buckler,E.S. IV.
TITLE	Direct Submission
JOURNAL	Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA
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Best Local Similarity:	91.9% Mismatches: 4
Query Match:	81.0% Indels: 3
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QY	41 AlaAepThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
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QY	61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db	1135 CGCCGCGGGCGGCGG-----TTCCGTCGCTCGTCTGCTGTC 1170
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LOCUS	Zea mays chromosome 9 BAC 9C20 complete sequence.
DEFINITION	AF488416
ACCESSION	AF488416.1 GI:33321038
VERSION	
KEYWORDS	Zea mays
SOURCE	Zea mays
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 143300)
AUTHORS	Ma,J., SanMiguel,P.J., Dubcovsky,J., Shiloff,B.A., Rostoks,N., Jiang,Z., Busso,C.S., Kleinhofs,A., Devos,K.M., Ramakrishna,W. and Bennetzen,J.L.
TITLE	Comparative sequence analysis of homologous wx1 regions in barley, maize, pearl millet, rice, sorghum and diploid wheat
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 143300)
AUTHORS	Ma,J., SanMiguel,P.J., Dubcovsky,J., Shiloff,B.A., Rostoks,N., Jiang,Z., Busso,C.S., Kleinhofs,A., Devos,K.M., Ramakrishna,W. and Bennetzen,J.L.
TITLE	Direct Submission
JOURNAL	Submitted (27-FEB-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA
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mrna	/product="putative selenium binding protein"
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US-10-628-525A-36 (1-74) x AF488416 (1-143300)

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Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArg-----His 56

Db 61528 GCGGACACGCTCAGCATGCGGACCCAGCGCGCGCGCGCGCTCCAGCACACGACGAG 61587

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RESULT 29

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LOCUS

DEFINITION

Sequence 25 from patent US 6350934.

AR195560

ACCESSION

AR195560.1 GI:20244997

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 2267)

Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P. Ann.Owens.,

Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.

Nucleic acid encoding delta-9 desaturase

JOURNAL

Patent: US 6350934-A 25 26-FEB-2002;

FEATURES

Location/Qualifiers

source

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ORIGIN

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Best Local Similarity:	82.1%	Mismatches:	5
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DB:	6	Gaps:	2

US-10-628-525A-36 (1-74) x AR195560 (1-2267)

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QY 52 AlaAlaProArgHisGlnGlnGlnAlaArgArgGlyGlyArgPheProPheProSerLeu 71  
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QY 72 ValValCys 74  
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Search completed: April 1, 2006, 15:15:52  
Job time : 1500.89 secs

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AF544093  
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DEFINITION Zea mays subsp. mays cultivar NC348 granule-bound starch synthase (waxy1) gene, partial sequence.  
ACCESSION AF544093  
VERSION AF544093.1 GI:23395314  
KEYWORDS .  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 4449)  
AUTHORS Whitt,S.R., Wilson,L.M., Tenaillon,M.I., Gaut,B.S. and Buckler,E.S. IV.  
Genetic diversity and selection in the maize starch pathway  
Proc. Natl. Acad. Sci. U.S.A. (2002) In press  
PUBMED 12244216  
REFERENCE 2 (bases 1 to 4449)  
AUTHORS Whitt,S.R. and Buckler,E.S. IV.  
TITLE Direct Submission  
JOURNAL Submitted (03-SEP-2002) Genetics, USDA-ARS, North Carolina State Univ., 2523 Gardner Hall, Raleigh, NC 27695-7614, USA  
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ORIGIN

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Query Match:	77.7%	Indels:	2
DB:	15	Gaps:	1

US-10-628-525A-36 (1-74) x AF544093 (1-4449)

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 00:15:06 ; Search time 174.223 Seconds  
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Title: US-10-628-525a-36

Perfect score: 368

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 21:\*  
1: Geneseqm1980s:\*  
2: Geneseqm1990s:\*  
3: Geneseqm2000s:\*  
4: Geneseqm2001s:\*  
5: Geneseqm2001bs:\*  
6: Geneseqm2002bs:\*  
7: Geneseqm2002bs:\*  
8: Geneseqm2003as:\*  
9: Geneseqm2003bs:\*  
10: Geneseqm2003cs:\*  
11: Geneseqm2003ds:\*  
12: Geneseqm2004as:\*  
13: Geneseqm2004bs:\*  
14: Geneseqm2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	90.5	1818	10	Aad63600 Maize UDP
2	333	90.5	1818	14	Adw87816 Maize gra
3	333	90.5	1818	14	Adw87799 Maize gra
4	333	90.5	1915	2	Aax60319 DNA seque

5	333	90.5	2263	11	ADM77903
6	333	90.5	2263	11	ADM77902
7	333	90.5	4627	14	Adw87817
8	333	90.5	4800	2	AAV29752
9	333	90.5	4800	8	ABX69931
10	333	90.5	4800	11	ADM77906
11	326	88.6	1406	13	ADX34893
12	326	88.6	1409	13	ADX33821
13	326	88.6	1416	13	ADX36735
14	316.5	86.0	1818	8	ACC44559
15	316.5	86.0	4207	14	Adw87804
16	306.5	83.3	1863	14	Adw87808
17	306.5	83.3	4442	14	Adw87815
18	306.5	83.3	4470	14	Adw87798
19	289	78.5	2267	2	AAx63355
20	183	49.7	121	6	ABK26694
21	183	49.7	121	6	ABK26693
22	183	49.7	121	12	ADN45385
23	183	49.7	121	12	ADN45384
24	175	47.6	121	6	ABK26690
25	175	47.6	121	6	ABK26689
26	175	47.6	121	12	ADN45381
27	175	47.6	121	12	ADN45380
28	159	43.2	121	6	ABK26698
29	159	43.2	121	6	ABK26697
30	159	43.2	121	12	ADN45388
31	159	43.2	121	12	ADN45389
32	155	42.1	121	6	ABK26702
33	155	42.1	121	6	ABK26701
34	155	42.1	121	12	ADN45392
35	155	42.1	121	12	ADN45393
36	128.5	34.9	1937	10	ADC53776
37	128.5	34.9	1937	2	ADC53778
38	128.5	34.9	2586	2	AAQ45913
39	128.5	34.9	2542	2	AAV29753
40	128.5	34.9	2597	10	ADC07867
41	113	30.7	121	6	ABK26685
42	113	30.7	121	6	ABK26686
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44	113	30.7	121	12	ADN45377
45	98.5	26.8	1714	10	ADN45377
46	97.5	26.5	2028	10	ADN45377
47	97.5	26.5	2886	9	ADN45377
48	97.5	26.5	2886	10	ADN45377
49	97.5	26.5	2886	14	AEA79538
50	97.5	26.5	2886	14	AEA79538
51	96	26.1	475	9	ACH45303
52	94	25.5	2818	10	ADN45377
53	94	25.5	2818	14	AEA79534
54	90.5	24.6	1752	8	ACA27181
55	88.5	24.0	6776	14	ACL64421
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57	87	23.6	1548	8	ACA23242
58	87	23.6	3123	10	ADN45377
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60	86	23.4	201	13	ADQ46475
61	86	23.4	2805	10	ADN45377
62	86	23.4	2805	14	AEA79536
63	86	23.4	3785	6	AAK98640
64	85.5	23.2	2870	2	AAQ91177
65	85	23.1	1278	13	ADN45377
66	84.5	23.0	75216	6	ABX09141
67	84.5	23.0	110000	4	AAI99682_13
68	84.5	23.0	110000	4	AAI99683_13
69	84	22.8	109519	5	AAK08693
70	84	22.8	113193	8	AAK08693
71	83.5	22.7	1350	6	ABA99445
72	83.5	22.7	22473	11	ACN43962
73	83.5	22.7	38064	6	ABA99469
74	83	22.6	201	13	ADQ46481
75	83	22.6	201	13	ADQ46481
76	83	22.6	1161	11	ACL29132
77	82	22.3	2778	5	AAK76843

Adm77903 Maize wax  
Adm77902 Maize wax  
Adw87817 Maize gra  
Aav29752 Zea maye  
Abx09931 DNA encod  
Adm77906 Granule-b  
Adx34893 Plant ful  
Adx33821 Plant ful  
Adx36735 Plant ful  
Acc44559 Maize gra  
Adw87804 Corn inbr  
Adw87808 Corn line  
Adw87815 Corn line  
Adw87798 Corn line  
Aax63355 Granule b  
Abk26694 Waxy star  
Abk26693 Waxy star  
Adn45385 Mutant ce  
Adn45384 Mutant ce  
Abk26690 Waxy star  
Abk26689 Waxy star  
Adn45381 Mutant ce  
Adn45380 Mutant ce  
Abk26698 Waxy star  
Abk26697 Waxy star  
Adn45388 Mutant ce  
Adn45389 Mutant ce  
Abk26702 Waxy star  
Abk26701 Waxy star  
Adn45392 Mutant ce  
Adn45393 Mutant ce  
Ades3776 Low amylo  
Ades3778 Low amylo  
Aaq45913 Rice star  
Aav29753 Oryza sat  
Abc07867 Rice DNA  
Abk26685 Waxy star  
Abk26686 Waxy star  
Adn45376 Mutant ce  
Adn45377 Mutant ce  
Adn45377 Mutant ce  
Adn45377 Mutant ce  
Adn45377 Mutant ce  
Adf92505 Bread whe  
Adf92505 Bread whe  
Adf92497 Bread whe  
Adf92503 Bread whe  
Adf92501 Bread whe  
Aea79534 waxy gene  
Aca27181 Prokaryot  
Acl64421 M. xanthu  
Adc10049 Human NOV  
Aca23242 Prokaryot  
Adf81459 Leukaemia  
Adg46462 Myocardia  
Adg46475 Myocardia  
Adf92499 Bread whe  
Aea79536 waxy gene  
Aak98640 Wheat car  
Aaq91177 Lipase an  
Adx49818 Plant ful  
Abx09141 Mycobacte  
Continuation (14 o  
Continuation (14 o  
Aas08693 Micromono  
Aad46465 Streptomy  
Aba99445 Actinopla  
Aca43962 Human gen  
Aba99469 Actinopla  
Adq46481 Myocardia  
Adq46468 Myocardia  
Acl29132 Rice abio  
Aas76843 DNA encod



Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 121 GCGGACACGCTCAGCATCGGACACGCGCGCGCGCCAGGACACGACGAGCG 180  
 Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 181 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 216

RESULT 2  
 ADW87816  
 ID ADW87816 standard; DNA; 1818 BP.  
 AC ADW87816;  
 XX  
 DT 07-APR-2005 (first entry)  
 DE Maize granule bound starch synthase (GBSS) coding region.  
 XX  
 DE Seed oil; feedstuff; food; crop improvement; transgenic plant;  
 KW granule bound starch synthase; plant; gene; ds.  
 KW  
 XX Zea mays.  
 OS  
 XX US2005005327-A1.  
 PN 06-JAN-2005.  
 XX  
 PD 25-JUN-2004; 2004US-00877645.  
 PF 27-JUN-2003; 2003US-0483491P.  
 PR  
 XX (RAVA/) RAVANELLO M P.  
 PA (FOLE/) FOLEY T J.  
 PA (LEDE/) LEDEAUX J R.  
 PA (WYRI/) WYRICK A E.  
 PA (SAVA/) SAVAGE T J.  
 XX  
 PI Ravanello MP, Foley TJ, Ledeaux JR, Wyrick AE, Savage TJ;  
 DR WPI; 2005-065279/07.  
 XX  
 DR New purified HOI001 granule bound starch synthase nucleic acid, useful  
 PT for increasing oil levels in maize plants or for creating maize plants  
 PT that include the nucleic acids.  
 XX  
 PS Disclosure; Fig 1; 74pp; English.  
 XX  
 CC The invention relates to HOI001 granule bound starch synthase (GBSS)  
 CC nucleic acid and its protein sequence. The invention also relates to a  
 CC method for increasing oil levels in corn kernel tissue by expression of  
 CC an HOI001 GBSS allele. The GBSS nucleic acid is useful for increasing oil  
 CC levels in maize plants and creating maize plants that include the nucleic  
 CC acids. The present sequence is the maize GBSS gene coding region.  
 XX  
 SQ Sequence 1818 BP; 345 A; 591 C; 613 G; 269 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2,16e-22 Length: 1818  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 14 Gaps: 1

US-10-628-525A-36 (1-74) x ADW87816 (1-1818)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 Db 1 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCGCGCTGGCGCTCCCGGAC 60  
 Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 |||

Db 61 GCCTCCACGTTCCGCGCGCGCGCGCGCTGAGGGGGCCCGCGGCTCGCGCGCG 120  
 Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 121 GCGGACACGCTCAGCATCGGACACGCGCGCGCGCCAGGACACGACGAGCG 180  
 Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 181 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 216

RESULT 3  
 ADW87799  
 ID ADW87799 standard; DNA; 1818 BP.  
 AC ADW87799;  
 XX  
 DT 07-APR-2005 (first entry)  
 DE Maize granule bound starch synthase (GBSS) gene.  
 XX  
 DE Seed oil; feedstuff; food; crop improvement; transgenic plant;  
 KW granule bound starch synthase; plant; gene; ds.  
 KW  
 XX Zea mays.  
 OS  
 XX US2005005327-A1.  
 PN 06-JAN-2005.  
 XX  
 PD 25-JUN-2004; 2004US-00877645.  
 PF 27-JUN-2003; 2003US-0483491P.  
 PR  
 XX (RAVA/) RAVANELLO M P.  
 PA (FOLE/) FOLEY T J.  
 PA (LEDE/) LEDEAUX J R.  
 PA (WYRI/) WYRICK A E.  
 PA (SAVA/) SAVAGE T J.  
 XX  
 PI Ravanello MP, Foley TJ, Ledeaux JR, Wyrick AE, Savage TJ;  
 DR WPI; 2005-065279/07.  
 DR P-PSDB; ADW87801.  
 DR EMBL; X03935.  
 XX  
 PT New purified HOI001 granule bound starch synthase nucleic acid, useful  
 PT for increasing oil levels in maize plants or for creating maize plants  
 PT that include the nucleic acids.  
 XX  
 PS Example 1; SEQ ID NO 2; 74pp; English.  
 XX  
 CC The invention relates to HOI001 granule bound starch synthase (GBSS)  
 CC nucleic acid and its protein sequence. The invention also relates to a  
 CC method for increasing oil levels in corn kernel tissue by expression of  
 CC an HOI001 GBSS allele. The GBSS nucleic acid is useful for increasing oil  
 CC levels in maize plants and creating maize plants that include the nucleic  
 CC acids. The present sequence is the maize GBSS gene. Note: This sequence  
 CC is stated to be similar to the sequence shown in figure 1, but these  
 CC sequences differ.  
 XX  
 SQ Sequence 1818 BP; 346 A; 592 C; 612 G; 268 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2,16e-22 Length: 1818  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2

DB: 14 Gaps: 1

US-10-628-525A-36 (1-74) x ADM87799 (1-1818)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20

DB 1 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTGCACACGCGCGCGCTGGCGCTCCCGGAC 60

QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 40

DB 61 GGTCTCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGGCCCGCGGCTGCGCGGCG 120

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60

DB 121 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 180

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74

DB 181 CGCCGCGGGGCGAGG-----TTCCGCTGCTCGTGTGTC 216

RESULT 4

AA660319

ID AAX60319 standard; DNA; 1915 BP.

XX AC AAX60319;

XX DT 23-AUG-1999 (first entry)

XX DE DNA sequence of the maize waxy gene.

XX KW Non-glycogen-like polysaccharide production; fermentation; waxy gene;

XX KW starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;

XX KW non-starch branching gene; amylopectin; amylose; plant-like starch; ss.

XX OS Zea mays.

XX PN WO9844780-A1.

XX PD 15-OCT-1998.

XX PF 03-APR-1998; 98WO-US006660.

XX PR 04-APR-1997; 97US-0042939P.

XX PA (EXSE-) EXSEED GENETICS LLC.

XX PI Guan H, Keeling PL;

XX DR WPI; 1998-568285/48.

XX DR P-PSDB; AAY16604.

XX PT Producing non-glycogen-like polysaccharides in bacteria, fungi or plants

XX PT - transformed with genes for enzymes involved in starch or glycogen

XX PT synthesis allows fermentative production of starches with engineered

XX PT properties.

XX PS Disclosure; Fig 49; 150pp; English.

XX CC The specification describes a method for the production of non-glycogen-

XX CC like polysaccharides in a host. The method comprises transforming a host,

XX CC suitable for fermentation, with genes encoding starch- or glycogen-

XX CC synthesis enzymes, and fermenting the transformants. The specification

XX CC also describes hosts transformed with a gene active in glycogen synthesis

XX CC and at least one non-starch branching gene, involved in production of

XX CC amylopectin or amylose in its original host. The method is used to

XX CC produce plant-like starches by fermentation and new starches in plants.

XX CC These starches are useful for all food and non-food applications of

XX CC starch. The present sequence is used in the course of the invention

XX SQ Sequence 1915 BP; 365 A; 610 C; 641 G; 299 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.28e-22 Length: 1915

Score: 333.00 Matches: 71

Percent Similarity: 95.9% Conservative: 0

Best Local Similarity: 95.9% Mismatches: 1

Query Match: 90.5% Indels: 2

DB: 2 Gaps: 1

US-10-628-525A-36 (1-74) x AAX60319 (1-1915)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20

DB 1 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTGCACACGCGCGCGCTGGCGCTCCCGGAC 60

QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 40

DB 61 GGTCTCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGGCCCGCGGCTGCGCGGCG 120

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60

DB 121 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 180

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74

DB 181 CGCCGCGGGGCGAGG-----TTCCGCTGCTCGTGTGTC 216

RESULT 5

ADM77903

ID ADM77903 standard; DNA; 2263 BP.

XX AC ADM77903;

XX DT 03-JUN-2004 (first entry)

XX DE Maize waxy-E starch EX385wx-E1 DNA G1643A SeqID 2.

XX KW maize; EX385wx-E1; ds; plant; starch; waxy-E starch; gel; paste;

XX KW starch storage organ; food stuff; coating; granule-bound starch synthase;

XX KW GBSS; mutant; gene.

XX OS Zea mays.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT CDS 194..2011

XX FT /\*tag= a

XX FT /product= "EX385wx-E1 protein"

XX FT mutation replace(1643,G)

XX FT /\*tag= b

XX PN WO2003033540-A2.

XX PD 24-APR-2003.

XX PF 17-OCT-2002; 2002WO-US033122.

XX PR 17-OCT-2001; 2001US-0329525P.

XX PA (BADI ) BASF PLANT SCI GMBH.

XX PI Klucinec JD, Keeling PL, Commuri P, Chang M;

XX DR WPI; 2003-481973/45.

XX DR P-PSDB; ADM77905.

XX PT Production of plant starch involves inducing mutation in starch affecting

XX PT locus of starch storage organ bearing plants, selecting propagative

XX PT structures, growing plants, and selecting and/or screening starch storing

XX PT organs.

XX PS Claim 23; SEQ ID NO 2; 181pp; English.

XX CC This invention relates to a novel method for producing a plant starch

XX CC through mutagenesis. Specifically, it refers to the granule-bound starch

XX CC synthase (GBSS) enzyme of waxy-E starch that exhibits elastic properties

CC with high viscosity useful for gels and pastes. The present invention  
CC describes inducing a mutation in a starch affecting locus of starch  
CC storage organ bearing plants and selecting propagative structures from  
CC the mutant plants in order to grow such plants and select and/or screen  
CC the starch storing organs. Accordingly, this method is useful for the  
CC production of plant starch used in food stuffs such as pies, puddings,  
CC soups, yogurts or sauces or for coatings and films in foodstuffs  
CC including batter. Furthermore, it provides a plant starch with unique  
CC cooking, thickening, and/or gelling properties that can be stained blue  
CC with iodine stain and exhibits a reduced amylose content compared to wild  
CC type. This polynucleotide sequence is the maize waxy-E starch EX385w-E1  
CC mutant DNA of the invention.

XX Sequence 2263 BP; 451 A; 699 C; 739 G; 374 T; 0 U; 0 Other;

Alignment Scores: 2.72e-22 Length: 2263  
Pred. No.: 333.00 Matches: 71  
Score: 333.00  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 11 Gaps: 1

US-10-628-525A-36 (1-74) x ADM77903 (1-2263)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 194 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCTGGCGCTGCCGGAC 253  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 254 GCGTCCACGCTTCGCGCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGCG 313  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 314 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 374 CGCGCGGGGGCAGG-----TTCCCGTCTGCTGCTGTGC 409

RESULT 6

ID ADM77902 standard; DNA; 2263 BP.

XX AC ADM77902;  
XX 03-JUN-2004 (first entry)  
DE Maize waxy-E starch EX385 DNA SeqID 1.  
XX maize; EX385w-E1; ds; plant; starch; waxy-E starch; gel; paste;  
KW starch storage organ; food stuff; coating; granule-bound starch synthase;  
KW GBSS; gene.

XX Zea mays.

XX Key Location/Qualifiers

XX CDS 194..2011

XX /\*tag= a

XX /product= "EX385 protein"

XX WO2003033540-A2.

XX 24-APR-2003.

XX 17-OCT-2002; 2002WO-US033122.

XX 17-OCT-2001; 2001US-0329525P.

XX (BADI ) BASF PLANT SCI GMBH.

XX Klucinec JD, Keeling PL, Commuri P, Chang M;

XX

DR WPI; 2003-481973/45.

XX P-PSDB; ADM77904.

XX Production of plant starch involves inducing mutation in starch affecting  
PT locus of starch storage organ bearing plants, selecting propagative  
PT structures, growing plants, and selecting and/or screening starch storing  
PT organs.

XX Example 13; SEQ ID NO 1; 181pp; English.

XX This invention relates to a novel method for producing a plant starch  
CC through mutagenesis. Specifically, it refers to the granule-bound starch  
CC synthase (GBSS) enzyme of waxy-E starch that exhibits elastic properties  
CC with high viscosity useful for gels and pastes. The present invention  
CC describes inducing a mutation in a starch affecting locus of starch  
CC storage organ bearing plants and selecting propagative structures from  
CC the mutant plants in order to grow such plants and select and/or screen  
CC the starch storing organs. Accordingly, this method is useful for the  
CC production of plant starch used in food stuffs such as pies, puddings,  
CC soups, yogurts or sauces or for coatings and films in foodstuffs  
CC including batter. Furthermore, it provides a plant starch with unique  
CC cooking thickening, and/or gelling properties that can be stained blue  
CC with iodine stain and exhibits a reduced amylose content compared to wild  
CC type. This polynucleotide sequence is the wild type maize waxy-E starch  
CC EX385 DNA of the invention.

XX Sequence 2263 BP; 450 A; 699 C; 740 G; 374 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.72e-22 Length: 2263  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 11 Gaps: 1

US-10-628-525A-36 (1-74) x ADM77902 (1-2263)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 194 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCTGGCGCTGCCGGAC 253  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 254 GCGTCCACGCTTCGCGCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGCG 313  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 314 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 374 CGCGCGGGGGCAGG-----TTCCCGTCTGCTGCTGTGC 409

RESULT 7

ID ADM7817

XX ADM7817 standard; DNA; 4627 BP.

XX AC ADM7817;

XX 07-APR-2005 (first entry)

XX Maize granule bound starch synthase (GBSS) gene, alternative form.

XX Seed oil; feedstuff; food; crop improvement; transgenic plant;  
KW granule bound starch synthase; plant; gene; ds.

XX Zea mays.

XX US2005005327-A1.

XX 06-JAN-2005.





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FT misc_feature 3570. .3572
FT            /*tag= kk
FT intron    /note= "target duplication site (Spm 18)"
FT            3682. .3792
FT            /*tag= ll
FT exon      3793. .3879
FT            /*tag= mm
FT intron    /number= 12
FT            3880. .3976
FT            /*tag= nn
FT exon      /number= 12
FT            3977. .4105
FT            /*tag= oo
FT intron    /number= 13
FT            4106. .4226
FT            /*tag= pp
FT exon      /number= 13
FT            4227. .4595
FT            /*tag= qq
FT polyA_signal /number= 14
FT            4570. .4575
FT polyA_signal /*tag= rr
FT            4593. .4598
FT polyA_signal /*tag= ss
FT            4597. .4602
FT            /*tag= tt
FT XX WO9814601-A1.
FT XX
FT XX 09-APR-1998.
FT XX
FT XX 30-SEP-1997; 97WO-US017555.
FT XX
FT XX 30-SEP-1996; 96US-0026855P.
FT XX
FT XX (EXSE-) EXSEED GENETICS LLC.

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XX Keeling P, Guan H;
XX WPI; 1998-240100/21.
XX P-PSDB; AAW56484.
XX Hybrid polypeptide comprising starch-encapsulating region and protein -
XX PT useful for, e.g. producing protein(s) resistant to degradation by stomach
XX PT acids.
XX Example 2; Page 29-31; 156pp; English.
XX The sequence is that of the waxy gene which codes for glucosyl
XX CC transferase. It can be used in the production of a hybrid polypeptide
XX CC comprising a starch-encapsulating region (SER) fused to a payload
XX CC protein. The hybrid polypeptide can be used to make modified starches
XX CC comprising the payload protein, selected from, e.g. hormones, growth
XX CC factors, antibodies, enzymes, dyes, immunoglobulins, etc. The modified
XX CC starch can also be used to provide grain feeds enriched in amino acids.
XX CC By encapsulating the payload protein in starch, it is more resistant to
XX CC degradation by stomach acids
XX SQ Sequence 4800 BP; 935 A; 1414 C; 1446 G; 1005 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.03e-22 Length: 4800
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 2 Gaps: 1

US-10-628-525A-36 (1-74) x AAV29752 (1-4800)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 1233 ATGGCGGCTCTGGCCACGTCGCGAGCTCTGCGCAACGCGCGCGCTGGCGCTCCCGGAC 1292

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40
DB 1293 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGGCCCGGGCTCGCGGCG 1352

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 60
DB 1353 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 1413 CGCCGCGGGGGCAGG-----TTCCGCTCGCTCGTGTGC 1448

RESULT 9
ABX09931
ID ABX09931 standard; DNA; 4800 BP.
XX
AC ABX09931;
XX
DT 17-FEB-2003 (first entry)
XX
DE DNA encoding maize granule bound starch synthase (GBSS).
XX
KW Starch; starch synthase; glucan association domain; GLASS; linker domain;
KW LINKR; glucosyl transferase domain; GLYTR; C-terminal end; CTEND;
KW granule bound starch synthase; GBSS; morphology; retrogradation;
KW waterbinding; swelling potential; gene; ds.
XX
OS Zea mays.
XX
PN WO200279410-A2.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009574.
XX

```



FT /number= 11  
PT 3977. .4105  
FT /\*tag= x  
FT /number= 12  
FT 4106. .4226  
FT /\*tag= y  
FT /number= 12  
FT 4227. .4343  
FT /\*tag= z  
FT /number= 13  
XX WO2003033540-A2.  
XX 24-APR-2003.  
XX 17-OCT-2002; 2002WO-US033122.  
XX 17-OCT-2001; 2001US-0329525P.  
XX (BADI ) BASF PLANT SCI GMBH.  
XX Klucinec JD, Keeling PL, Commuri P, Chang M;  
XX WPI; 2003-481973/45.  
XX P-PSDB; ADM77907.  
XX Production of plant starch involves inducing mutation in starch affecting  
PT locus of starch storage organ bearing plants, selecting propagative  
PT structures, growing plants, and selecting and/or screening starch storing  
PT organs.  
XX Example 13; SEQ ID NO 5; 181pp; English.  
XX This invention relates to a novel method for producing a plant starch  
CC through mutagenesis. Specifically, it refers to the granule-bound starch  
CC synthase (GBSS) enzyme of waxy-E starch that exhibits elastic properties  
CC with high viscosity useful for gels and pastes. The present invention  
CC describes inducing a mutation in a starch affecting locus of starch  
CC storage organ bearing plants and selecting propagative structures from  
CC the mutant plants in order to grow such plants and select and/or screen  
CC the starch storing organs. Accordingly, this method is useful for the  
CC production of plant starch used in food stuffs such as pies, puddings,  
CC soups, yogurts or sauces or for coatings and films in foodstuffs  
CC including batter. Furthermore, it provides a plant starch with unique  
CC cooking, thickening, and/or gelling properties that can be stained blue  
CC with iodine stain and exhibits a reduced amylose content compared to wild  
CC type. This polynucleotide sequence is the maize GBSS DNA of the  
XX invention.  
XX Sequence 4800 BP; 935 A; 1413 C; 1447 G; 1005 T; 0 U; 0 Other;  
SQ Alignment Scores:  
Pred. No.: 6,03e-22 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservatives: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 11 Gaps: 1  
US-10-628-525A-36 (1-74) x ADM77906 (1-4800)  
QY 1 MetaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1233 ATGGCGGCTCTGGCCACGTCGAGCTCGTCGCAACGCGCGCGCTGGCGTCCGGAC 1292  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
DB 1293 GGGTCACAGTTCGCGCGCGCGCGCGCGCGCTGAGGGGCGCGCGCGCGCGG 1352  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 1353 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412

QY 61 ArgArgGlyGlyArgPhePropSerLeuValValCys 74  
DB 1413 CGCGCGCGCGCGCAGG-----TTCCCGTGGCTCGTGGTGGC 1448  
RESULT 11  
ADX34893  
ID ADX34893 standard; cDNA; 1406 BP.  
XX AC ADX34893;  
XX 21-APR-2005 (first entry)  
XX Plant full length insert polynucleotide seqid 17713.  
XX plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX Unidentified.  
XX US2004034888-A1.  
XX 19-FEB-2004.  
XX 28-APR-2003; 2003US-00425114.  
XX 06-MAY-1999; 99US-00304517.  
XX 05-NOV-2001; 2001US-00985678.  
XX (LIU/) LIU J.  
XX (ZHOU/) ZHOU Y.  
XX (KOVA/) KOVALIC D K.  
XX (SCRE/) SCREEN S E.  
XX (TABA/) TABASKA J E.  
XX (CAOV/) CAO Y.  
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX Claim 1; SEQ ID NO 17713; 15pp; English.  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
XX invention.  
XX Sequence 1406 BP; 275 A; 468 C; 457 G; 206 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 7,63e-22 Length: 1406  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservatives: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 13 Gaps: 1

US-10-628-525A-36 (1-74) x ADX34893 (1-1406)

QY 1 MetaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20  
Db 172 ATGGGGGCTCTGGCCACGTCGAGCTCGTCGCAACGCCCGCGGCTGGCGCTCCCGGAC 231  
QY 21 AlaSerThrPheArgGlyAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 232 GGTTCACGTTCCGGCGCGCCCGCGAGGCCCTGAGGGGGGCCCGCGCTCGCGGGCG 291  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 292 GCGGACACGCTCAGCATCGGACCGAGCGCGCGCGCGCGCCAGGACACGAGCAGGCGG 351  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 352 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTC 387

RESULT 12  
ADX33821  
ID ADX33821 standard; cDNA; 1409 BP.  
XX  
AC ADX33821;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 16641.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
XX  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAJ/) TABASKA J E.  
PA (CAOY/) CAO Y.  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX  
XX WPI; 2004-180133/17.  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
XX Claim 1; SEQ ID NO 16641; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 1409 BP; 275 A; 470 C; 458 G; 206 T; 0 U; 0 Other;  
XX

Alignment Scores:  
Pred. No.: 7,65e-22 Length: 1409  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservatives: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 13 Gaps: 1

US-10-628-525A-36 (1-74) x ADX33821 (1-1409)

QY 1 MetaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20  
Db 175 ATGGCGGCTCTGGCCACGTCGAGCTCGTCGCAACGCCCGCGGCTGGCGCTCCCGGAC 234  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 235 GGTTCACGTTCCGGCGCGCCCGCGAGGCCCTGAGGGGGGCCCGCGCTCGCGGGCG 294  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 295 GCGGACACGCTCAGCATCGGACCGAGCGCGCGCGCGCCAGGACACGAGCAGGCGG 354  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 355 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTC 390

RESULT 13  
ADX36735  
ID ADX36735 standard; cDNA; 1416 BP.  
XX  
AC ADX36735;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 19555.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX

PF 28-APR-2003; 2003US-00425114.  
XX 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX (LIUJ//) LIU J.  
PA (ZHOU//) ZHOU Y.  
PA (KOVA//) KOVALIC D K.  
PA (SCRE//) SCREEN S E.  
PA (TABA//) TABASKA J E.  
PA (CAOY//) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 19555; 15pp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.secdatas.uspto.gov/sequence.html?docID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
XX Sequence 1416 BP; 275 A; 471 C; 463 G; 207 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 7.69e-22 Length: 1416  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 13 Gaps: 1  
US-10-628-525A-36 (1-74) x ADX36735 (1-1416)  
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 173 ATGGCGGCTGTGGCCACGTGCGAGCTGTCGCAACGCCGCCGCGCTGGCGTCCCGGAC 232  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValAlaArgAlaSerAlaAla 40  
Db 233 GCGTCCACGTTCG 292  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 293 GCGGACACGCTCAGCATGCGGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 352  
QY 61 ArgArgGlyGlyValGlyPheProPheProSerLeuValValCys 74  
Db 353 CGCCG 388  
RESULT 14  
ACC44559  
ID ACC44559 standard; cDNA; 1818 BP.

XX ACC44559;  
XX 02-JUN-2003 (first entry)  
XX Maize granule-bound starch synthase encoding cDNA SEQ ID NO:7.  
XX Self-processing plant; plant; processing enzyme; alpha-amylase; grain;  
XX pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase;  
XX mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;  
XX maltodextrin; ethanol; fermentation; beverage; enzyme; gene; ss.  
XX Zea mays.  
XX Key Location/Qualifiers  
XX CDS 1..1818  
XX FT /\*tag= a  
XX FT /partial  
XX FT /product= "granule-bound starch synthase (waxy)"  
XX FT /note= "no stop codon given"  
XX  
XX WO2003018766-A2.  
XX  
XX 06-MAR-2003.  
XX 27-AUG-2002; 2002WO-US027129.  
XX 27-AUG-2001; 2001US-0315281P.  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX Lanahan MB, Basu SS, Batie CJ, Chen W, Craig J, Kinkema M;  
XX WPI; 2003-268420/26.  
XX P-PSDB; ABP96605.  
XX Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.  
XX alpha-amylase, useful for producing plant to produce food products having  
XX improved taste or fermentable substrates for ethanol.  
XX  
XX Example 2; Page 90-91; 158pp; English.  
XX  
XX The present invention describes polynucleotides which encode processing  
XX enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose  
XX isomerase, or glucoamylase) that are optimised for expression in plants.  
XX The polynucleotides encode mesophilic, thermophilic or hyperthermophilic  
XX processing enzymes, which are activated under suitable conditions to act  
XX upon the desired substrate. Also described are self-processing transgenic  
XX plants and plant parts, e.g. grain, which express one or more of these  
XX enzymes and have an altered composition that facilitates plant and grain  
XX processing. Also described is a method (M) for converting starch to  
XX starch-derived products in a transformed plant part (TPP), by activating  
XX the starch processing enzyme contained in it. Transgenic grain is useful  
XX for preparing maltodextrin. A transformed plant (TP) can be used to  
XX produce food products having improved taste and to produce fermentable  
XX substrates for ethanol and fermented beverages. (M) eliminates the need  
XX to mill or physically disrupt the integrity of plant parts prior to  
XX recovery of starch-derived products. The present sequence encodes maize  
XX granule-bound starch synthase (waxy), which is given in the  
XX exemplification of the present invention  
SQ Sequence 1818 BP; 346 A; 596 C; 609 G; 267 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 8.02e-21 Length: 1818  
Score: 316.50 Matches: 70  
Percent Similarity: 93.3% Conservative: 0  
Best Local Similarity: 93.3% Mismatches: 2  
Query Match: 86.0% Indels: 3  
DB: 8 Gaps: 2  
US-10-628-525A-36 (1-74) x ACC44559 (1-1818)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1 ATGGCGGCTCTGGCCACGTCGAGCTCGTCGCAACGCGCGCCGCTGGCGCTCCCGGAC 60  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaSerAlaAla 40  
DB 61 GCGTCCACGTTCCGCGCGCGCGCGCGAGGCTCGAGGGGGCGCGCGGCTCGCGGCG 120  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln---GlnGln 59  
DB 121 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
QY 60 AlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 181 GCGGCGCGCGGGGCCAGG-----TTCCCGTCTGCTGTGTGC 219  
RESULT 15  
ADW87804  
ID ADW87804 standard; DNA; 4207 BP.  
XX ADW87804;  
XX  
DT 07-APR-2005 (first entry)  
DE Corn inbred line LH59 granule bound starch synthase (GBSS) DNA.  
KW Seed oil; feedstuff; food; crop improvement; transgenic plant;  
KW granule bound starch synthase; plant; ds.  
XX  
OS Zea mays.  
XX  
PN US2005005327-A1.  
XX  
PD 06-JAN-2005.  
XX  
PF 25-JUN-2004; 2004US-00877645.  
XX  
PR 27-JUN-2003; 2003US-0483491P.  
XX  
PA (RAVA/) RAVANELLO M P.  
PA (FOLE/) FOLEY T J.  
PA (LEDE/) LEDEUX J R.  
PA (WYRI/) WYRICK A E.  
PA (SAVA/) SAVAGE T J.  
XX  
PI Ravanello MP, Foley TJ, Ledeaux JR, Wyrick AE, Savage TJ;  
DR WPI; 2005-065279/07.  
XX  
PT New purified HOI001 granule bound starch synthase nucleic acid, useful  
PT for increasing oil levels in maize plants or for creating maize plants  
PT that include the nucleic acids.  
XX  
PS Example 1; SEQ ID NO 7; 74pp; English.  
XX  
CC The invention relates to HOI001 granule bound starch synthase (GBSS)  
CC nucleic acid and its protein sequence. The invention also relates to a  
CC method for increasing oil levels in corn kernel tissue by expression of  
CC an HOI001 GBSS allele. The GBSS nucleic acid is useful for increasing oil  
CC levels in maize plants and creating maize plants that include the nucleic  
CC acids. The present sequence is the corn inbred line LH59 GBSS DNA. Note:  
CC This sequence is said to encode seqid:8, however this does not appear to  
CC be the case.  
XX  
SQ Sequence 4207 BP; 805 A; 1282 C; 1299 G; 821 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: Length: 4207  
Score: 316.50 Matches: 70  
Percent Similarity: 93.3% Conservative: 0  
Best Local Similarity: 93.3% Mismatches: 2  
Query Match: 86.0% Indels: 3  
DB: 14 Gaps: 2

US-10-628-525A-36 (1-74) x ADW87804 (1-4207)  
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1130 ATGGCGGCTCTGGCCACGTCGAGCTCGTCGCAACGCGCGCGCTGGCGCTCCCGGAC 1189  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaSerAlaAla 40  
DB 1190 GCGTCCACGTTCCGCGCGCGCGCGAGGCTCGAGGGGGCGCGCGGCTCGCGGCG 1249  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln---GlnGln 59  
DB 1250 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCG 1309  
QY 60 AlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 1310 GCGCGCGCGGGGCCAGG-----TTCCCGTCTGCTGTGTGC 1348  
RESULT 16  
ADW87808  
ID ADW87808 standard; DNA; 1863 BP.  
XX ADW87808;  
XX  
DT 07-APR-2005 (first entry)  
DE Corn line HOI001 GBSS cDNA coding region.  
XX  
KW Seed oil; feedstuff; food; crop improvement; transgenic plant;  
KW granule bound starch synthase; plant; gene; ss.  
XX  
OS Zea mays.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1863  
FT /tag= a  
FT /product= "Corn line HOI001 granule bound starch synthase  
FT (GBSS)"  
XX  
US2005005327-A1.  
XX  
PN 06-JAN-2005.  
XX  
PD 25-JUN-2004; 2004US-00877645.  
XX  
PF 27-JUN-2003; 2003US-0483491P.  
XX  
PA (RAVA/) RAVANELLO M P.  
PA (FOLE/) FOLEY T J.  
PA (LEDE/) LEDEUX J R.  
PA (WYRI/) WYRICK A E.  
PA (SAVA/) SAVAGE T J.  
XX  
PI Ravanello MP, Foley TJ, Ledeaux JR, Wyrick AE, Savage TJ;  
DR WPI; 2005-065279/07.  
XX  
PT P-PSDB; ADW87800.  
XX  
PT New purified HOI001 granule bound starch synthase nucleic acid, useful  
PT for increasing oil levels in maize plants or for creating maize plants  
PT that include the nucleic acids.  
XX  
PS Claim 1; SEQ ID NO 11; 74pp; English.  
XX  
CC The invention relates to HOI001 granule bound starch synthase (GBSS)  
CC nucleic acid and its protein sequence. The invention also relates to a  
CC method for increasing oil levels in corn kernel tissue by expression of  
CC an HOI001 GBSS allele. The GBSS nucleic acid is useful for increasing oil  
CC levels in maize plants and creating maize plants that include the nucleic  
CC acids. The present sequence is the corn line HOI001 GBSS cDNA coding  
XX region.

SQ Sequence 1863 BP; 355 A; 596 C; 614 G; 298 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 7.36e-20 Length: 1863  
Score: 306.50 Matches: 69  
Percent Similarity: 87.3% Conservative: 0  
Best Local Similarity: 87.3% Mismatches: 3  
Query Match: 83.3% Indels: 7  
DB: 14 Gaps: 2

US-10-628-525A-36 (1-74) x ADM87808 (1-1863)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCCGCTGGGGCGTCCCGGAC 60

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 61 GCGTCCACGTTCCG 120

QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArg----- 55  
DB 121 GCGGACACGCTCAGCATGCGGACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

QY 56 HisGlnGlnGlnAlaArgArgGlyArgPheProPheProSerLeuValValCys 74  
DB 181 CAGCAGCAGCAGCG 231

RESULT 17  
ADM87815  
ID ADM87815 standard; DNA; 4442 BP.  
XX ADM87815;  
AC  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Corn line HO1001 granule bound starch synthase gene, alternative form.  
XX  
KW Seed oil; feedstuff; food; crop improvement; transgenic plant;  
KW granule bound starch synthase; plant; gene; ds.  
XX  
OS Zea mays.  
XX  
XX  
PN US2005005327-A1.  
XX  
XX  
PD 06-JAN-2005.  
XX  
PF 25-JUN-2004; 2004US-00877645.  
XX  
PR 27-JUN-2003; 2003US-0483491P.  
XX  
PA (RAVA/) RAVANELLO M P.  
PA (FOLE/) FOLEY T J.  
PA (LEDE/) LEDEUX J R.  
PA (WYRI/) WYRICK A E.  
PA (SAVA/) SAVAGE T J.  
XX  
XX  
PI Ravanello MP, Foley TJ, Ledoux JR, Wyrick AE, Savage TJ;  
XX WPI; 2005-065279/07.  
XX  
DR  
XX  
XX  
PT New purified HO1001 granule bound starch synthase nucleic acid, useful  
PT for increasing oil levels in maize plants or for creating maize plants  
PT that include the nucleic acids.  
XX  
XX  
PS Claim 1; Fig 1; 74pp; English.  
XX  
CC The invention relates to HO1001 granule bound starch synthase (GBSS)  
CC nucleic acid and its protein sequence. The invention also relates to a  
CC method for increasing oil levels in corn kernel tissue by expression of  
CC an HO1001 GBSS allele. The GBSS nucleic acid is useful for increasing oil  
CC levels in maize plants and creating maize plants that include the nucleic  
CC acids. The present sequence is the corn line HO1001 GBSS gene,  
CC

CC alternative form. Note: This sequence is stated to be similar to the  
CC sequence shown as seqid:1 in the sequence listing, but these sequences  
CC differ.  
XX  
SQ Sequence 4442 BP; 877 A; 1300 C; 1350 G; 915 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.84e-19 Length: 4442  
Score: 306.50 Matches: 69  
Percent Similarity: 87.3% Conservative: 0  
Best Local Similarity: 87.3% Mismatches: 3  
Query Match: 83.3% Indels: 7  
DB: 14 Gaps: 2

US-10-628-525A-36 (1-74) x ADM87815 (1-4442)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1127 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCCGCTGGGGCGTCCCGGAC 1186

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 1187 GCGTCCACGTTCCG 1246

QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArg----- 55  
DB 1247 GCGGACACGCTCAGCATGCGGACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1306

QY 56 HisGlnGlnGlnAlaArgArgGlyArgPheProPheProSerLeuValValCys 74  
DB 1307 CAGCAGCAGCAGCG 1357

RESULT 18  
ADM87798  
ID ADM87798 standard; DNA; 4470 BP.  
XX ADM87798;  
AC  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Corn line HO1001 granule bound starch synthase (GBSS) gene.  
XX  
KW Seed oil; feedstuff; food; crop improvement; transgenic plant;  
KW granule bound starch synthase; single nucleotide polymorphism; SNP;  
KW SNP detection; plant; gene; ds.  
XX  
OS Zea mays.  
XX  
XX  
FH Key  
FT variation  
FT Location/Qualifiers  
FT replace(158,T)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism"  
FT replace(343,A)  
FT /\*tag= b  
FT /standard\_name= "Single nucleotide polymorphism"  
FT replace(349,A)  
FT /\*tag= c  
FT /standard\_name= "Single nucleotide polymorphism"  
FT replace(441,A)  
FT /\*tag= d  
FT /standard\_name= "Single nucleotide polymorphism"  
FT replace(1450,A)  
FT /\*tag= e  
FT /standard\_name= "Single nucleotide polymorphism"  
FT replace(1709,C)  
FT /\*tag= f  
FT /standard\_name= "Single nucleotide polymorphism"  
FT replace(1761,T)  
FT /\*tag= g  
FT /standard\_name= "Single nucleotide polymorphism"  
FT replace(1836,A)  
FT /\*tag= h  
FT /standard\_name= "Single nucleotide polymorphism"  
FT

[illegible]





PF 01-JUN-2001; 2001WO-US017672.  
 XX  
 PR 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 PR 27-MAR-2001; 2001US-00818875.  
 XX  
 PA (UYDE ) UNIV DELAWARE.  
 XX  
 XX Kmiec EB, Gamper HB, Rice MC, Kim J;  
 XX WPI; 2002-106307/14.  
 DR  
 XX  
 XX New oligonucleotides with modified nuclease-resistant termini, useful for  
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.  
 XX  
 XX Claim 7; Page 165; 220pp; English.  
 PS  
 XX The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an RNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 XX altering oligonucleotide of the invention  
 XX  
 SQ Sequence 121 BP; 15 A; 48 C; 50 G; 8 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2.3e-09 Length: 121  
 Score: 183.00 Matches: 38  
 Percent Similarity: 97.4% Conservative: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 49.7% Indels: 0  
 DB: 6 Gaps: 0  
 US-10-628-525A-36 (1-74) x ABK26693 (1-121)  
 QY 19 ProAspAlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaArgAlaSer 38  
 Db 3 CGGACGCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTAG 62  
 QY 39 AlaAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57  
 Db 63 GCGGCGGCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCAG 119  
 RESULT 22  
 ADN45385/c  
 ID ADN45385 standard; DNA; 121 BP.  
 XX  
 AC ADN45385;  
 XX  
 XX 15-JUL-2004 (first entry)  
 DT  
 XX Mutant cell identification-related mutagenic oligonucleotide SeqID2054.  
 DE  
 XX cell identification; oligonucleotide-directed sequence alteration;  
 KW

KW selectable phenotype; transgenic plant; herbicide resistance;  
 KW sterile plant; abiotic stress tolerance; albino plant;  
 KW amino acid production; ss.  
 XX  
 OS Zea mays.  
 OS Synthetic.  
 XX  
 PN WO2004033708-A2.  
 XX  
 XX 22-APR-2004.  
 PD  
 XX  
 XX 07-OCT-2003; 2003WO-US031862.  
 PF  
 XX 07-OCT-2002; 2002US-0416983P.  
 PR  
 PR 07-MAR-2003; 2003US-0453360P.  
 XX  
 XX (UYDE ) UNIV DELAWARE.  
 PA  
 PA (NAPR-) NAPRO BIO THERAPEUTICS INC.  
 XX  
 XX Kmiec EB, Van Brabant A;  
 PI  
 XX WPI; 2004-340941/31.  
 DR  
 XX  
 XX Identifying a cell with a desired oligonucleotide-directed sequence  
 PT alteration at a nucleic acid target site within the cell by identifying  
 PT the desired sequence alteration in cells selected for the presence of a  
 PT selectable phenotype.  
 XX  
 XX Example 28; SEQ ID NO 2054; 303pp; English.  
 PS  
 XX This invention relates to a novel method of identifying a cell having a  
 CC desired oligonucleotide-directed sequence alteration at a first nucleic  
 CC acid target site within the cell. The method comprises identifying the  
 CC desired sequence alteration in cells that have been selected for the  
 CC presence of a selectable phenotype conferred by a concurrent  
 CC oligonucleotide-directed sequence alteration at a second nucleic acid  
 CC target site within the cells. The method is useful in identifying a cell  
 CC having a desired oligonucleotide-directed sequence alteration at a first  
 CC nucleic acid target site within the cell. The method may be useful for  
 CC the production of plants with herbicide resistance, male or female  
 CC sterile plants, abiotic stress tolerance, albino plants or plants with  
 CC altered amino acid production as well as for use in mammalian cell lines.  
 CC The present example is that of a mutagenic oligonucleotide which was  
 CC used in the exemplification of the invention.  
 XX  
 SQ Sequence 121 BP; 8 A; 50 C; 48 G; 15 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2.3e-09 Length: 121  
 Score: 183.00 Matches: 38  
 Percent Similarity: 97.4% Conservative: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 49.7% Indels: 0  
 DB: 12 Gaps: 0  
 US-10-628-525A-36 (1-74) x ADN45385 (1-121)  
 QY 19 ProAspAlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaArgAlaSer 38  
 Db 119 CGGACGCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTAG 60  
 QY 39 AlaAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57  
 Db 59 GCGGCGGCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCAG 3  
 RESULT 23  
 ADN45384  
 ID ADN45384 standard; DNA; 121 BP.  
 XX  
 AC ADN45384;  
 XX  
 XX 15-JUL-2004 (first entry)  
 DT  
 XX

DE Mutant cell identification-related mutagenic oligonucleotide SeqID2053.  
 XX cell identification; oligonucleotide-directed sequence alteration;  
 KW selectable phenotype; transgenic plant; herbicide resistance;  
 KW sterile plant; abiotic stress tolerance; albino plant;  
 KW amino acid production; ss.  
 OS Zea mays.  
 OS Synthetic.  
 XX WO2004033708-A2.  
 PN 22-APR-2004.  
 PD 07-OCT-2003; 2003WO-US031862.  
 XX 07-OCT-2002; 2002US-0416983P.  
 PR 07-MAR-2003; 2003US-0453360P.  
 XX (UYDE ) UNIV DELAWARE.  
 PA (NAPR-) NAPRO BIO THERAPEUTICS INC.  
 XX Kmiec EB, Van Brabant A;  
 XX WPI; 2004-340941/31.  
 DR Identifying a cell with a desired oligonucleotide-directed sequence  
 PT alteration at a nucleic acid target site within the cell by identifying  
 PT the desired sequence alteration in cells selected for the presence of a  
 PT selectable phenotype.  
 XX Example 28; SEQ ID NO 2053; 303pp; English.  
 PS This invention relates to a novel method of identifying a cell having a  
 XX desired oligonucleotide-directed sequence alteration at a first nucleic  
 CC acid target site within the cell. The method comprises identifying the  
 CC desired sequence alteration in cells that have been selected for the  
 CC presence of a selectable phenotype conferred by a concurrent  
 CC oligonucleotide-directed sequence alteration at a second nucleic acid  
 CC target site within the cells. The method is useful in identifying a cell  
 CC having a desired oligonucleotide-directed sequence alteration at a first  
 CC nucleic acid target site within the cell. The method may be useful for  
 CC the production of plants with herbicide resistance, male or female  
 CC sterile plants, abiotic stress tolerance, albino plants or plants with  
 CC altered amino acid production as well as for use in mammalian cell lines.  
 CC The present sequence is that of a mutagenic oligonucleotide which was  
 CC used in the exemplification of the invention.  
 XX SQ Sequence 121 BP; 15 A; 48 C; 50 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2.3e-09 Length: 121  
 Score: 183.00 Matches: 38  
 Percent Similarity: 97.4% Conservatives: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 49.7% Indels: 0  
 DB: 12 Gaps: 0

US-10-628-525A-36 (1-74) x ADN45384 (1-121)

QY 19 ProApsAlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSer 38  
 Db 3 CCGGACGCGCTCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTAG 62  
 QY 39 AlaAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57  
 Db 63 GCGCGCGCGCGACACGCTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGAC 119

RESULT 24  
 ABK26690/c  
 ID ABK26690 standard; DNA; 121 BP.  
 XX  
 AC ABK26690;

XX 09-APR-2002 (first entry)  
 DT Waxy starch production genome altering oligonucleotide #346.  
 DE Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 XX o-methyl modification; LNA modification; phosphorothioate linkage;  
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
 KW abiotic stress tolerance; improved nutritional value; hygromycin-B;  
 KW amino acid over production; herbicide resistance; glyphosate resistance;  
 KW imidazolinone herbicide resistance; herbicide resistance; sulphonylurea herbicide resistance;  
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KW modified oil production; modified starch production; waxy starch;  
 KW altered floral morphology; male-sterile plant; albino mutant;  
 KW modified fatty acid content; reduced palmitate production; albino plant;  
 KW increased stearate production; reduced linolenic acid production;  
 KW photosynthetic process.  
 XX Zea mays.  
 OS Synthetic.  
 OS WO200192512-A2.  
 PN 06-DEC-2001.  
 PD 01-JUN-2001; 2001WO-US017672.  
 XX 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 PR 27-MAR-2001; 2001US-00818875.  
 XX (UYDE ) UNIV DELAWARE.  
 PA Kmiec EB, Gamper HB, Rice MC, Kim J;  
 XX WPI; 2002-106307/14.  
 DR New oligonucleotides with modified nuclease-resistant termini, useful for  
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.  
 XX Claim 7; Page 165; 220pp; English.  
 PS The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 XX SQ Sequence 121 BP; 11 A; 52 C; 46 G; 12 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.33e-08 Length: 121  
 Score: 175.00 Matches: 38  
 Percent Similarity: 95.0% Conservatives: 0

```
Best Local Similarity: 95.0%
Query Match: 47.6%
DB: 6
Mismatches: 2
Indels: 0
Gaps: 0
```

US-10-628-525A-36 (1-74) x ABK26690 (1-121)

Qy	10	ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgHrgGlyAlaLa	29
Db	121	GTGCGAACGGCGCCGGGCTGTGGCGTGTCCCGACGCGCTCCACGTTCGCGCGGGCGCCGCG	62
Qy	30	GlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSer	49
Db	61	TAGGGGCTGAGGGGGCCCGGGCGTTCGGCGGGGGCGGACACGCTCAGCATGCGGACCAAGC	2

## RESULT 25

ABK26689  
ID ABK26689 standard; DNA: 121 BP.

AC ABK26689;

09-APR-2002 (first entry)

DE Waxy starch production genome altering oligonucleotide #345.

Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
O-methyl modification; LNA modification; phosphorothioate linkage;  
DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
abiotic stress tolerance; improved nutritional value; hygromycin; primer;  
amino acid over production; herbicide resistance; glyphosate resistance;  
imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
porphyrin herbicide resistance; triazine resistance; disease resistance;  
modified oil production; modified starch production; waxy starch;  
altered floral morphology; male-sterile plant; albino mutant;  
modified fatty acid content; reduced palmitate production; albino plant;  
increased stearate production; reduced linolenic acid production;  
photosynthetic process.

OS Zea mays.  
OS Synthetic.

AA  
PN  
WO200192512-A2.

06-DEC-2001.

01-JUN-2001: 2001WO-US017672.

PR 01-JUN-2000; 2000US-0208538P.

20-DEC-2000; 2000US-0244383E;  
PR 27-MAR-2001; 2001US-00818875;

PA (UYDE ) UNIV DELAWARE.

PI Kmiec EB, Gamper HB,

DR WPI; 2002-106307/14.

New oligonucleotides

PT nutritional value, herbicide or disease resistance, or modified oil production.

PS Claim 7: Page 165: 220pp: English.

The invention relates to an oligonucleotide for targeted alteration of a genetic sequence, which comprises a single-stranded oligonucleotide having a DNA domain. The DNA domain has at least one mismatch with respect to the genetic sequence to be altered and further comprises chemical modifications of the oligonucleotide. The chemical modifications consist of o-methyl modification, an LNA modification, two or more phosphorothioate linkages on a terminus, or a combination of any two or more of these modifications. The oligonucleotides are useful for directing repair or alteration of plant genetic information. The oligonucleotides are particularly useful for creating plants with desired

XX This invention relates to a novel method of identifying a cell having a  
 CC desired oligonucleotide-directed sequence alteration at a first nucleic  
 CC acid target site within the cell. The method comprises identifying the  
 CC desired sequence alteration in cells that have been selected for the  
 CC presence of a selectable phenotype conferred by a concurrent  
 CC oligonucleotide-directed sequence alteration at a second nucleic acid  
 CC target site within the cells. The method is useful in identifying a cell  
 CC having a desired oligonucleotide-directed sequence alteration at a first  
 CC nucleic acid target site within the cell. The method may be useful for  
 CC the production of plants with herbicide resistance, male or female  
 CC sterile plants, abiotic stress tolerance, albino plants or plants with  
 CC altered amino acid production as well as for use in mammalian cell lines.  
 CC The present sequence is that of a mutagenic oligonucleotide which was  
 CC used in the exemplification of the invention.

SQ Sequence 121 BP; 11 A; 52 C; 46 G; 12 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.33e-08 Length: 121  
 Score: 175.00 Matches: 38  
 Percent Similarity: 95.0% Conservative: 0  
 Best Local Similarity: 95.0% Mismatches: 2  
 Query Match: 47.6% Indels: 0  
 DB: 12 Gaps: 0

US-10-628-525A-36 (1-74) x ADM45381 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAla 29  
 DB 121 GTGCAAGCGCGCGCGCGCTGGGGCGTCCCGACGCGTCCACGTTCCCGCGCGCGCG 62  
 QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSer 49  
 DB 61 TAGGGCTGTAGGGGGGCGCGCGCGTCCGGCGCGGACACACGCTCAGCATGCGGACCG 2

#### RESULT 27

ADM45380  
 ID ADM45380 standard; DNA; 121 BP.

AC ADM45380;

DT 15-JUL-2004 (first entry)

XX Mutant cell identification-related mutagenic oligonucleotide SeqID2049.

DE cell identification; oligonucleotide-directed sequence alteration;  
 KW selectable phenotype; transgenic plant; herbicide resistance;  
 KW sterile plant; abiotic stress tolerance; albino plant;  
 KW amino acid production; ss.

XX Zea mays.  
 OS Synthetic.

XX WO2004033708-A2.

XX 22-APR-2004.

XX 07-OCT-2003; 2003WO-US031862.

XX 07-OCT-2002; 2002US-0416983P.

XX 07-MAR-2003; 2003US-0453360P.

XX (UYDE ) UNIV DELAWARE.

PA (NAPR-) NAPRO BIO THERAPEUTICS INC.

XX Kmiec EB, Van Brabant A;

XX WPI; 2004-340941/31.

XX Identifying a cell with a desired oligonucleotide-directed sequence  
 PT alteration at a nucleic acid target site within the cell by identifying  
 PT the desired sequence alteration in cells selected for the presence of a

#### selectable phenotype.

XX Example 28; SEQ ID NO 2049; 303pp; English.

XX This invention relates to a novel method of identifying a cell having a  
 CC desired oligonucleotide-directed sequence alteration at a first nucleic  
 CC acid target site within the cell. The method comprises identifying the  
 CC desired sequence alteration in cells that have been selected for the  
 CC presence of a selectable phenotype conferred by a concurrent  
 CC oligonucleotide-directed sequence alteration at a second nucleic acid  
 CC target site within the cells. The method is useful in identifying a cell  
 CC having a desired oligonucleotide-directed sequence alteration at a first  
 CC nucleic acid target site within the cell. The method may be useful for  
 CC the production of plants with herbicide resistance, male or female  
 CC sterile plants, abiotic stress tolerance, albino plants or plants with  
 CC altered amino acid production as well as for use in mammalian cell lines.  
 CC The present sequence is that of a mutagenic oligonucleotide which was  
 CC used in the exemplification of the invention.

SQ Sequence 121 BP; 12 A; 46 C; 52 G; 11 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.33e-08 Length: 121  
 Score: 175.00 Matches: 38  
 Percent Similarity: 95.0% Conservative: 0  
 Best Local Similarity: 95.0% Mismatches: 2  
 Query Match: 47.6% Indels: 0  
 DB: 12 Gaps: 0

US-10-628-525A-36 (1-74) x ADM45380 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAla 29

DB 1 GTGCAAGCGCGCGCGCGCTGGGGCGTCCCGACGCGTCCACGTTCCCGCGCGCGCG 60

QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSer 49

DB 61 TAGGGCTGTAGGGGGGCGCGCGCGTCCGGCGCGGACACACGCTCAGCATGCGGACCG 120

#### RESULT 28

ABK26698/C

ID ABK26698 standard; DNA; 121 BP.

XX ABK26698;

XX 09-APR-2002 (first entry)

XX Waxy starch production genome altering oligonucleotide #354.

DE Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KW o-methyl modification; LNA modification; phosphorothioate linkage;  
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
 KW abiotic stress tolerance; improved nutritional value; hygromycin-B;  
 KW amino acid over production; herbicide resistance; glyphosate resistance;  
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KW modified oil production; modified starch production; waxy starch;  
 KW altered floral morphology; male-sterile plant; albino mutant;  
 KW modified fatty acid content; reduced palmitate production; albino plant;  
 KW increased stearate production; reduced linolenic acid production;  
 KW photosynthetic process.

XX Zea mays.

OS Synthetic.

XX WO200192512-A2.

XX 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.

XX 30-OCT-2000; 2000US-0244989P.



QY 57 GlnGlnGlnAlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 61 TAGCAGCAGGCGCGCGCGGGGAGG-----TTCCCGTGGCTCGTGTGTC 108

RESULT 30  
ADN45388  
ID ADN45388 standard; DNA; 121 BP.  
XX  
AC ADN45388;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Mutant cell identification-related mutagenic oligonucleotide SeqID2057.  
XX  
KW cell identification; oligonucleotide-directed sequence alteration;  
KW selectable phenotype; transgenic plant; herbicide resistance;  
KW sterile plant; abiotic stress tolerance; albino plant;  
KW amino acid production; ss.  
XX  
OS Zea mays.  
OS Synthetic.  
XX  
PN WO2004033708-A2.  
XX  
PD 22-APR-2004.  
XX  
PF 07-OCT-2003; 2003WO-US031862.  
XX  
PR 07-OCT-2002; 2002US-0416983P.  
PR 07-MAR-2003; 2003US-0453360P.  
XX  
PX (UYDE ) UNIV DELAWARE.  
PA (NAPR-) NAPRO BIO THERAPEUTICS INC.  
XX  
PI Kmiec EB, Van Brabant A;  
XX  
WPI; 2004-340941/31.  
XX  
PT Identifying a cell with a desired oligonucleotide-directed sequence  
PT alteration at a nucleic acid target site within the cell by identifying  
PT the desired sequence alteration in cells selected for the presence of a  
PT selectable phenotype.  
XX  
PS Example 28; SEQ ID NO 2057; 303pp; English.  
XX  
CC This invention relates to a novel method of identifying a cell having a  
CC desired oligonucleotide-directed sequence alteration at a first nucleic  
CC acid target site within the cell. The method comprises identifying the  
CC desired sequence alteration in cells that have been selected for the  
CC presence of a selectable phenotype conferred by a concurrent  
CC oligonucleotide-directed sequence alteration at a second nucleic acid  
CC target site within the cells. The method is useful in identifying a cell  
CC having a desired oligonucleotide-directed sequence alteration at a first  
CC nucleic acid target site within the cell. The method may be useful for  
CC the production of plants with herbicide resistance, male or female  
CC sterile plants, abiotic stress tolerance, albino plants or plants with  
CC altered amino acid production as well as for use in mammalian cell lines.  
CC The present sequence is that of a mutagenic oligonucleotide which was  
CC used in the exemplification of the invention.  
XX  
SQ Sequence 121 BP; 14 A; 46 C; 50 G; 11 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 4.42e-07 Length: 121  
Score: 159.00 Matches: 35  
Percent Similarity: 92.1% Conservative: 0  
Best Local Similarity: 92.1% Mismatches: 1  
Query Match: 43.2% Indels: 2  
DB: 12 Gaps: 1

US-10-628-525A-36 (1-74) x ADN45388 (1-121)

QY 37 AlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAlaProArgHis 56

Db 1 GCCTCGCGCGCGCGGACACGCTCAGCATGCGGACACAGCGCGCGCGCCAGGCAC 60  
QY 57 GlnGlnGlnAlaArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 61 TAGCAGCAGGCGCGCGCGGGGAGG-----TTCCCGTGGCTCGTGTGTC 108

Search completed: April 1, 2006, 04:26:16  
Job time : 183.223 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 1193.34 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

Title: US-10-628-525a-36

Perfect score: 368

Sequence: 1 MAALATSQLVATAGHVPD.....RHQQQARRGRPPFPLVVC 74

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23193541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abss/ABSSWEB spool/US10628525/runat\_31032006\_095118\_16742/app\_query.fasta\_1  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0\_1 -LOOPECL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOALIGN=200 -THR\_SCORE=pcp -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss06h  
-USER=US10628525 @CGN\_1\_11098 @runat\_31032006\_095118\_16742 -NCPUs=6 -ICPU=3  
-NO MAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hc1:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gse1:\*  
10: gb\_gse2:\*  
11: gb\_gse3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	90.5	735	7	CO455159
2	333	90.5	771	6	CD440347
3	333	90.5	803	7	CO460657
4	333	90.5	805	7	CO456300
5	333	90.5	811	7	CO469376
6	333	90.5	812	7	CO461143
7	333	90.5	813	7	CO464185
					CO464185 MZCCL1504

8	333	90.5	816	7	CO462292
9	333	90.5	828	7	CO460606
10	333	90.5	830	7	CO456895
11	333	90.5	837	7	CO460923
12	333	90.5	844	7	CO455063
13	333	90.5	849	7	CO455764
14	333	90.5	850	7	CO456306
15	333	90.5	853	7	CO460568
16	333	90.5	854	7	CO464201
17	333	90.5	858	7	CO468515
18	333	90.5	860	7	CO458241
19	333	90.5	863	7	CO457215
20	333	90.5	873	7	CO463484
21	333	90.5	876	7	CO461256
22	333	90.5	880	7	CO462929
23	333	90.5	883	7	CO463816
24	333	90.5	893	7	CO462071
25	333	90.5	895	7	CO459176
26	333	90.5	895	7	CO463621
27	333	90.5	903	7	CO456060
28	333	90.5	911	7	CO460347
29	333	90.5	927	7	CO464483
30	329	89.4	785	7	CO457630
31	329	89.4	869	7	CO463624
32	327	88.9	857	7	CO460324
33	326	88.6	825	6	CD433331
34	324	88.0	781	7	CO466939
35	319	86.7	883	7	CO463466
36	316.5	86.0	709	7	CO467050
37	316.5	86.0	904	7	CO459604
38	316.5	86.0	910	7	CO456170
39	316	85.9	822	7	CO459171
40	314	85.3	883	7	CO456807
41	307	83.4	594	6	CD440356
42	304	82.6	797	7	CO463719
43	304	82.6	882	7	CO467445
44	304	82.6	938	7	CO454267
45	303.5	82.5	905	7	CO456470
46	295	80.2	832	7	CO465006
47	294	79.9	621	7	CO460486
48	293	79.6	436	8	DR824971
49	293	79.6	495	8	DR789179
50	293	79.6	536	6	CF647689
51	293	79.6	546	7	CO525196
52	293	79.6	598	8	DR795136
53	293	79.6	606	8	DR795417
54	293	79.6	615	9	BZ525328
55	293	79.6	620	7	CO533103
56	293	79.6	620	8	DR795335
57	293	79.6	648	8	CO530133
58	293	79.6	648	8	DR800471
59	293	79.6	652	8	DR795561
60	293	79.6	656	8	DR964842
61	293	79.6	658	8	CO525078
62	293	79.6	685	7	CO518712
63	293	79.6	692	8	DR969773
64	293	79.6	695	8	DR817915
65	293	79.6	696	8	DR822256
66	293	79.6	698	8	DR797257
67	293	79.6	706	8	DR826952
68	293	79.6	724	8	DR803147
69	293	79.6	724	8	DR824972
70	293	79.6	726	8	DR814212
71	293	79.6	727	8	DR964919
72	293	79.6	728	8	DR830479
73	293	79.6	728	8	DR968616
74	293	79.6	730	8	DR968586
75	293	79.6	732	8	DR966935
76	293	79.6	734	8	DR792755
77	293	79.6	742	8	DR965242
78	293	79.6	743	8	DR820739
79	293	79.6	745	7	CO527273
80	293	79.6	754	8	DR797255

81	293	79.6	776	8	DR821516	DR821516 ZM BFB006	RESULT 1
82	293	79.6	780	7	CO518868	CO518868 3530_1_12	CO455159
83	293	79.6	782	8	DR804832	DR804832 ZM BFB003	LOCUS
84	293	79.6	786	8	DR814441	DR814441 ZM BFB004	DEFINITION
85	293	79.6	789	8	DR968570	DR968570 ZM BFB008	sequence.
86	293	79.6	790	8	DR823764	DR823764 ZM BFB006	CO455159
87	293	79.6	790	8	DR830404	DR830404 ZM BFB007	CO455159.1
88	293	79.6	806	8	DR797875	DR797875 ZM BFB002	GI:67026410
89	293	79.6	809	8	DR814663	DR814663 ZM BFB004	EST.
90	293	79.6	812	10	CG261938	CG261938 OGYAE73TH	Zea mays
91	293	79.6	826	8	DR794686	DR794686 ZM BFB001	Zea mays
92	293	79.6	837	8	DR825687	DR825687 ZM BFB006	Zea mays
93	293	79.6	864	8	DR808766	DR808766 ZM BFB003	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
94	290	78.0	877	7	CO467381	CO467381 MZCCL2000	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
95	287	78.0	834	9	CC726093	CC726093 CGWEI189TV	clade; Panicoideae; Andropogoneae; Zea.
96	285	77.4	694	10	CU983517	CU983517 ZMWBH000	1 (bases 1 to 735)
97	284	77.2	401	6	CF649007	CF649007 3530_1_12	Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,
98	284	77.2	427	6	CF650004	CF650004 3530_1_80	De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and
99	277	75.3	809	7	CO462949	CO462949 MZCCL2003	Arruda,P.
100	273	74.2	445	6	CF647636	CF647636 3530_1_45	EndospERM-preferred expression of maize genes as revealed by
101	262	71.2	925	7	CO459474	CO459474 MZCCS1502	transcriptome-wide analysis of expressed sequence tags
102	261	70.9	296	6	CF648232	CF648232 3530_1_53	Plant Mol. Biol. (2005) In press
103	261	70.9	379	3	BM500492	BM500492 PAC000000	Contact: Arruda P
104	259	70.4	381	8	DR800828	DR800828 ZM BFB002	Centro de Biologia Molecular e Engenharia Genetica
105	251	68.2	428	6	CD433222	CD433222 EL01N0306	Universidade Estadual de Campinas
106	250	67.9	334	8	DR793659	DR793659 ZM BFB001	Caixa Postal 6010, 13083-970, Campinas SP, Brazil
107	249.5	67.8	626	6	CA269213	CA269213 SCBGR1307	Tel: 55 19 3788 1137
108	247	67.1	952	7	CO460528	CO460528 MZCCL1502	Fax: 55 19 3788 1089
109	237.5	64.5	593	10	CW036057	CW036057 104_267_1	Email: parruda@unicamp.br.
110	237.5	64.5	636	6	CF489136	CF489136 POL1_54_G	Location/Qualifiers
111	237.5	64.5	669	10	CW191886	CW191886 104_614_1	1. 735
112	233	63.3	337	6	CF648691	CF648691 3530_1_58	/organism="Zea mays"
113	226	61.4	221	8	DR787732	DR787732 ZM BFB000	/mol_type="mRNA"
114	224.5	61.0	637	6	CF486436	CF486436 POL1_37_E	/cultivar="F-352 near isogenic line"
115	197	53.5	271	6	CF244032	CF244032 3530_1_26	/db_xref="taxon:4577"
116	185	50.3	430	8	DN150586	DN150586 5215_B02	/sex="hermaphrodite"
117	179	48.6	967	7	CO464206	CO464206 MZCCL1504	/tissue type="endospERM"
118	171	46.5	577	7	CO455868	CO455868 MZCCS2000	/dev stage="multiple stages (10 to 25 days after
119	161	43.8	283	6	CF649487	CF649487 3530_1_70	pollination, see publication for more information)"
120	145	39.4	726	7	CO467589	CO467589 MZCCL2004	/lab host="E. coli DH10B"
121	130	35.3	263	6	CF647907	CF647907 3530_1_49	/clone lib="Maize EndospERM cDNA Library"
122	128.5	34.9	2543	10	CU957023	CU957023 OsJURA000	/note="Organ: seed; Vector: pSPORT1; Site 1: SalI; Site 2:
123	127	34.5	822	7	CO467310	CO467310 MZCCL2004	Not; Plant Material and RNA Isolation: Field grown maize
124	116	31.5	757	6	CF488108	CF488108 POL1_47_G	plants from inbred line F352 were used. Bars were
125	116	31.5	829	7	CO464830	CO464830 MZCCS1504	harvested at 10, 15, 20 and 25 days after pollination
126	113.5	30.8	470	5	C73133	C73133 C73133 Rice	(DAP), seeds were cut from the ear and the upper third of
127	109.5	29.8	558	2	BE602243	BE602243 HVSMEH009	the endosperms, containing only endospERM, aleurone and
128	109.5	29.8	586	3	BM368238	BM368238 EBed01_SQ	pericarpal tissues, was removed, frozen in liquid nitrogen
129	109.5	29.8	638	1	AL508959	AL508959 AL508959	and stored at -80o C. Frozen endosperms were pulverized in
130	109.5	29.8	700	1	AL508163	AL508163 AL508163	liquid nitrogen and total RNA was isolated according the
131	107	29.1	631	7	CV059967	CV059967 BNEJ52h9	method of Manning (9). Poly(A)+RNA was isolated using
132	105.5	28.7	513	1	AL508933	AL508933 AL508933	Oligotex-dT. cDNA libraries were constructed using
133	98.5	26.8	1619	4	CR612874	CR612874 full-length	Superscript Plasmid System for cDNA Synthesis and Plasmid
134	97.5	26.5	451	3	BQ240789	BQ240789 TaE05012H	Cloning Kit as described in Vettore, et al., (2001) The
135	97.5	26.5	502	3	BQ246003	BQ246003 TaE15017D	libraries that made SUCREST. Genet Mol Biol 24: 1-7. cDNAs
136	97.5	26.5	583	1	AL812068	AL812068 AL812068	ranging from 500 to 800 bp in size were assigned as short
137	97.5	26.5	650	5	BQ608470	BQ608470 BRY_4375	libraries (S10, S15, S20), and cDNAs >800 were assigned as
138	95.5	26.0	1061	10	CW932270	CW932270 EDDCC45TF	long libraries (L10, L15, M15, L20, L25). Unamplified
139	94.5	25.7	529	6	CA741461	CA741461 wiaic.pk0	libraries were plated and individual colonies picked and
140	94.5	25.7	649	6	CD907459	CD907459 G468_106P	transferred to 96 well plates containing liquid Circle
141	94	25.5	460	3	BQ239647	BQ239647 TaE05028D	Grow (CG) medium supplemented with 100 mg/L of ampicillin
142	94	25.5	473	8	BQ245208	BQ245208 TaE15029C	and 8% glycerol. Three copies of each cDNA clone were
143	94	25.5	474	3	COX009230	COX009230 io39d03.b	stored at -80o C. Additional information can be found in :
144	94	25.5	503	5	BQ606794	BQ606794 BRY_2666	Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,
145	94	25.5	539	7	CK504019	CK504019 rswc0_00	Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
146	94	25.5	541	1	AL814469	AL814469 AL814469	A.L., da Silva, F.R. and Arruda, P. (2005)
147	94	25.5	556	5	BQ607263	BQ607263 BRY_3155	EndospERM-preferred expression of maize genes as revealed
148	94	25.5	579	6	CA717812	CA717812 wdk4c.pk0	by transcriptome-wide analysis of expressed sequence tags.
149	94	25.5	598	6	CD890114	CD890114 G118_113O	Plant Molecular Biology (/in press/)"
150	94	25.5	639	2	BE414303	BE414303 SCU008.C0	

ORIGIN

Alignment Scores:  
Pred. No.:  
Score:

7.22e-24  
333.00

Length:  
Matches:

735  
71

Percent Similarity: 95.9%      Conservative: 0  
 Best Local Similarity: 95.9%      Mismatches: 1  
 Query Match: 90.5%      Indels: 2  
 DB: 7      Gaps: 1

US-10-628-525A-36 (1-74) x C0455159 (1-735)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
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 Db 211 ATGGCGGCTCTGGCCACGTCGCGACGTCGTCACACGCGCGCCGCGCTGGGGCGTCCCGGAC 270  
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 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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 Db 271 GCGTCCAGGTTCCG 330  
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 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 331 GCGGACACGCTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 390  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 391 CGCCGCGGGGGCAGG-----TTCCCGTCGTCGTCGTGTGC 426  
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## RESULT 2

CD440347      771 bp      mRNA      linear      EST 03-JUN-2003  
 LOCUS  
 DEFINITION EL01N053F08.b Endosperm\_5 Zea mays cDNA, mRNA sequence.  
 ACCESSION CD440347  
 VERSION CD440347.1 GI:31355990  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 771)

TITLE  
 AUTHORS Lai J., Dev N., Kim, C.S., Bharti, A.K., Rudd, S., Mayer, K.F.,  
 Larkins, B., Becraft, P. and Messing, J.  
 TITLE Characterization of the maize endosperm transcriptome and its  
 comparison to the rice genome  
 JOURNAL Genome Res. 14 (10), 1932-1937 (2004)  
 PUBMED 15466291

COMMENT  
 Contact: Lai, Jinheng  
 Dr. Joachim Messing's lab  
 Wakeman Institute, Rutgers University  
 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA  
 Tel: 732-445-3801  
 Fax: 732-445-5735  
 Email: jlai@wakeman.rutgers.edu  
 Seq primer: T3.

## FEATURES

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 XhoI"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,61e-24      Length: 771  
 Score: 333.00      Matches: 71  
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 Best Local Similarity: 95.9%      Mismatches: 1  
 Query Match: 90.5%      Indels: 2  
 DB: 6      Gaps: 1

US-10-628-525A-36 (1-74) x CD440347 (1-771)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20

Db 185 ATGGCGGCTCTGGCCACGTCGCGACGTCGTCACACGCGCGCCGCGCTGGGGCGTCCCGGAC 244  
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 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 305 GCGGACACGCTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 364  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 365 CGCCGCGGGGGCAGG-----TTCCCGTCGTCGTCGTGTGC 400  
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## RESULT 3

CO460657      803 bp      mRNA      linear      EST 08-JUN-2005  
 LOCUS  
 DEFINITION MZCL20024G08.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
 sequence.  
 ACCESSION CO460657  
 VERSION CO460657.1 GI:67031908  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 803)

TITLE  
 AUTHORS Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H.,  
 De Rosa, V.B. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and  
 Arruda, P.

COMMENT  
 Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 Plant Mol. Biol. (2005) In press

CONTACT: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

## FEATURES

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 /tissue\_type="endosperm"  
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 /lab\_host="E. coli DH10B"  
 /clone\_lib="Maize Endosperm cDNA Library"  
 /note="Organ: seed; Vector: pSPORT1; Site\_1: SalI; Site\_2:  
 NotI; Plant Material and RNA Isolation: Field grown maize  
 plants from inbred line F352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
 the endosperms, containing only endosperm, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -80o C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the  
 method of Manning (9). Poly(A)+RNA was isolated using  
 Oligotex-dT. cDNA libraries were constructed using  
 Superscript Plasmid System for cDNA Synthesis and Plasmid  
 Cloning Kit as described in Vettore, et al., (2001) The  
 libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs  
 ranging from 500 to 800 bp in size were assigned as short  
 libraries (S10, S15, S20), and cDNAs >800 were assigned as  
 long libraries (L10, L15, L20, L25). Unamplified  
 libraries were plated and individual colonies picked and  
 transferred to 96 well plates containing liquid Circle

Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80°C. Additional information can be found in: Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) EndospERM-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (in press//)

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,97e-24 Length: 803  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO460657 (1-803)

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QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValaAlaSerAlaAla 40  
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 Db 231 GGTCTCACGTTTCGGCGCGCGCGCGAGGCTGTAGGGGGCGCGCGCTCGGGCGG 290  
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QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 291 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 350  
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QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 351 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 386  
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RESULT 4  
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 LOCUS MZCC15012D08.g Maize EndospERM cDNA Library Zea mays cDNA, mRNA  
 DEFINITION  
 ACCESSION CO456300  
 VERSION CO456300.1 GI:67027551  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.  
 TITLE EndospERM-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

## FEATURES

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 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="P-352 near isogenic line"  
 /db\_xref="taxon:4577"  
 /sex="hermaphrodite"  
 /tissue\_type="endospERM"  
 /dev\_stage="multiple stages (10 to 25 days after

pollination, see publication for more information)"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="Maize EndospERM cDNA Library"  
 /note="Organ: seed; Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; Plant Material and RNA isolation: Field grown maize plants from inbred line P352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP). seeds were cut from the ear and the upper third of the endosperms, containing only endospERM, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -80°C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, N15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80°C. Additional information can be found in: Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) EndospERM-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (in press//)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,99e-24 Length: 805  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
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US-10-628-525A-36 (1-74) x CO456300 (1-805)

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 Db 201 ATGGCGGCTCTGGCCACGTCGAGCTCGTGCACAGCGCGCGCTGGCGCTCCCGGAC 260  
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QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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 Db 261 GGTCTCACGTTTCGGCGCGCGCGCGAGGCTGTAGGGGGCGCGCGCTCGGGCGG 320  
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QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 321 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGG 380  
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QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 381 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 416  
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RESULT 5  
 CO469376  
 LOCUS MZCCS15042H10.g Maize EndospERM cDNA Library Zea mays cDNA, mRNA  
 DEFINITION  
 ACCESSION CO469376  
 VERSION CO469376.1 GI:67043121  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE  
 1 (bases 1 to 811)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

**AUTHORS**  
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H.,  
De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and  
Arruda, P.

**TITLE**  
Endosperm-preferred expression of maize genes as revealed by  
transcriptome-wide analysis of expressed sequence tags

**JOURNAL**  
Plant Mol. Biol. (2005) In press

**COMMENT**  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br.

**FEATURES**  
source  
Location/Qualifiers

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/organism="Zea mays"
/mol_type="mRNA"
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/tissue_type="endosperm"
/dev_stage="multiple stages (10 to 25 days after
pollination, see publication for more information)"
/lab_host="E. coli DH10B"
/clone_lib="Maize Endosperm cDNA Library"
/notes="Organ: seed; Vector: pSPORT1; Site: 1: Sali; Site: 2:
NotI; Plant Material and RNA Isolation: Field grown maize
plants from inbred line F352 were used. Bars were
harvested at 10, 15, 20 and 25 days after pollination
(DAP). seeds were cut from the ear and the upper third of
the endosperms, containing only endosperm, aleurone and
pericarpal tissues, was removed, frozen in liquid nitrogen
and stored at -800 C. Frozen endosperms were pulverized in
liquid nitrogen and total RNA was isolated according the
method of Manning (9). Poly(A)+RNA was isolated using
Oligotex-dT. cDNA libraries were constructed using
SuperScript Plasmid System for cDNA Synthesis and Plasmid
Cloning Kit as described in Vettore, et al., (2001) The
libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs
ranging from 500 to 800 bp in size were assigned as short
libraries (S10, S15, S20), and cDNAs >800 were assigned as
long libraries (L10, L15, M15, L20, L25). Unamplified
libraries were plated and individual colonies picked and
transferred to 96 well plates containing liquid circle
Growth (CG) medium supplemented with 100 mg/L of ampicillin
and 8% glycerol. Three copies of each cDNA clone were
stored at -800 C. Additional information can be found in :
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
A.L., da Silva, F.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed
by transcriptome-wide analysis of expressed sequence tags.
Plant Molecular Biology (/in press//)"
```

## ORIGIN

Alignment Scores:  
Pred. No.: 8,05e-24 Length: 811  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x C0469376 (1-811)

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**Db** 184 ATGGCGGCTCTGGCCACGTCGACGTCGTCTGCAACGCGCGCCGCTGGCGGTCGCCGAC 243  
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**Db** 244 GCGTCCACGTTCCGCGCGCGCGCGCGGAGGCTGAGGGGGGCCCGCGGCTCGCGGCG 303  
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**QY** 41 AlaAspThrLeuSerMetArgThrSerAlaAlaProArgHisGlnGlnAla 60  
|||||  
**Db** 304 GCGGACACGCTCAGCATGCGGACGCGCGCGCGCCAGCCACGACGACGCG 363  
|||||

**QY** 61 ArgArgGlyValArgPheProPheProSerLeuValValCys 74  
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**Db** 364 CGCGCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 399  
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**RESULT 6**  
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LOCUS MZCCS20023B02.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
DEFINITION  
C0461143  
VERSION C0461143.1 GI:67032394  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

**REFERENCE**  
**AUTHORS**  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 812)  
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H.,  
De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and  
Arruda, P.

**TITLE**  
Endosperm-preferred expression of maize genes as revealed by  
transcriptome-wide analysis of expressed sequence tags

**JOURNAL**  
Plant Mol. Biol. (2005) In press

**COMMENT**  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br.

**FEATURES**  
source  
Location/Qualifiers

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/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F-352 near isogenic line"
/db_xref="taxon:4577"
/sex="hermaphrodite"
/tissue_type="endosperm"
/dev_stage="multiple stages (10 to 25 days after
pollination, see publication for more information)"
/lab_host="E. coli DH10B"
/clone_lib="Maize Endosperm cDNA Library"
/notes="Organ: seed; Vector: pSPORT1; Site: 1: Sali; Site: 2:
NotI; Plant Material and RNA Isolation: Field grown maize
plants from inbred line F352 were used. Bars were
harvested at 10, 15, 20 and 25 days after pollination
(DAP). seeds were cut from the ear and the upper third of
the endosperms, containing only endosperm, aleurone and
pericarpal tissues, was removed, frozen in liquid nitrogen
and stored at -800 C. Frozen endosperms were pulverized in
liquid nitrogen and total RNA was isolated according the
method of Manning (9). Poly(A)+RNA was isolated using
Oligotex-dT. cDNA libraries were constructed using
SuperScript Plasmid System for cDNA Synthesis and Plasmid
Cloning Kit as described in Vettore, et al., (2001) The
libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs
ranging from 500 to 800 bp in size were assigned as short
libraries (S10, S15, S20), and cDNAs >800 were assigned as
long libraries (L10, L15, M15, L20, L25). Unamplified
libraries were plated and individual colonies picked and
transferred to 96 well plates containing liquid circle
Growth (CG) medium supplemented with 100 mg/L of ampicillin
and 8% glycerol. Three copies of each cDNA clone were
stored at -800 C. Additional information can be found in :
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
A.L., da Silva, F.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed
```

by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press/)"

## ORIGIN

## Alignment Scores:

Pred. No.: 8,06e-24 Length: 812  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO461143 (1-812)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
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Db 202 ATGGCGGCTCTGGCCACGTCGCAGCTCTGCAACGCGCGCGCTGGCGCTCCGGAC 261  
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QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValAlaArgAlaSerAlaAla 40  
|||||  
Db 262 GCGTCACGCTTCG 321  
|||||  
QY 41 AlaAapThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
|||||  
Db 322 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 381  
|||||

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
|||||

Db 382 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTC 417  
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## RESULT 7

CO464185

LOCUS MZCC115045G11.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
DEFINITION

ACCESSION CO464185

VERSION CO464185.1 GI:67037339

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 813)

Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,P.T.S., Fisch,P.H.,  
De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and

Arruda,P.

Endosperm-preferred expression of maize genes as revealed by

transcriptome-wide analysis of expressed sequence tags

Plant Mol. Biol. (2005) In press

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br.

## FEATURES

source

1..813

/location/Qualifiers

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/dev\_stage="multiple stages (10 to 25 days after

pollination, see publication for more information)"

/lab\_host="E. coli DH10B"

/clone\_lib="Maize Endosperm cDNA Library"

/note="Organ: seed; Vector: pSPORII; Site\_1: Sall; Site\_2:

NotI; Plant Material and RNA Isolation: Field grown maize

plants from inbred line P352 were used. Ears were

harvested at 10, 15, 20 and 25 days after pollination

(DAP), seeds were cut from the ear and the upper third of  
the endosperms, containing only endosperm, aleurone and  
pericarpal tissues, was removed, frozen in liquid nitrogen  
and stored at -80o C. Frozen endosperms were pulverized in  
liquid nitrogen and total RNA was isolated according the  
method of Manning (9). Poly(A)+RNA was isolated using  
Oligotex-dT. cDNA libraries were constructed using  
SuperScript Plasmid System for cDNA Synthesis and Plasmid  
Cloning Kit as described in Vettore, et al., (2001). The  
libraries that made SUCSEST. Genet Mol Biol 24: 1-7. cDNAs  
ranging from 500 to 800 bp in size were assigned as short  
libraries (S10, S15, S20), and cDNAs >800 were assigned as  
long libraries (L10, L15, L20, L25). Unamplified  
libraries were plated and individual colonies picked and  
transferred to 96 well plates containing liquid Circle  
Grow (CG) medium supplemented with 100 mg/L of ampicillin  
and 8% glycerol. Three copies of each cDNA clone were  
stored at -80o C. Additional information can be found in :  
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,  
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
A.L., da Silva, F.R. and Arruda, P. (2005)  
Endosperm-preferred expression of maize genes as revealed  
by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press/)"

## ORIGIN

## Alignment Scores:

Pred. No.: 8,08e-24 Length: 813  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO464185 (1-813)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
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Db 166 ATGGCGGCTCTGGCCACGTCGCAGCTCTGCAACGCGCGCGCTGGCGCTCCGGAC 225  
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QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValAArgAlaSerAlaAla 40  
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Db 226 GCGTCACGCTTCG 285  
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Db 286 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 345  
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QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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Db 346 CGCCGCGGGGCGAG-----TTCCCGTCGCTCGTGTGTC 381  
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## RESULT 8

CO462292

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 816)

Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,P.T.S., Fisch,P.H.,  
De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and

Arruda,P.

Endosperm-preferred expression of maize genes as revealed by

transcriptome-wide analysis of expressed sequence tags

Plant Mol. Biol. (2005) In press

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br.

# FEATURES

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/tissue\_type="endosperm"

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/clone\_lib="Maize Endosperm cDNA Library"  
/notes="Organ: seed; Vector: pSPORT1; Site: 1: SalI; Site: 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -800 C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCREST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -800 C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

## ORIGIN

### Alignment Scores:

Pred. No.:	Score:	8.11e-24	Length:	816
Percent Similarity:	333.00	Matches:	71	
Best Local Similarity:	95.9%	Conservative:	0	
Query Match:	95.9%	Mismatches:	1	
DB:	90.5%	Indels:	2	
	7	Gaps:	1	

US-10-628-525A-36 (1-74) x CO462292 (1-816)

QY	1	MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp	20
Db	196	ATGGCGGCTCTGGCCACGTCGCGAGCTGTCGACACCGCGCGCGCTGGCGGCTGCCGGAC	255
QY	21	AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla	40
Db	256	GCCTCCACGTTCCGCGCGCGCGCGCGAGGGCTTGAGGGGGCCCGGGCGCTGGCGGGC	315
QY	41	AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla	60
Db	316	GGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCCAGGCACCGACGACGAGCGG	375
QY	61	ArgArgGlyGlyValArgPheProPheProSerLeuValValCys	74
Db	376	CGCCCGCGGGGGGAGG-----TTCCGTCGCTCGTGTGTGC	411

## RESULT 9

### CO460606

#### LOCUS

#### DEFINITION

#### ACCESSION

#### VERSION

#### KEYWORDS

#### SOURCE

#### ORGANISM

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

#### COMMENT

#### FEATURES

#### source

#### 1. .828

#### /organism="Zea mays"

#### /mol\_type="mRNA"

#### /cultivar="P-352 near isogenic line"

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#### /tissue\_type="endosperm"

#### /dev\_stage="multiple stages (10 to 25 days after pollination, see publication for more information)"

#### /lab\_host="E. coli DH10B"

#### /clone\_lib="Maize Endosperm cDNA Library"

#### /notes="Organ: seed; Vector: pSPORT1; Site: 1: SalI; Site: 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -800 C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCREST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -800 C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

#### Alignment Scores:

#### Pred. No.:

#### Score:

#### 8.24e-24

#### Length:

#### 828

#### Matches:

#### 333.00

#### Conservative:

#### 0

#### Mismatches:

#### 1

#### Indels:

#### 2

#### Gaps:

#### 1

CO460606 828 bp mRNA linear EST 08-JUN-2005  
M2CC120024C02.9 Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
sequence.

CO460606

CO460606.1 GI:67031857

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 828)

Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.

Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags

Plant Mol. Biol. (2005) In press

Contact: Arruda, P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br.

Location/Qualifiers

1. .828

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="P-352 near isogenic line"

/db\_xref="taxon:4577"

/sex="hermaphrodite"

/tissue\_type="endosperm"

/dev\_stage="multiple stages (10 to 25 days after pollination, see publication for more information)"

/lab\_host="E. coli DH10B"

/clone\_lib="Maize Endosperm cDNA Library"

/notes="Organ: seed; Vector: pSPORT1; Site: 1: SalI; Site: 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -800 C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCREST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -800 C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

Alignment Scores:

Pred. No.:

Score:

8.24e-24

Length:

828

Matches:

333.00

Conservative:

0

Mismatches:

1

Indels:

2

Gaps:

1

## ORIGIN

### Alignment Scores:

#### Pred. No.:

#### Score:

#### 8.24e-24

#### Length:

#### 828

#### Matches:

#### 333.00

Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO460606 (1-828)

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QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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RESULT 10  
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 ACCESSION CO456895  
 VERSION CO456895.1 GI:67028146  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
 Arruda,P.  
 Title Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

FEATURES  
 source 1..830  
 /organism="Zea mays"  
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 /db\_xref="taxon:4577"  
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 /tissue\_type="endosperm"  
 /dev\_stages="multiple stages (10 to 25 days after  
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 /clone\_lib="Maize Endosperm cDNA Library"  
 /note="Organ: seed; Vector: pSPORT1; Site 1: SalI; Site 2:  
 NotI; Plant Material and RNA Isolation: Field grown maize  
 plants from inbred line P352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
 the endosperms, containing only endosperm, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -800 C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the  
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SuperScript Plasmid System for cDNA Synthesis and Plasmid  
 Cloning Kit as described in Vettore, et al., (2001) The  
 libraries that made SUCREST. Genet Mol Biol 24: 1-7. cDNAs  
 ranging from 500 to 800 bp in size were assigned as short  
 libraries (S10, S15, S20), and cDNAs >800 bp were assigned as  
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 libraries were plated and individual colonies picked and  
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 A.L., da Silva, F.R. and Arruda, P. (2005)  
 Endosperm-preferred expression of maize genes as revealed  
 by transcriptome-wide analysis of expressed sequence tags.  
 Plant Molecular Biology (/in press/)"

ORIGIN

Alignment Scores: 8,26e-24 Length: 830  
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 Score: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO456895 (1-830)

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 Db 177 ATGGCGGCTCTGGCCACGTCGACGCTCGTGCACCGCGCGCGCTGGCGGCTCCGGAC 236  
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QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 |||||  
 Db 237 GGTCCACGCTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGCGCG 296  
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QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 297 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 356  
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QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 357 CGCCGCGGGGGGAGG-----TTCCCGTCGTCGTCGTGTGC 392  
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RESULT 11  
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 ACCESSION CO460923  
 VERSION CO460923.1 GI:67032174  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 837)  
 Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
 Arruda,P.  
 Title Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Centro de Biologia Molecular e Engenharia Genetica  
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 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
 Location/Qualifiers



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/notes="Organ: seed; Vector: pSPORT1; Site: 1: Salt1; Site 2:
Not1; Plant Material and RNA Isolation: Field grown maize
plants from inbred line F352 were used. Ears were
harvested at 10, 15, 20 and 25 days after pollination
(DAP), seeds were cut from the ear and the upper third of
the endosperms, containing only endosperm, aleurone and
pericarpal tissues, was removed, frozen in liquid nitrogen
and stored at -800 C. Frozen endosperms were pulverized in
liquid nitrogen and total RNA was isolated according the
method of Manning (9). Poly(A)+RNA was isolated using
Oligotex-dT. cDNA libraries were constructed using
SuperScript plasmid system for cDNA synthesis and Plasmid
Cloning Kit as described in Vettore, et al., (2001). The
libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs
ranging from 500 to 800 bp in size were assigned as short
libraries (S10, S15, S20), and cDNAs >800 were assigned as
long libraries (L10, L15, M15, L20, L25). Unamplified
libraries were plated and individual colonies picked and
transferred to 96 well plates containing liquid circle
Growth (CG) medium supplemented with 100 mg/L of ampicillin
and 8% glycerol. Three copies of each cDNA clone were
stored at -800 C. Additional information can be found in :
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
A.L., da Silva, F.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed
by transcriptome-wide analysis of expressed sequence tags.
Plant Molecular Biology (/in press/)"

FEATURES
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1. .844
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/clone_lib="Maize Endosperm cDNA Library"
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Not1; Plant Material and RNA Isolation: Field grown maize
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harvested at 10, 15, 20 and 25 days after pollination
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Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
A.L., da Silva, F.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed
by transcriptome-wide analysis of expressed sequence tags.
Plant Molecular Biology (/in press/)"

ORIGIN
US-10-628-525A-36 (1-74) x CO460923 (1-837)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20
Db 203 ATGGCGGCTCTGGCCAGCTCGCAGCTCTGTCACACGGCGCGGCTGGCGGAC 262
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40
Db 263 GGTCTCACGTTCCGCGCGCGCGCGGCGGCGCTGAGGGGGCGCGGCGGCGG 322
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 323 GCGACACGCTAGCATGGGACACGCGCGCGCGCGCGCCAGGCGCCAGCAGCAGCGG 382
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
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LOCUS MZCCS15035D06.g 844 bp mRNA linear EST 08-JUN-2005
DEFINITION Maize Endosperm cDNA Library Zea mays cDNA, mRNA
sequence.
ACCESSION CO465063

VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 844)
De Rosa, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H.,
De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and
Arruda, P.
Endosperm-preferred expression of maize genes as revealed by
transcriptome-wide analysis of expressed sequence tags
Plant Mol. Biol. (2005) In press
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1137
Email: parruda@unicamp.br.
Location/Qualifiers
1. .844
/organism="Zea mays"
/mol_type="mRNA"
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/db_xref="taxon:4577"
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Not1; Plant Material and RNA Isolation: Field grown maize
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harvested at 10, 15, 20 and 25 days after pollination
(DAP), seeds were cut from the ear and the upper third of
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Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
A.L., da Silva, F.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed
by transcriptome-wide analysis of expressed sequence tags.
Plant Molecular Biology (/in press/)"

ORIGIN
Alignment Scores:
Pred. No.: 8 34e-24 Length: 837
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO465063 (1-844)
Alignment Scores:
Pred. No.: 8 42e-24 Length: 844
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO465063 (1-844)

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 QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 381 CGCGCGGGGGCAGG-----TTCCGTCGCTCGTGTGTGC 416  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 849)  
 AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,P.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
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 TITLE Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Centro de Biologia Molecular e Engenharia Genetica  
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 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
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 Email: parruda@unicamp.br.  
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 /organism="Zea mays"  
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 NotI; Plant Material and RNA Isolation: Field grown maize  
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 and stored at -80o C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the  
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 Cloning Kit as described in Vettore, et al., (2001) The  
 libraries that made SUCRST. Genet Mol Biol 24: 1-7. cDNAs  
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 libraries (S10, S15, S20), and cDNAs >800 were assigned as  
 long libraries (L10, L15, L20, L25). Unamplified  
 libraries were plated and individual colonies picked and

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 and 8% glycerol. Three copies of each cDNA clone were  
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 Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
 A.L., da Silva, F.R. and Arruda, P. (2005)  
 Endosperm-preferred expression of maize genes as revealed  
 by transcriptome-wide analysis of expressed sequence tags.  
 Plant Molecular Biology (/in press//)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8 47e-24 Length: 849  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1  
 US-10-628-525A-36 (1-74) x CO455764 (1-849)  
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 QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 235 GGTCCACGCTTCGCGCGCGCGCGAGGCGCTGAGGGGGCGCGCGCGCGCG 294  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 295 GCGGACACGCTCAGCATCGGACCGAGCGCGCGCGCGCGCGCGCGCGCG 354  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 355 CGCGCGGGGGCAGG-----TTCCGTCGCTCGTGTGTGC 390  
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 DEFINITION MZCCL15012E06.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
 ACCESSION CO456306  
 VERSION CO456306.1 GI:67027557  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 850)  
 AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,P.T.S., Fisch,P.H.,  
 De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and  
 Arruda,P.  
 TITLE Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
 FEATURES  
 source  
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 /organism="Zea mays"  
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 /cultivar="F-352 near isogenic line"  
 /db\_xref="taxon:4577"  
 /sex="hermaphrodite"  
 /tissue\_type="endosperm"





harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -80o C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according to the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001). The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80o C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
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 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

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 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 ORGANISM Zea mays  
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 1 (bases 1 to 860)  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.  
 TITLE Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press

## COMMENT

Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
 Location/Qualifiers

## FEATURES

## source

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 /organism="Zea mays"  
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## ORIGIN

Alignment Scores:  
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 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO458241 (1-860)

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 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
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ACCESSION CO457215
VERSION   CO457215.1   GI:67028466
KEYWORDS EST.
SOURCE    Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 863)
Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,
De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and
Arruda,P.
Endosperm-preferred expression of maize genes as revealed by
transcriptome-wide analysis of expressed sequence tags
Plant Mol. Biol. (2005) In press
Contact: Arruda P
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br.
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NotI; Plant Material and RNA Isolation: Field grown maize
plants from inbred line F352 were used. Ears were
harvested at 10, 15, 20 and 25 days after pollination
(DAP), seeds were cut from the ear and the upper third of
the endosperms, containing only endosperm, aleurone and
pericarpal tissues, was removed, frozen in liquid nitrogen
and stored at -80o C. Frozen endosperms were pulverized in
liquid nitrogen and total RNA was isolated according the
method of Manning (9). Poly(A)+RNA was isolated using
Oligotex-dT. cDNA libraries were constructed using
Superscript Plasmid System for cDNA Synthesis and Plasmid
Cloning Kit as described in Vettore, et al., (2001) The
libraries that made SUCSEST. Genet Mol Biol 24: 1-7. cDNAs
ranging from 500 to 800 bp in size were assigned as short
libraries (S10, S15, S20), and cDNAs >800 were assigned as
long libraries (L10, L15, L20, L25). Unamplified
libraries were plated and individual colonies picked and
transferred to 96 well plates containing liquid Circle
Grow (CG) medium supplemented with 100 mg/L of ampicillin
and 8% glycerol. Three copies of each cDNA clone were
stored at -80o C. Additional information can be found in :
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,
A.L., da Silva, F.R. and Arruda, P. (2005)
Endosperm-preferred expression of maize genes as revealed
by transcriptome-wide analysis of expressed sequence tags.
Plant Molecular Biology (/in press/)"

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Pred. No.:      8.63e-24      Length:      863

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Query Match: 90.5%      Indels: 2
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VERSION   CO463484.1   GI:67034951
KEYWORDS EST.
SOURCE    Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 873)
Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H.,
De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and
Arruda,P.
Endosperm-preferred expression of maize genes as revealed by
transcriptome-wide analysis of expressed sequence tags
Plant Mol. Biol. (2005) In press
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br.
Location/Qualifiers
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NotI; Plant Material and RNA Isolation: Field grown maize
plants from inbred line F352 were used. Ears were
harvested at 10, 15, 20 and 25 days after pollination
(DAP), seeds were cut from the ear and the upper third of
the endosperms, containing only endosperm, aleurone and
pericarpal tissues, was removed, frozen in liquid nitrogen
and stored at -80o C. Frozen endosperms were pulverized in
liquid nitrogen and total RNA was isolated according the
method of Manning (9). Poly(A)+RNA was isolated using

```

Oligotex-dT. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80°C. Additional information can be found in: Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endospem-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8,74e-24 Length: 873  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO461256 (1-873)

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CO461256 876 bp mRNA linear EST 08-JUN-2005  
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 ACCESSION CO461256  
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 ORGANISM Zea mays  
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 REFERENCE 1 (bases 1 to 876)  
 AUTHORS Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.  
 TITLE Endospem-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

FEATURES  
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Location/Qualifiers  
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## ORIGIN

Alignment Scores:  
 Pred. No.: 8,77e-24 Length: 876  
 Score: 333.00 Matches: 71  
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 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO461256 (1-876)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
 DB 201 ATGGCGGCTCTGGCCACGTCGACGCTGTCGCAACGCGCGCGCTGGCGCGTCCCGGAC 260  
 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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 DB 321 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCCAGGCGCCAGGCGAGCGG 380  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 DB 381 CGCCGCGGGGCGAGG-----TTCCCGTCGCTGCTGTGC 416

## RESULT 22

LOCUS CO462929 880 bp mRNA linear EST 08-JUN-2005  
 DEFINITION MZCCL20030H11.g Maize Endospem cDNA Library Zea mays cDNA, mRNA sequence.

ACCESSION CO462929  
 VERSION CO462929.1 GI:67034379  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 880)  
 AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.  
 TITLE Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
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 ORIGIN  
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 Score: 333.00 Matches: 71  
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 Query Match: 90.5% Indels: 2  
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 US-10-628-525A-36 (1-74) x CO462929 (1-880)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThArGAlaGlyHisGlyValP-rAaP 20  
 Db 227 ATGGCGGGCTCTGGCCACGCTCGCGAGCTCGCAACGCGCGCGCTGGCGGCTCCGGAC 286  
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 Db 287 GGGTCCAGTTCCGGCGGGCGCGCGGAGGCGCTAGGGGGGGCGGCGGCGTCCGGCGG 346  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 347 GCGGACACGCTCAGCATCGGACACGCGCGCGCGCGCGCGCCAGGCGCCAGCAGCAGGCG 406  
 QY 61 ArgArgGlyGlyAcqPheProPheProSerLeuValValCys 74  
 Db 407 CGCCCGCGGGGCGAGG-----TTCCCGTCGCTCGCTCGTGTGC 442  
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 LOCUS CO463816  
 DEFINITION MZCCL1503SD06.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA sequence.  
 ACCESSION CO463816  
 VERSION CO463816.1 GI:67035283  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 883)  
 AUTHORS Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.  
 TITLE Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags  
 JOURNAL Plant Mol. Biol. (2005) In press  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
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 /lab\_host="E. coli DH10B"  
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 /note="Organ: seed; Vector: pSPORT1; Site 1: Sall; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -80o C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according to the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dt. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, L20, L25). Unamplified



libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -80°C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) EndospERM-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8,85e-24 Length: 893  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO463816 (1-893)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
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 Db 218 ATGGGGCTCTGGCCAGCTCGCAGCTGTCGACCGCCGCCCTGGCGCTCCCGGAC 277  
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 Db 278 GCGTCCACGTTCCGCGCGCGCGCGCGAGCGCTGAGGGGGCCCGCGGGCTCGCGGGCG 337  
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 Db 338 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCCAGGACCAGCAGCAGCGCG 397  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 398 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 433  
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## RESULT 24

CO462071  
 LOCUS CO462071.1 GI:67033322  
 DEFINITION MZCCS20028G05.g Maize EndospERM cDNA Library Zea mays cDNA, mRNA  
 ACCESSION CO462071  
 VERSION EST.  
 KEYWORDS Zea mays  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

AUTHORS Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.

## TITLE

EndospERM-preferred expression of maize genes as revealed by

## JOURNAL

transcriptome-wide analysis of expressed sequence tags

## COMMENT

Plant Mol. Biol. (2005) In press  
 Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.

## FEATURES

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 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="P-352 near isogenic line"  
 /db\_xref="taxon:4577"  
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 /notes="Organ: seed; Vector: pSPORT1; Site: 1: SalI; Site 2:  
 NotI; Plant Material and RNA Isolation: Field grown maize  
 plants from inbred line P352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP). seeds were cut from the ear and the upper third of  
 the endosperms, containing only endospERM, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -80°C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the  
 method of Manning (9). Poly(A)+RNA was isolated using  
 Oligotex-dT. cDNA libraries were constructed using  
 Cloning Kit as described in Vettore, et al., (2001) the  
 libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs  
 ranging from 500 to 800 bp in size were assigned as short  
 libraries (S10, S15, S20), and cDNAs >800 were assigned as  
 long libraries (L10, L15, M15, L20, L25). Unamplified  
 libraries were plated and individual colonies picked and  
 transferred to 96 well plates containing liquid Circle  
 Grow (CG) medium supplemented with 100 mg/L of ampicillin  
 and 8% glycerol. Three copies of each cDNA clone were  
 stored at -80°C. Additional information can be found in :  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,  
 Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
 A.L., da Silva, F.R. and Arruda, P. (2005)  
 EndospERM-preferred expression of maize genes as revealed  
 by transcriptome-wide analysis of expressed sequence tags.  
 Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 8,96e-24 Length: 893  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO462071 (1-893)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
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 Db 190 ATGGGGCTCTGGCCAGCTCGCAGCTGTCGACCGCCGCCCTGGCGCTCCCGGAC 249  
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 QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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 Db 250 GCGTCCACGTTCCGCGCGCGCGCGAGCGCTGAGGGGGCCCGCGGGCTCGCGGGCG 309  
 |||||  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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 Db 310 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCCAGGACCAGCAGCAGCGCG 369  
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 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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 Db 370 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 405  
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## RESULT 25

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 LOCUS MZCCS15018E09.g Maize EndospERM cDNA Library Zea mays cDNA, mRNA  
 DEFINITION sequence.  
 ACCESSION CO459176  
 VERSION CO459176.1 GI:67030427  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

REFERENCE	clade; Panicoidae; Andropogoneae; Zea.	
AUTHORS	1 (bases 1 to 895) Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.	
TITLE	Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags	
JOURNAL	Plant Mol. Biol. (2005) In press	
COMMENT	Contact: Arruda P Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137 Fax: 55 19 3788 1089 Email: parruda@unicamp.br.	
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ORIGIN		
Alignment Scores:		
Pred. No.:	8,98e-24	Length: 895
Score:	333.00	Matches: 71
Percent Similarity:	95.9%	Conservative: 0
Best Local Similarity:	95.9%	Mismatches: 1
Query Match:	90.5%	Indels: 2
DB:	7	Gaps: 1
US-10-628-525A-36 (1-74) x CO459176 (1-895)		
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Db	229	ATGGCGGCTCTGGCACGTCGCAGCTCTGCGACAGCGCGCGCTGGCGCTCCCGAC 288 
Qy	21	AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyValaArgAlaSerAlaAla 40 
Db	289	GGTCCACGTTCCG 348 
Qy	41	AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60 
Db	349	GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 408 
Qy	61	ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74 
Db	409	CGCCCGCGGCGCGCGCG-----TTCCCGTCGCTCGTCGTGTGC 444 
RESULT 26		
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LOCUS	MZCCL20034H03.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA	
DEFINITION	sequence.	
ACCESSION	CO463621	
VERSION	CO463621.1 GI:67035088	
KEYWORDS	EST.	
SOURCE	Zea mays	
ORGANISM	Zea mays	
REFERENCE	1 (bases 1 to 895) Verza,N.C., Silva,T.R., Cord-Neto,G., Nogueira,F.T.S., Fisch,P.H., De Rosa,V.E. Jr., Martins,M.M., Vettore,A.L., da Silva,F.R. and Arruda,P.	
AUTHORS	Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags Plant Mol. Biol. (2005) In press	
TITLE	Contact: Arruda P Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137 Fax: 55 19 3788 1089 Email: parruda@unicamp.br.	
JOURNAL	Location/Qualifiers	
COMMENT	1..895 /organism="Zea mays" /mol_type="mRNA" /cultivar="P-352 near isogenic line" /db_xref="taxon:4577" /sex="hermaphrodite" /tissue_type="endosperm" /dev_stage="multiple stages (10 to 25 days after pollination, see publication for more information)" /lab_host="E. coli DH10B" /clone_lib="Maize Endosperm cDNA Library" /note="Organ: seed; Vector: pSPORT1; Site 1: Sall; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP), seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -800 C. Frozen endosperms were pulverized in liquid nitrogen and total RNA was isolated according the method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dt. cDNA libraries were constructed using SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001) The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circle Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -800 C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005) Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags. Plant Molecular Biology (/in press/)"	

A.L., da Silva, F.R. and Arruda, P. (2005)  
Endosperm-preferred expression of maize genes as revealed  
by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press/)"

## ORIGIN

Alignment Scores:  
Pred. No.: 8.98e-24 Length: 895  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO463621 (1-895)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
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|||||  
Db 347 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 406  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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Db 407 CGCGCGGGGGGCGAGG-----TTCCCGTCGCTGCTGTGTGC 442

RESULT 27  
CO456060  
LOCUS MZCCL20018D05.g 903 bp mRNA linear EST 08-JUN-2005  
DEFINITION Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags

ACCESSION CO456060.1 GI:67027311  
VERSION EST.  
KEYWORDS  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.

TITLE Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags

JOURNAL Plant Mol. Biol. (2005) In press  
COMMENT Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br.

FEATURES  
source

1..903  
/organism="Zea mays"  
/mol\_type="mRNA"  
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/db\_xref="taxon:4577"  
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/clone\_lib="Maize Endosperm cDNA Library"  
/note="Organ: seed; Vector: pSPORT1; Site: 1: SalI; Site 2: NotI; Plant Material and RNA Isolation: Field grown maize

plants from inbred line F352 were used. Ears were harvested at 10, 15, 20 and 25 days after pollination (DAP). seeds were cut from the ear and the upper third of the endosperms, containing only endosperm, aleurone and pericarpal tissues, was removed, frozen in liquid nitrogen and stored at -800 C. Frozen endosperms were pulverized in method of Manning (9). Poly(A)+RNA was isolated using Oligotex-dT. cDNA libraries were constructed using Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning Kit as described in Vettore, et al., (2001). The libraries that made SUCEST. Genet Mol Biol 24: 1-7. cDNAs ranging from 500 to 800 bp in size were assigned as short libraries (S10, S15, S20), and cDNAs >800 were assigned as long libraries (L10, L15, M15, L20, L25). Unamplified libraries were plated and individual colonies picked and transferred to 96 well plates containing liquid Circles Grow (CG) medium supplemented with 100 mg/L of ampicillin and 8% glycerol. Three copies of each cDNA clone were stored at -800 C. Additional information can be found in : Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P. (2005)

Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press/)"

Alignment Scores:  
Pred. No.: 9.07e-24 Length: 903  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO456060 (1-903)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
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Db 228 ATGGCGGCTCTGGCCACGTCGCAGCTGTCGCACGCGCGCGCGCTGGGGCTCCCGGAC 287  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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Db 288 GCGTCCACGTTCCGCCGCGCGCGCGCGCGCTGAGGGCGCGCGCGCTGGCGGCG 347  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
|||||  
Db 348 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 407  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
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Db 408 CGCGCGGGGGGCGAGG-----TTCCCGTCGCTGCTGTGTGC 443

RESULT 28  
CO460347

LOCUS MZCCL15023D11.g 911 bp mRNA linear EST 08-JUN-2005  
DEFINITION Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags

ACCESSION CO460347.1 GI:67031598  
VERSION EST.  
KEYWORDS  
SOURCE Zea mays  
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 911)  
AUTHORS Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H., De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, F.R. and Arruda, P.

TITLE Endosperm-preferred expression of maize genes as revealed by transcriptome-wide analysis of expressed sequence tags

JOURNAL  
COMMENT

Plant Mol. Biol. (2005) In press  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br.

## FEATURES

## source

1. .911  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="F-352 near isogenic line"  
/db\_xref="taxon:4577"  
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/tissue\_type="endosperm"  
/dev\_stage="multiple stages (10 to 25 days after  
pollination, see publication for more information)"  
/lab\_host="E. coli DH10B"  
/clone\_lib="Maize Endosperm cDNA Library"  
/note="Organ: seed; Vector: pSPORT1; Site 1: Sall; Site 2:  
NotI; Plant Material and RNA Isolation: Field grown maize  
plants from inbred line F352 were used. Ears were  
harvested at 10, 15, 20 and 25 days after pollination  
(DAP), seeds were cut from the ear and the upper third of  
the endosperms, containing only endosperm, aleurone and  
pericarpal tissues, was removed, frozen in liquid nitrogen  
and stored at -800 C. Frozen endosperms were pulverized in  
liquid nitrogen and total RNA was isolated according to the  
method of Manning (9). Poly(A)+RNA was isolated using the  
Oligotex-dT. cDNA libraries were constructed using  
SuperScript Plasmid System for cDNA Synthesis and Plasmid  
Cloning Kit as described in Vettore, et al., (2001) The  
libraries from 500 to 800 bp in size were assigned as short  
ranging from 500 to 800 bp in size were assigned as short  
libraries (S10, S15, S20), and cDNAs >800 were assigned as  
long libraries (L10, L15, L20, L25). Unamplified  
libraries were plated and individual colonies picked and  
transferred to 96 well plates containing liquid Circle  
Grow (CG) medium supplemented with 100 mg/L of ampicillin  
and 8% glycerol. Three copies of each cDNA clone were  
stored at -800 C. Additional information can be found in :  
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,  
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
A.L., da Silva, F.R. and Arruda, P. (2005)  
Endosperm-preferred expression of maize genes as revealed  
by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press//)"

## ORIGIN

Alignment Scores:  
Pred. No.: 9,16e-24 Length: 911  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO460347 (1-911)

OY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAep 20  
DB 238 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCGCTGGCGTCCCGGAC 297  
OY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 298 GGTCCACGTTCCCGCGCGCGCGCGCGAGGCCCTGAGGGGGCGCGCGTCGCGCGC 357  
OY 41 AlaAepThrLeuSerMetArgThrSerAlaAlaProArgHisGlnGlnAla 60  
DB 358 GCGGACACGCTCAGCATCGGACCAAGCGCGCGCGCGCGCCAGGACACAGCAGCGCG 417  
OY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74

Db 418 CGCCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGC 453

## RESULT 29

## LOCUS

## DEFINITION

CO464483  
MZCCS15033H11.g Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

## 1. .927

## /organism="Zea mays"

## /mol\_type="mRNA"

## /cultivar="F-352 near isogenic line"

## /db\_xref="taxon:4577"

## /sex="hermaphrodite"

## /tissue\_type="endosperm"

/dev\_stage="multiple stages (10 to 25 days after  
pollination, see publication for more information)"

## /lab\_host="E. coli DH10B"

## /clone\_lib="Maize Endosperm cDNA Library"

/note="Organ: seed; Vector: pSPORT1; Site 1: Sall; Site 2:  
NotI; Plant Material and RNA Isolation: Field grown maize  
plants from inbred line F352 were used. Ears were  
harvested at 10, 15, 20 and 25 days after pollination  
(DAP), seeds were cut from the ear and the upper third of  
the endosperms, containing only endosperm, aleurone and  
pericarpal tissues, was removed, frozen in liquid nitrogen  
and stored at -800 C. Frozen endosperms were pulverized in  
liquid nitrogen and total RNA was isolated according to the  
method of Manning (9). Poly(A)+RNA was isolated using the  
Oligotex-dT. cDNA libraries were constructed using  
SuperScript Plasmid System for cDNA Synthesis and Plasmid  
Cloning Kit as described in Vettore, et al., (2001) The  
libraries from 500 to 800 bp in size were assigned as short  
ranging from 500 to 800 bp in size were assigned as short  
libraries (S10, S15, S20), and cDNAs >800 were assigned as  
long libraries (L10, L15, L20, L25). Unamplified  
libraries were plated and individual colonies picked and  
transferred to 96 well plates containing liquid Circle  
Grow (CG) medium supplemented with 100 mg/L of ampicillin  
and 8% glycerol. Three copies of each cDNA clone were  
stored at -800 C. Additional information can be found in :  
Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,  
Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
A.L., da Silva, F.R. and Arruda, P. (2005)  
Endosperm-preferred expression of maize genes as revealed  
by transcriptome-wide analysis of expressed sequence tags.  
Plant Molecular Biology (/in press//)"

## ORIGIN

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## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

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## DB 238 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCGCTGGCGTCCCGGAC 297

## OY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40

## DB 298 GGTCCACGTTCCCGCGCGCGCGCGCGAGGCCCTGAGGGGGCGCGCGTCGCGCGC 357

## OY 41 AlaAepThrLeuSerMetArgThrSerAlaAlaProArgHisGlnGlnAla 60

## DB 358 GCGGACACGCTCAGCATCGGACCAAGCGCGCGCGCGCCAGGACACAGCAGCGCG 417

## OY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74

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 Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 259 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGGCGCGCGCGCG 318  
 Qy 41 AlaAspThrLeuSerMetAspThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
 Db 319 GCGGACACGCTCAGCTACGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 378  
 Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 Db 379 CGCGCGGGGGCAGG-----TTCCCGTCTCGTCTGTGTGC 414

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 LOCUS M2CCS15011P02.5 Maize Endosperm cDNA Library Zea mays cDNA, mRNA  
 DEFINITION sequence.  
 ACCESSION CO457630  
 VERSION CO457630.1 GI:67028881  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 785)  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S., Fisch, P.H.,  
 De Rosa, V.E. Jr., Martins, M.M., Vettore, A.L., da Silva, P.R. and  
 Arruda, P.  
 Endosperm-preferred expression of maize genes as revealed by  
 transcriptome-wide analysis of expressed sequence tags  
 Plant Mol. Biol. (2005) In press  
 Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br.  
 Location/Qualifiers  
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 /cultivar="P-352 near isogenic line"  
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 /tissue\_type="endosperm"  
 /dev\_stage="multiple stages (10 to 25 days after  
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 /clone\_lib="Maize Endosperm cDNA Library"  
 /notes="Organ: seed; Vector: pSPORT1; Site 1: Salt; Site 2:  
 Not1; Plant Material and RNA Isolation: Field grown maize  
 plants from inbred line F352 were used. Ears were  
 harvested at 10, 15, 20 and 25 days after pollination  
 (DAP), seeds were cut from the ear and the upper third of  
 the endosperms, containing only endosperm, aleurone and  
 pericarpal tissues, was removed, frozen in liquid nitrogen  
 and stored at -800 C. Frozen endosperms were pulverized in  
 liquid nitrogen and total RNA was isolated according the

method of Manning (9). Poly(A)+RNA was isolated using  
 Oligotex-dT. cDNA libraries were constructed using  
 SuperScript Plasmid System for cDNA Synthesis and plasmid  
 Cloning Kit as described in Vettore, et al., (2001) The  
 libraries that made SUCSEST. Genet Mol Biol 24: 1-7. cDNAs  
 ranging from 500 to 800 bp in size were assigned as short  
 long libraries (L10, L15, S20), and cDNAs >800 were assigned as  
 libraries were plated and individual colonies picked and  
 transferred to 96 well plates containing liquid Circle  
 Grow (CG) medium supplemented with 100 mg/L of ampicillin  
 and 8% glycerol. Three copies of each cDNA clone were  
 stored at -800 C. Additional information can be found in :  
 Verza, N.C., Silva, T.R., Cord-Neto, G., Nogueira, F.T.S.,  
 Fisch, P.H., De Rosa Jr., V.E., Martins, M.M., Vettore,  
 A.L., da Silva, P.R. and Arruda, P. (2005)  
 Endosperm-preferred expression of maize genes as revealed  
 by transcriptome-wide analysis of expressed sequence tags.  
 Plant Molecular Biology (/in press/)

ORIGIN

Alignment Scores:  
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 Score: 329.00 Matches: 70  
 Percent Similarity: 94.6% Conservative: 0  
 Best Local Similarity: 94.6% Mismatches: 2  
 Query Match: 89.4% Indels: 2  
 DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x CO457630 (1-785)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 Db 211 ATGGCGGCTCTGGCCAGCTCGTGCACAGCGCGCGCTGGGGGCTCCCGGAC 270  
 Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
 Db 271 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGGCGCGCGCGCG 330  
 Qy 41 AlaAspThrLeuSerMetAspThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: March 31, 2006, 22:47:42 ; Search time 98.966 Seconds  
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Title: US-10-628-525A-36

Perfect score: 368

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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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					US-09-103-840A-2

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13	83.5	22.7	10333	3	US-09-949-016-15678	Sequence 15678, A
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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/941.445A  
FILING DATE: 30-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,855  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 89-97  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4800 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1449..1553, 1685..1765, 1860..1958, 2055  
LOCATION: ..2144, 2226..2289, 2413..2513, 2651..2760, 2858  
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US-08-941-445A-4

Alignment Scores:  
Pred. No.: 1-5e-24 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 3 Gaps: 1

US-10-628-525A-36 (1-74) x US-08-941-445A-4 (1-4800)

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Db 1233 ATGGCGGCTCTGGCCACGTCGCAGCTCGTCCAAACGCGCGCGCTGGGGCGTCCCGGAC 1292  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
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QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrAlaAlaProArgHisGlnGlnAla 60  
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QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 1413 CGCGCGCGGGGCGAGG-----TTCCCGTCTGCTGCTGTCG 1448

## RESULT 3

US-08-679-645-25  
; Sequence 25, Application US/08679645  
; Patent No. 6350934  
; GENERAL INFORMATION:  
; APPLICANT: Zwick, Michael G.  
; APPLICANT: Edington, Brent E.  
; APPLICANT: McSwiggen, James A.  
; APPLICANT: Merlo, Patricia Ann Owens  
; APPLICANT: Guo, Lining  
; APPLICANT: Skokut, Thomas A.  
; APPLICANT: Young, Scott A.  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Merlo, Donald J.

; TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1263  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/679,645  
; FILING DATE: July 12, 1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/001,135  
; FILING DATE: July 13, 1995  
; APPLICATION NUMBER: 08/300,726  
; FILING DATE: September 2, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 219/247  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2267 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-679-645-25

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Score: 289.00 Matches: 64  
Percent Similarity: 85.9% Conservative: 3  
Best Local Similarity: 82.1% Mismatches: 5  
Query Match: 78.5% Indels: 6  
DB: 3 Gaps: 2

US-10-628-525A-36 (1-74) x US-08-679-645-25 (1-2267)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 177 ATGGCGGCTCTAGCCACGTCGCAGCTCGTCCAAACGCGCGCGCTGGGGCGTCCCGGAC 236  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 237 GCGTCCACGTTCCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGTCCGGCGG 296  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrAlaAlaProArg-----His 56  
Db 297 GCGGACACGCTCAGCATTCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 356  
QY 57 GlnGlnAlaArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 357 CAGCAGCAGCGCGCGCGCGCGCGCGG-----TTCCCGTCTGCTGCTGTCG 404

## RESULT 4

US-08-941-445A-6  
; Sequence 6, Application US/08941445A  
; Patent No. 6107060

```

; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Heping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 453..2282
; US-08-941-445A-6

Alignment Scores:
Pred. No.: 0.000583 Length: 2542
Score: 128.50 Matches: 35
Percent Similarity: 60.3% Conservative: 12
Best Local Similarity: 44.9% Mismatches: 24
Query Match: 34.9% Indels: 7
DB: 3 Gaps: 4

US-10-628-525A-36 (1-74) x US-08-941-445A-6 (1-2542)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20
Db 453 ATGTGGCTCTCACCAGCTCCCGACCTCGGCCACCGGCTTCGGCATCGCCGAC 512
QY 21 -----AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAla 37
Db 513 AGGTGGCGCGCTCGTGGCTGCTCCGCCACGGTTCAGGGGCTCAAG---CCCCGCAGC 569
QY 38 SerAlaAlaAlaAsp-----ThrLeuSerMetArgThrSerAlaArgAlaAlaProArg 55
Db 570 CCCGCGCGCGCGACGCGACGCTCGCTCAGCGTGCAGCAGCAGCGCGCGCGCGCGCCAA 629
QY 56 HisGlnGlnAlaAlaArgGlyGlyArgPheProPheProSerLeuValVal 73
Db 630 CAGCAGCGGTGCGTGCAGCGTGGCAGCCGG---AGTTCCCTCCGTGCTG 680

RESULT 5
; Sequence 1085, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1085
; LENGTH: 1714
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-104-047-1085

Alignment Scores:
Pred. No.: 0.432 Length: 1714
Score: 98.50 Matches: 31
Percent Similarity: 44.6% Conservative: 6
Best Local Similarity: 37.3% Mismatches: 28
Query Match: 26.8% Indels: 18
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-10-104-047-1085 (1-1714)
QY 6 ThrSerGlnLeuValAla---ThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24
Db 784 TCCAAGATGCTGTGTGGCCCGGTGAGTGTGCTGCTGCCAGGTCCCTCTGCACGTG 843
QY 25 Arg-ArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrIle 44
Db 844 AGGCAGGGGAGGCCAGCAAGGACTTCAGGGCTGCAGAGCCTTCCTGCAGTTCCTACCTT 903
QY 44 u-----SerMetArgThrSerAlaArgAlaAlaPr 54
Db 904 ACAACACAGGATCTAATCCCTAACCTGGGGTACGTGTGAGACCACAGGGAGAGGCCCTC 963
QY 54 oArgHisGlnGlnAlaAlaArg-----ArgGlyGlyArgPheProPh 68
Db 964 GAGGCATGGGCACCATGCCAGGCTGTAGGCACCTTCTCTGCAGCAGGAGCAGAAATCCCTT 1023
QY 68 eProSer 70
Db 1024 CCCAAGT 1030

RESULT 6
; Sequence 884, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 884
; LENGTH: 6776
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-884

Alignment Scores:
Pred. No.: 22.3 Length: 6776
```

```

; Sequence 1085, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1085
; LENGTH: 1714
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-104-047-1085

Alignment Scores:
Pred. No.: 0.432 Length: 1714
Score: 98.50 Matches: 31
Percent Similarity: 44.6% Conservative: 6
Best Local Similarity: 37.3% Mismatches: 28
Query Match: 26.8% Indels: 18
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-10-104-047-1085 (1-1714)
QY 6 ThrSerGlnLeuValAla---ThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24
Db 784 TCCAAGATGCTGTGTGGCCCGGTGAGTGTGCTGCTGCCAGGTCCCTCTGCACGTG 843
QY 25 Arg-ArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrIle 44
Db 844 AGGCAGGGGAGGCCAGCAAGGACTTCAGGGCTGCAGAGCCTTCCTGCAGTTCCTACCTT 903
QY 44 u-----SerMetArgThrSerAlaArgAlaAlaPr 54
Db 904 ACAACACAGGATCTAATCCCTAACCTGGGGTACGTGTGAGACCACAGGGAGAGGCCCTC 963
QY 54 oArgHisGlnGlnAlaAlaArg-----ArgGlyGlyArgPheProPh 68
Db 964 GAGGCATGGGCACCATGCCAGGCTGTAGGCACCTTCTCTGCAGCAGGAGCAGAAATCCCTT 1023
QY 68 eProSer 70
Db 1024 CCCAAGT 1030

RESULT 6
; Sequence 884, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 884
; LENGTH: 6776
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-884

Alignment Scores:
Pred. No.: 22.3 Length: 6776
```

```
Score: 88.50 Matches: 25
Percent Similarity: 44.9% Conservative: 10
Best Local Similarity: 32.1% Mismatches: 22
Query Match: 24.0% Indels: 21
DB: 3 Gaps: 2

US-10-628-525A-36 (1-74) x US-09-902-540-884 (1-6776)

QY 15 GlyHisGlyValProAspAlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGly 34
DQ 4655 GGCATTCTCCACCGCGGTCTATCTCCGACCGCGAGATCTCAGCACCTCCGCTCA 4596
QY 35 AlaArgAlaSerAla-----AlaAlaAspThrLeuSer 45
DQ 4595 TCTCAATCTCCCGCGCTTCCATGACGACCACTGGAGCGCGCTCTCGACCTCAAT 4536
QY 46 MetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAlaArg----- 61
DQ 4535 GCCCGCTGTGCGCATCCACCGCGCTCGCAGGTCTATGACACCCGTCGGAGCCCGGC 4476
QY 62 -----ArgGlyGlyArgPheProPheProSerLeu 71
DQ 4475 TCCAGGCCCACTGTCTCCAGATGAGTGGAGGCGCTCGAACAATCCGGCAATC 4422

RESULT 7
US-09-949-016-13016/c
; Sequence 13016, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13016
; LENGTH: 49315
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13016

Alignment Scores:
Pred. No.: 316 Length: 49315
Score: 87.00 Matches: 25
Percent Similarity: 53.7% Conservative: 4
Best Local Similarity: 46.3% Mismatches: 21
Query Match: 23.6% Indels: 4
DB: 3 Gaps: 2

US-10-628-525A-36 (1-74) x US-09-949-016-13016 (1-49315)

QY 15 GlyHisGlyValProAspAlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGly 34
DQ 2093 GGCATTGTGTGCGACCGCGGTCTATCTCCGACCGCGAGTACCGCGCTCGACGCC 2037
QY 35 AlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAlaArg----- 51
DQ 2036 AGCGCGGACCGCGGAGAACCCAGATCTGGGGCGGGGACCTACCGCGCTCGACGCC 1977
QY 52 AlaAlaProArgHisGlnGlnGlnAlaArgArgGlyArg 65
DQ 1976 GCGCGCCCGCGCGGTCCCGCTGACGCCACAAAGCGCGGCGG 1935

RESULT 8
US-09-899-718A-1

; Sequence 1, Application US/09899718A
; Patent No. 6949693
; GENERAL INFORMATION:
; APPLICANT: Aventis CropScience GmbH
; TITLE OF INVENTION: Promotor for gene expression in caryopses of plants
; FILE REFERENCE: 51413-3886
; CURRENT APPLICATION NUMBER: US/09/899,718A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: DE 100 41 861.9
; PRIOR FILING DATE: 2000-08-26
; PRIOR APPLICATION NUMBER: DE 100 32 379.0
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3785
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-899-718A-1

Alignment Scores:
Pred. No.: 20.5 Length: 3785
Score: 86.00 Matches: 31
Percent Similarity: 53.7% Conservative: 5
Best Local Similarity: 46.3% Mismatches: 23
Query Match: 23.4% Indels: 8
DB: 3 Gaps: 4

US-10-628-525A-36 (1-74) x US-09-899-718A-1 (1-3785)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAsp 20
DQ 3140 ATGGCGGCTCTGTCTACGTCCAGCTCGCCACCTCGCGGACCCGCTCTCAGCGTCACCGAC 3199
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DQ 3200 -----AGATTCGCGGCTCCAGGTTTTCAGGGGCTGAGGCGCCCGGAAACCGCGGATGCG 3253
QY 41 AlaAspThrLeuSerMetArgThr-----SerAlaArgAlaAlaProArgHisGlnGln 59
DQ 3254 GCG-----CTCGCATGAGGACTGTCGAGGCGGAGCGCGCCCGCCCAAG-----CAA 3298
QY 60 AlaArgArgGlyGlyArgPhe 66
DQ 3299 AGCAGGAACCGCACCGCATTC 3319

RESULT 9
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
```





Score: 82.00 Matches: 29  
Percent Similarity: 53.0% Conservative: 6  
Best Local Similarity: 43.9% Mismatches: 24  
Query Match: 22.3% Indels: 7  
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-09-949-016-14168 (1-21490)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAla 29  
Db 1416 GTGTGGGCGCGAGGGAGGCGCGCCCGGGCGCCCGAGTGAGGGCGGGCGGCG 1475  
QY 30 GlnGlyLeuArg---GlyAlaArgAlaSerAlaAlaAspThrLeuSerMetArgThr 48  
Db 1476 AAGGAGCGCGGTGCGCGCACTTGTGCGCGGCTTGATGGCTGGGC-----CCC 1529  
QY 49 SerAlaArgAlaAla-ProArgHisGlnGlnAlaArgArgGlyGlyArgPhe----- 66  
Db 1530 CCTCGCGCTCGCTCTCCACAGCGCGCGCGCGCGCGCGGCGGCGCGCGCGCG 1589  
QY 67 ----ProPheProSer 70  
Db 1590 GGGCCCGGCACCTTCG 1605

## RESULT 16

US-09-949-016-13338  
; Sequence 13338, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13338  
; LENGTH: 25709  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13338

## Alignment Scores:

Pred. No.: 482 Length: 25709  
Score: 82.00 Matches: 29  
Percent Similarity: 53.0% Conservative: 6  
Best Local Similarity: 43.9% Mismatches: 24  
Query Match: 22.3% Indels: 7  
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-09-949-016-13338 (1-25709)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAla 29  
Db 1416 GTGTGGGCGCGAGGGAGGCGCGCCCGGGCGCCCGAGTGAGGGCGGGCGGCG 1475  
QY 30 GlnGlyLeuArg---GlyAlaArgAlaSerAlaAlaAspThrLeuSerMetArgThr 48  
Db 1476 AAGGAGCGCGGTGCGCGCACTTGTGCGCGGCTTGATGGCTGGGC-----CCC 1529  
QY 49 SerAlaArgAlaAla-ProArgHisGlnGlnAlaArgArgGlyGlyArgPhe----- 66  
Db 1530 CCTCGCGCTCGCTCTCCACAGCGCGCGCGCGCGCGCGGCGGCGGCGCGCG 1589  
QY 67 ----ProPheProSer 70  
Db 1590 GGGCCCGGCACCTTCG 1605

Db 1590 GGGCCCGGCACCTTCG 1605

## RESULT 17

US-09-252-991A-15592/c  
; Sequence 15592, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 15592  
; LENGTH: 1008  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15592

## Alignment Scores:

Pred. No.: 14.4 Length: 1008  
Score: 81.00 Matches: 24  
Percent Similarity: 48.4% Conservative: 6  
Best Local Similarity: 38.7% Mismatches: 30  
Query Match: 22.0% Indels: 2  
DB: 3 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-252-991A-15592 (1-1008)

QY 5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24  
Db 315 GCGCCTCGCGAAGGCTTGCCTGTCAGCGCGGTTGGAGCTGGCGGTGGACCGCTGT 256  
QY 25 ArgArgGlyAlaGlnGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeu 44  
Db 255 CGGCGCGGATCTGCAGCGCGGCTTGTCTGAGCGGCTTCGACGGGCTCGCCCTGGCGGCTT 196  
QY 45 SerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAlaArgArgGlyGly 64  
Db 195 CGGCAAGGCGGAGCTGCGCTGCTCAGCCCGC-----TCGGGAGCGCGCGCGGCG 142  
QY 65 ArgPhe 66  
Db 141 CGGTTC 136

## RESULT 18

US-09-252-991A-15755  
; Sequence 15755, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 15755  
; LENGTH: 1266  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15755  
Alignment Scores:

```
Pred. No.: 18.7 Length: 1266
Score: 81.00 Matches: 24
Percent Similarity: 48.4% Conservative: 6
Best Local Similarity: 38.7% Mismatches: 30
Query Match: 22.0% Indels: 2
DB: 3 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-252-991A-15755 (1-1266)

QY 5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24
   |||
   ::
   |||
Db 559 GCCTCGCCGAGGCTTGGCTGTCAGAGCGGGTTGGAGCTGGCGTGGAGACCGTGCT 618

QY 25 ArgArgAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeu 44
   |||
   ::
   |||
Db 619 CGGCGGGATCTGAGCGGCTTGTGTGAGCGCTTCGACGGGCTCGCCCTGGCCCGGCTT 678

QY 45 SerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAlaArgArgGlyGly 64
   |||
   ::
   |||
Db 679 CGGCAAGGCGAGCTGGCTGCTCAGCCCGC-----TCGGGAGCCGCGAGCGCGC 732

QY 65 ArgPhe 66
   |||
   |||
Db 733 CGGTTT 738

RESULT 19
US-08-656-393-1/c
; Sequence 1, Application US/08656393
; Patent No. 5837258
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; TITLE OF INVENTION: METHODS AND USES OF CONNECTIVE TISSUE
; TITLE OF INVENTION: GROWTH FACTOR AS AN INDUCTION AGENT
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,393
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2541 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-656-393-1

Alignment Scores:
Pred. No.: 41.9 Length: 2541
Score: 81.00 Matches: 23
Percent Similarity: 49.2% Conservative: 6
Best Local Similarity: 39.0% Mismatches: 20
Query Match: 22.0% Indels: 10
```

```
DB: 2 Gaps: 2
US-10-628-525A-36 (1-74) x US-08-656-393-1 (1-2541)

QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
   |||
   ::
   |||
Db 2264 ACACCGGATCTTGGCGTTGGCCGGGAGCCGAAGTCACAGAGAGGCCCTTGTGCGGGT 2205

QY 32 LeuArgGly-----AlaArgAlaSerAlaAlaAlaAspThrLeuSerMet 46
   |||
   ::
   |||
Db 2204 CGCAGGGTGGCGTGGTGCACAGCTGCCAGCTGCTTGGCGAGAC----- 2157

QY 47 ArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAlaArgArgGlyGlyArg 65
   |||
   ::
   |||
Db 2156 ---GCCGAGCAGCCGCGCTCCAGCAGAGGCTCAGCCCGCGGCGAGCGCG 2103

RESULT 20
US-09-252-991A-15560/c
; Sequence 15560, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15560
; LENGTH: 3402
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15560

Alignment Scores:
Pred. No.: 58.8 Length: 3402
Score: 81.00 Matches: 24
Percent Similarity: 48.4% Conservative: 6
Best Local Similarity: 38.7% Mismatches: 30
Query Match: 22.0% Indels: 2
DB: 3 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-252-991A-15560 (1-3402)

QY 5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24
   |||
   ::
   |||
Db 1552 GCCTCGCCGAGGCTTGGCTGTCAGCGGGTTGGAGCTGGCGTGGAGACCGTGCT 1493

QY 25 ArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAspThrLeu 44
   |||
   ::
   |||
Db 1492 CGGCGGGATCTGACGGCGCTTGTCTGACCGGCTTCGACGGCTCGCCCTGGCCGGCTT 1433

QY 45 SerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAlaArgArgGlyGly 64
   |||
   ::
   |||
Db 1432 CGGCAAGGCGGAGCTGGCTGCTCAGCCCGC-----TCGGGAGCCGCGAGCGCGC 1379

QY 65 ArgPhe 66
   |||
   |||
Db 1378 CGGTTT 1373

RESULT 21
US-09-252-991A-15688
; Sequence 15688, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
```

[illegible]



```
; PRIOR APPLICATION NUMBER: 09/232,279
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2799
; TYPE: DNA
; ORGANISM: Bovine herpesvirus 2
US-10-085-519-1

Alignment Scores:
Pred. No.: 52.7      Length: 2799
Score: 80.50        Matches: 28
Percent Similarity: 51.6%      Conservative: 4
Best Local Similarity: 45.2%    Mismatches: 18
Query Match: 21.9%            Indels: 12
DB: 3                  Gaps: 2

US-10-628-525A-36 (1-74) x US-10-085-519-1 (1-2799)
QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26
Db 1833 GCCCAGCTGTGGCAGTACGTACGCCCATGGGTCCCC-----CAA 1792
QY 27 GlyAlaAlaGlnGlyLeu-ArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMe 46
Db 1791 CATGCGCGCGCGCGCGCGGTCACGCGAGCGCTGCGCGCGCTGGGGTTGAGCTT 1732
QY 46 tArgThrSerAlaArgAlaAala-----ProArgHisGlnGlnAlaAr 61
Db 1731 AGCGGCTCGGCCACAGGCGCGCTCTTGTTCGACGACGACGACGACGACGTCGCCAG 1672
QY 61 gArg 62
Db 1671 GCGG 1668

RESULT 25
US-08-682-847-1/c
; Sequence 1, Application US/08682847
; Patent No. 5858989
; GENERAL INFORMATION:
; APPLICANT: BABIUK, LORNE
; APPLICANT: VAN DEN HURK, SYLVIA
; APPLICANT: ZAMB, TIM
; APPLICANT: FITZPATRICK, DAVID
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1
; TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,847
; FILING DATE: 12-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: PARK, FREDDIE K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 29310-20005.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3382 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 432..3230
US-08-682-847-1

Alignment Scores:
Pred. No.: 65.7      Length: 3382
Score: 80.50        Matches: 28
Percent Similarity: 51.6%      Conservative: 4
Best Local Similarity: 45.2%    Mismatches: 18
Query Match: 21.9%            Indels: 12
DB: 2                  Gaps: 2

US-10-628-525A-36 (1-74) x US-08-682-847-1 (1-3382)
QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26
Db 2267 GCCCAGCTGTGGCAGTACGTACGCCCATGGGTCCCC-----CAA 2226
QY 27 GlyAlaAlaGlnGlyLeu-ArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMe 46
Db 2225 CATGCGCGCGCGCGCGGTCACGCGAGCGCTGCGCGCGCTGGGGTTGAGCTT 2166
QY 46 tArgThrSerAlaArgAlaAala-----ProArgHisGlnGlnAlaAr 61
Db 2165 AGCGGCTCGGCCACAGGCGCGCTCTTGTTCGACGACGACGACGACGACGTCGCCAG 2106
QY 61 gArg 62
Db 2105 GCGG 2102

RESULT 26
US-09-252-991A-6863/c
; Sequence 6863, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6863
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6863

Alignment Scores:
Pred. No.: 11.3      Length: 666
Score: 80.00        Matches: 32
Percent Similarity: 45.6%      Conservative: 9
Best Local Similarity: 35.6%    Mismatches: 30
Query Match: 21.7%            Indels: 19
DB: 3                  Gaps: 3

US-10-628-525A-36 (1-74) x US-09-252-991A-6863 (1-666)
QY 2 AlaAlaLeuAlaThrSerGlnLeuValAlaThr-----ArgAlaGlyHisGlyVal 18
Db 392 GCAGCACTGCGCGCGGATCGGTAGTGATCGGTGCGCGCGGTGCAGTGGCGG 333
```

QY 19 ProAspAlaSerThr-----PheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArg 36  
Db 332 CCGGACCGCGCACACAGACGAGCGGCGATCGCGCGCGCTCGGTGGCGAGCGGCA 273  
QY 37 AlaSerAlaAla-AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHi 56  
Db 272 AGCTCATCGCGCGGAGATCGGTGGCAGCACCGGTGGCTGATCGCGCGCGCTCGGCG 213  
QY 56 sGlnGlnGlnAlaArgArgGlyGly----- 64  
Db 212 GCGCGCGCGCGCGCGCTGGTGGCAACCATATATGGCGACGCAACCGCCGCTACGACGACG 153  
QY 65 ----ArgPheProPheProSerLeuVal 72  
Db 152 ATGACGACTACCGGACCGCTCGCTACTA 125

RESULT 27  
US-09-902-540-7146  
; Sequence 7146, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 7146  
; LENGTH: 813  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-7146

Alignment Scores:  
Pred. No.: 14.2 Length: 813  
Score: 80.00 Matches: 27  
Percent Similarity: 42.6% Conservative: 2  
Best Local Similarity: 39.7% Mismatches: 25  
Query Match: 21.7% Indels: 14  
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-09-902-540-7146 (1-813)

QY 8 GlnLeuValAlaThrArgAlaGlyHis-----GlyValPro 19  
Db 12 CGCCTACTTCTTACAGGAAGAGCCACCGCGGACGCGCGCGGGGGCGGAGTCCCC 71  
QY 20 AspAlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAla 39  
Db 72 GGTGCTGGA-----AGAGGTGCTGCCAAGGCCTCGCGCTGGCGGTGCGCGCGCT 122  
QY 40 AlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGln 59  
Db 123 GCGCAACCAATGACACACAGCGCTGCGAAGTGGGGGACACCGCCATCCAGGTGGC 182  
QY 60 Ala-----ArgArgGlyGly 64  
Db 183 GCGCGTGGAGTAGCAGAGGTGCG 206

RESULT 28  
US-09-252-991A-6763  
; Sequence 6763, Application US/09252991A  
; Patent No. 6851795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6763  
; LENGTH: 1164  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6763

Alignment Scores:  
Pred. No.: 21.5 Length: 1164  
Score: 80.00 Matches: 32  
Percent Similarity: 45.6% Conservative: 9  
Best Local Similarity: 35.6% Mismatches: 30  
Query Match: 21.7% Indels: 19  
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-09-252-991A-6763 (1-1164)

QY 2 AlaAlaLeuAlaThr-SerGlnLeuValAlaThr-----ArgAlaGlyHisGlyVal 18  
Db 785 GCAGCACTGGCGCGCGGATCGGTAGTGGCATCGGTGGCGCTCGGGCGGTGAGTCGGCG 844  
QY 19 ProAspAlaSerThr-----PheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArg 36  
Db 845 CCGGACCGCGCACACAGACGAGCGGCGATCGCGCGCGCTCGGTGGCGCGCGCGCA 904  
QY 37 AlaSerAlaAla-AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHi 56  
Db 905 AGTCATCGCGCGGAGATCGGTGGCAGCACCGGTGGCTGATCGCGCGCGCTCGGCG 964  
QY 56 sGlnGlnGlnAlaArgArgGlyGly----- 64  
Db 965 GCGCGCGCGCGCGCGCTGGGCAACCATATATGGCGACGCGCAACCGCCGCTACGACGACG 1024  
QY 65 ----ArgPheProPheProSerLeuVal 72  
Db 1025 ATGACGACTACCGGACCGCTCGCTACTA 1052

RESULT 29

US-09-902-540-656  
; Sequence 656, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 656  
; LENGTH: 5163  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-656

Alignment Scores:  
Pred. No.: 121 Length: 5163  
Score: 80.00 Matches: 27  
Percent Similarity: 42.6% Conservative: 2  
Best Local Similarity: 39.7% Mismatches: 25  
Query Match: 21.7% Indels: 14  
DB: 3 Gaps: 3

US-10-628-525A-36 (1-74) x US-09-902-540-656 (1-5163)					
	Qy	8 GlnLeuValAlaThrArgAlaGlyHis-----GlyValPro 19			
	Db	4362 CGCTACTTCTACAGAGAGCCACC CGGGACGCCGGCGGGCGGCAGTCCTCCC 4421			
	Qy	20 AspAlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAla 39			
	Db	4422 GTGTCTGGA-----AGAGTGTCGCCAAGGCCCTCCGCGTGGCGGTGCGCGCCT 4472			
	Qy	40 AlaAlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnGln 59			
	Db	4473 GCSCCAANTGGACACAACGACGCGCTGTGCGAAGTTGGGGGACACCGGCATCCAGGTGGC 4532			
	Qy	60 Ala-----ArgArgGlyGly 64			
	Db	4533 GCGCTGGAGTAGCACGACGAGGTGGC 4556			
RESULT 30					
US-08-998-416-689/c ; Sequence 689, Application US/08998416					
Patent No. 6239264					

  

Percent Similarity:	43.9%	Conservative:	3
Best Local Similarity:	39.4%	Mismatches:	28
Query Match:	21.6%	Indels:	9
DB:	3	Gaps:	1

  

US-10-628-525A-36 (1-74) x US-08-998-416-689 (1-696)	
Qy	11 AlathrArgAlaGly-----HisGlyValProaspAla 21
Db	590 GCAGAGAAGGCGCAGAAAGCGCGGGTTCAGGCGGCGAGCGGCGGCTCGTGCA 531
Qy	22 SerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 41
Db	530 TGTACTCGGAGCGCGGCTGCCAGGCTGGATGACGTGTGAAGACGATCTCGAAGCGCG 471
Qy	42 AspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAlaArg 61
Db	470 AGTCGGCGCGCGCGGGGAAAAGGGCGTCTGCCAGCGGAGGAGGCGCGCGCAGA 411
Qy	62 ArgGlyGlyArgPhePro 67
Db	410 AGGGGCGAGCATAGTCCA 393

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 00:58:46 ; Search time 349.614 Seconds  
(without alignments)  
1750.313 Million cell updates/sec

Title: US-10-628-525A-36

Perfect score: 368

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	333	90.5	2111	8	US-10-425-115-155307
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4	333	90.5	2263	6	US-10-272-291-2
5	333	90.5	4800	6	US-10-272-291-5
6	333	90.5	4800	7	US-10-109-048-1141
7	333	90.5	4800	8	US-10-628-525-4
GENERAL INFORMA					

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Sequence 15641, A  
Sequence 19555, A  
Sequence 155340, A  
Sequence 7, Appli  
Sequence 1, Appli  
Sequence 25, Appli  
Sequence 46, Appli  
Sequence 42638, A  
Sequence 15855, A  
Sequence 2053, Ap  
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Sequence 2049, Ap  
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Sequence 2057, Ap  
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Sequence 2062, Ap  
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Sequence 8144, Ap  
Sequence 30548, A  
Sequence 54227, A  
Sequence 83514, A  
Sequence 1863, Ap  
Sequence 624, App  
Sequence 12647, A  
Sequence 35966, A  
Sequence 2318, Ap  
Sequence 2165, Ap

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81 81.5 22.1 9025608 6 US-10-156-761-1 Sequence 1, Appli
82 82 22.0 864 7 US-10-437-963-48278 Sequence 48278, A
83 83 22.0 1302 7 US-10-282-122A-14357 Sequence 14357, A
84 84 22.0 2562 6 US-10-156-761-1133 Sequence 1133, Ap
85 85 22.0 3489 3 US-09-815-242-7731 Sequence 7731, Ap
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138 138 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
139 139 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
140 140 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
141 141 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
142 142 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
143 143 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
144 144 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
145 145 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
146 146 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
147 147 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
148 148 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
149 149 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli
150 150 22.0 137560 8 US-10-481-112-1 Sequence 1, Appli

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ALIGNMENTS

```

RESULT 1
US-10-877-645-2
; Sequence 2, Application US/10877645
; Publication No. US20050005327A1
; GENERAL INFORMATION:
; APPLICANT: Ravanello, Monica P
; APPLICANT: Foley, Terry J
; APPLICANT: LeDeaux, John R
; APPLICANT: Wyrick, Annette E
; APPLICANT: Savage, Thomas J
; TITLE OF INVENTION: Elevation of Oil Levels in Plants
; FILE REFERENCE: REN-00-119
; CURRENT APPLICATION NUMBER: US/10/877,645
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 1818
; TYPE: DNA
; ORGANISM: Zea mays
US-10-877-645-2
Alignment Scores:
Pred. No.: 4,9e-31 Length: 1818
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 8 Gaps: 1
US-10-628-525A-36 (1-74) x US-10-877-645-2 (1-1818)
QY 1 MetAlaLaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20
Db 1 ATGGCGGCTCTGGCCACGCTCGTCGACACGCGCGCGGCTGGCGCTCGCGGAC 60
QY 21 AlaSerThrPheArgGlyValAlaGlnGlyLeuArgGlyValAlaSerAlaAla 40
Db 61 GCGTCCAGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 121 GCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 ArgArgGlyGlyArgPhePropheProSerLeuValValCys 74
Db 181 CGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 216
RESULT 2
US-10-425-115-155307
; Sequence 155307, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 155307
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MMT4577_7321C.1
US-10-425-115-155307
Alignment Scores:

```

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Pred. No.: 5.67e-31 Length: 2111
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-115-155307 (1-2111)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 1 ATGGCGGCTCTGGCCACGTCGACGTCGTGCAACGCGCGCCGCTGGGGCTCCCGGAC 60
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 61 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 121 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 181 CGCGCGCGGGGCGAGG-----TTCCCGTCGCTGCTGTGTGC 216

RESULT 3
US-10-272-291-1
; Sequence 1, Application US/10272291
; Publication No. US20030150023A1
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The mutation is at position 1643 in the sequence,
; OTHER INFORMATION: 1450 bp after the start codon.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The change is a "G" in the wild type (EX385) to an
; OTHER INFORMATION: "A" in the mutant
US-10-272-291-2

Alignment Scores:
Pred. No.: 6.07e-31 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 6 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-272-291-2 (1-2263)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 194 ATGGCGGCTCTGGCCACGTCGACGTCGTGCAACGCGCGCGCGCTGGGGCTCCCGGAC 253
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 254 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 313
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 314 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 374 CGCGCGGGGGGCGAGG-----TTCCCGTCGCTGCTGTGTGC 409

RESULT 5
US-10-272-291-5
; Sequence 5, Application US/10272291
; Publication No. US20030150023A1
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4800
; TYPE: DNA
```

```
Pred. No.: 5.67e-31 Length: 2111
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-115-155307 (1-2111)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 1 ATGGCGGCTCTGGCCACGTCGACGTCGTGCAACGCGCGCCGCTGGGGCTCCCGGAC 60
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 61 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 121 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 181 CGCGCGGGGGGCGAGG-----TTCCCGTCGCTGCTGTGTGC 216

RESULT 3
US-10-272-291-1
; Sequence 1, Application US/10272291
; Publication No. US20030150023A1
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The mutation is at position 1643 in the sequence,
; OTHER INFORMATION: 1450 bp after the start codon.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The change is a "G" in the wild type (EX385) to an
; OTHER INFORMATION: "A" in the mutant
US-10-272-291-2

Alignment Scores:
Pred. No.: 6.07e-31 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 6 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-272-291-1 (1-2263)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 194 ATGGCGGCTCTGGCCACGTCGACGTCGTGCAACGCGCGCGCGCTGGGGCTCCCGGAC 253
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 254 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 313
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 314 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 374 CGCGCGGGGGGCGAGG-----TTCCCGTCGCTGCTGTGTGC 409
```

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; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1233)..(1448)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1554)..(1684)
; OTHER INFORMATION: number 2
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1766)..(1859)
; OTHER INFORMATION: number 3
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1959)..(2054)
; OTHER INFORMATION: number 4
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2145)..(2225)
; OTHER INFORMATION: number 5
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2290)..(2412)
; OTHER INFORMATION: number 6
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2514)..(2650)
; OTHER INFORMATION: number 7
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2761)..(2857)
; OTHER INFORMATION: number 8
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3102)..(3211)
; OTHER INFORMATION: number 9
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3395)..(3489)
; OTHER INFORMATION: number 10
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3682)..(3792)
; OTHER INFORMATION: number 11
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3880)..(3976)
; OTHER INFORMATION: number 12
; FEATURE:
; NAME/KEY: intron
; LOCATION: (4106)..(4226)
; OTHER INFORMATION: number 13
US-10-272-291-5
Alignment Scores:
Pred. No.: 1,27e-30 Length: 4800
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 6 Gaps: 1
US-10-628-525A-36 (1-74) x US-10-272-291-5 (1-4800)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 1233 ATGGCGGCTCTGGCACGTCGTCGCAACGCGCGGCTGGCGGTCCCGGAC 1292
QY 21 AlaSerThrPheArgGlyAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 1293 GCGTCCAGCTTCGCGCGGCGCGGCGCTGAGGGGGCCCGGCGCGCGGCG 1352
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 1353 GCGGACACGTCAGCATGGGACCGCGCGGCGCGGCGCGCGCGCGCGCGCGG 1412
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 1413 CGCGCGCGGCGGCGAGG-----TTCCCGTGGTCTCGTGTGTGC 1448
RESULT 7
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:

```



Alignment Scores:  
Pred. No.: 1,278-30 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-628-525-4 (1-4800)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1233 ATGGCGGCTCTGGCCAGCTCGAGCTGCTCGCAACGGCGCGCTGGCGTCCCGGAC 1292

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
DB 1293 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCTCGCGGGCG 1352

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60  
DB 1353 GCGGACACGCTCAGCATGGGACCGCGCGCGCGCGCGCGCGCCCGCCAGCAGCAGGCG 1412

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 1413 CGCGCGCGGGGCGAGG-----TTCCCGTCTGCTGCTGTCG 1448

RESULT 8  
US-10-425-114-17713  
; Sequence 17713, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 17713  
; LENGTH: 1406  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3075-006-H11\_FLI

Alignment Scores:  
Pred. No.: 1,278-30 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-628-525-4 (1-4800)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1233 ATGGCGGCTCTGGCCAGCTCGAGCTGCTCGCAACGGCGCGCTGGCGTCCCGGAC 1292

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
DB 1293 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCTCGCGGGCG 1352

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60  
DB 1353 GCGGACACGCTCAGCATGGGACCGCGCGCGCGCGCGCGCGCCCGCCAGCAGCAGGCG 1412

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 1413 CGCGCGCGGGGCGAGG-----TTCCCGTCTGCTGCTGTCG 1448

RESULT 8  
US-10-425-114-17713  
; Sequence 17713, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 17713  
; LENGTH: 1406  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3075-006-H11\_FLI

Alignment Scores:

Pred. No.: 2,768-30 Length: 1406  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-114-17713 (1-1406)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 172 ATGGCGGCTCTGGCCAGCTCGAGCTGCTCGCAACGGCGCGCTGGCGTCCCGGAC 231

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
DB 232 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCTCGCGGGCG 291

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60  
DB 292 GCGGACACGCTCAGCATGGGACCGCGCGCGCGCGCGCGCCCGCCAGCAGCAGGCG 351

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 352 CGCGCGGGGCGAGG-----TTCCCGTCTGCTGCTGTCG 387

RESULT 9

US-10-425-114-16641  
; Sequence 16641, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 16641  
; LENGTH: 1409  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3066-030-H5\_FLI

Alignment Scores:  
Pred. No.: 2,768-30 Length: 1409  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-114-16641 (1-1409)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 175 ATGGCGGCTCTGGCCAGCTCGAGCTGCTCGCAACGGCGCGCTGGCGTCCCGGAC 234

QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAla 40  
DB 235 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCTCGCGGGCG 294

QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60  
DB 295 GCGGACACGCTCAGCATGGGACCGCGCGCGCGCGCGCGCCCGCCAGCAGCAGGCG 354

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 355 CGCCGGGGGGGAGG-----TTCCGTCGCTCGTGTGTC 390

RESULT 10

US-10-425-114-19555  
; Sequence 19555, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 19555  
; LENGTH: 1416  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-022-D3\_FLI  
US-10-425-114-19555

Alignment Scores:  
Pred. No.: 2,78e-30 Length: 1416  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservatives: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 7 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-114-19555 (1-1416)

QY 1 MetalAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 173 ATGGCGGCTCTGGCCACGCTCGCAGCTCGTCGCAACGCCCGCGGCTGGGGCTCCCGGAC 232  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 233 GCGTCCACGTTCCG 292  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 293 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 352  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 353 CGCCGGGGGGGAGG-----TTCCGTCGCTCGTGTGTC 388

RESULT 11

US-10-425-115-155340  
; Sequence 155340, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 155340  
; LENGTH: 2442

; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_7324C.1  
US-10-425-115-155340

Alignment Scores:  
Pred. No.: 4,73e-30 Length: 2442  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservatives: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-115-155340 (1-2442)

QY 1 MetalAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 234 ATGGCGGCTCTGGCCACGCTCGCAGCTCGTCGCAACGCCCGCGGCTGGGGCTCCCGGAC 293  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 294 GCGTCCACGTTCCG 353  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 354 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 413  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 414 CGCCGGGGGGGAGG-----TTCCGTCGCTCGTGTGTC 449

RESULT 12

US-10-228-063-7  
; Sequence 7, Application US/10228063  
; Publication No. US20030135885A1  
; GENERAL INFORMATION:  
; APPLICANT: Lanahan, Mike  
; TITLE OF INVENTION: Self-processing Plants and Plant Parts  
; FILE REFERENCE: 109846.317  
; CURRENT APPLICATION NUMBER: US/10/228,063  
; CURRENT FILING DATE: 2002-12-12  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-228-063-7

Alignment Scores:  
Pred. No.: 5,19e-29 Length: 1818  
Score: 316.50 Matches: 70  
Percent Similarity: 93.3% Conservatives: 0  
Best Local Similarity: 93.3% Mismatches: 2  
Query Match: 86.0% Indels: 3  
DB: 6 Gaps: 2

US-10-628-525A-36 (1-74) x US-10-228-063-7 (1-1818)

QY 1 MetalAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 1 ATGGCGGCTCTGGCCACGCTCGCAGCTCGTCGCAACGCCCGCGGCTGGGGCTCCCGGAC 60  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 61 GCGTCCACGTTCCG 120  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln---GlnGln 59  
Db 121 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180





```
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 42638
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_138892C.1
US-10-425-115-42638

Alignment Scores:
Pred. No.: 3 98e-23 Length: 365
Score: 263.00 Matches: 58
Percent Similarity: 82.4% Conservative: 3
Best Local Similarity: 78.4% Mismatches: 11
Query Match: 71.5% Indels: 2
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-115-42638 (1-365)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 126 ATGTGGGCTGTGCACATGTCAGATCTTGTCAACGCCCGCGGCTGTGCTGGAC 185
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAla 40
Db 186 GCCTGTACATTTCCCGCGCGCGCGCGCGCGCGCTGTGGGGCGCGCGGCTGTGCGGCG 245
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 246 GCGGACACACTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 305
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 306 CGCGCGCGGGGCGAGG-----TTCCCGTCTGCTGCTGTGTC 341

RESULT 19
US-10-767-701-15855
; Sequence 15855, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53235)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 15855
; LENGTH: 2287
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 1255713
US-10-767-701-15855

Alignment Scores:
Pred. No.: 3 23e-19 Length: 2287
Score: 237.50 Matches: 58
Percent Similarity: 76.6% Conservative: 1
Best Local Similarity: 75.3% Mismatches: 15
Query Match: 64.5% Indels: 3
DB: 7 Gaps: 3
```

```
US-10-628-525A-36 (1-74) x US-10-767-701-15855 (1-2287)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 207 ATGTGACTCTAGCCAGCTGCGAGCTGTCGCCACGACGCCGCCCTAGGCGTCCCCGAC 266
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArg---GlyAlaArgAlaSerAla 39
Db 267 GCCTCCATGTTCCGCGCGCGCGCGCTGAGGGCGCTGAGGGCGCGCGGCGCATCGCG 326
QY 40 AlaAla---AspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGln 58
Db 327 GCAGCAGGGGACCGGCTCAGCATGCGGACCGAGCGGTGTCGCGCTCCGAGGCGAGCGCG 386
QY 59 GlnAlaArgArgGlyGlyArg---PheProPheProSerLeuValValCys 74
Db 387 GCGGCGCGCGCGCGCGCGCGCGGAGGTTCCCGTCTGCTGCTGTGTC 437

RESULT 20
US-10-307-005-2053
; Sequence 2053, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Camper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2053
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2053

Alignment Scores:
Pred. No.: 8 91e-14 Length: 121
Score: 183.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 49.7% Indels: 0
DB: 6 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-307-005-2053 (1-121)

QY 19 ProAspAlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSer 38
Db 3 CCGGACGCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTAG 62
QY 39 AlaAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57
Db 63 GCGGCGCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCG 119

RESULT 21
US-10-307-005-2054/c
; Sequence 2054, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
```

```
; APPLICANT: Eric B. Kniec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2054
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2054

Alignment Scores:
Pred. No.:      8 91e-14      Length:      121
Score:          133.00      Matches:      38
Percent Similarity: 97.4%      Conservative: 0
Best Local Similarity: 97.4%      Mismatches: 1
Query Match:    49.7%      Indels:      0
DB:             6          Gaps:          0

US-10-628-525A-36 (1-74) x US-10-307-005-2054 (1-121)

QY 19 ProAspAlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaArgAlaSer 38
|
|
|
Db 119 CGGAGCGGTCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGTAG 60
|
|
|
QY 39 AlaAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57
|
|
|
Db 59 GCGGCGGCGGACACGCTCAGCATGCGGACCGGCGCGCGCGCGCGCGCGCGCGCGCCAG 3

RESULT 22
US-10-307-005-2049
; Sequence 2049, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kniec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2049
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2049
```

```
Alignment Scores:
Pred. No.:      8.55e-13      Length:      121
Score:          175.00      Matches:      38
Percent Similarity: 95.0%      Conservative: 0
Best Local Similarity: 95.0%      Mismatches: 2
Query Match:    47.6%      Indels:      0
DB:             6          Gaps:          0

US-10-628-525A-36 (1-74) x US-10-307-005-2049 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgGlyAlaAla 29
|
|
|
Db 1  GTCCGAACGCGCGCGCGCTCGGGCGTCCCGGACGCGTCCACGTTCCGCGCGCGCGCGCG 60
|
|
|
QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSer 49
|
|
|
Db 61 TAGGGCCTGAGGGGGGGCGGGCGTCCGGCGGCGGCGGACACGCTCAGCATGCGGACCGAGC 120

RESULT 23
US-10-307-005-2050/c
; Sequence 2050, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kniec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2050
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2050

Alignment Scores:
Pred. No.:      8.55e-13      Length:      121
Score:          175.00      Matches:      38
Percent Similarity: 95.0%      Conservative: 0
Best Local Similarity: 95.0%      Mismatches: 2
Query Match:    47.6%      Indels:      0
DB:             6          Gaps:          0

US-10-628-525A-36 (1-74) x US-10-307-005-2050 (1-121)

QY 10 ValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgGlyAlaAla 29
|
|
|
Db 121 GTCCGAACGCGCGCGCGCTCGGGCGTCCCGGACGCGTCCACGTTCCGCGCGCGCGCGCG 62
|
|
|
QY 30 GlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSer 49
|
|
|
Db 61 TAGGGCCTGAGGGGGGGCGGGCGTCCGGCGGCGGCGGACACGCTCAGCATGCGGACCGAGC 2

RESULT 24
US-10-425-115-148056
; Sequence 148056, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
```



```
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/818,875
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2061
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2061

Alignment Scores:
Pred. No.:          2,44e-10      Length:      121
Score:              155.00        Matches:     34
Percent Similarity: 91.9%         Conservat:    0
Best Local Similarity: 91.9%      Mismatches:  1
Query Match:        42.1%         Indels:      2
DB:                  6            Gaps:        1

US-10-628-525A-36 (1-74) x US-10-307-005-2061 (1-121)

QY 38 SerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57
Db 1 TCGGCGCGCGGACACACGCTCAGCATGCGGACGCGCGCGCGCGCCAGGCACCA 60
QY 58 GlnGlnAlaArgGlyGlyArgPheProPheSerLeuValValCys 74
Db 61 TAGCAGCGCGCGCGCGCGGAGG-----TTCCCGTCGCTCGTGTGTC 105

RESULT 28
US-10-307-005-2062/c
; Sequence 2062, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/818,875
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2062
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2062

Alignment Scores:
Pred. No.:          2,44e-10      Length:      121
Score:              155.00        Matches:     34
Percent Similarity: 91.9%         Conservat:    0
Best Local Similarity: 91.9%      Mismatches:  1
Query Match:        42.1%         Indels:      2
DB:                  6            Gaps:        1

US-10-628-525A-36 (1-74) x US-10-307-005-2061 (1-121)

QY 38 SerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57
Db 1 TCGGCGCGCGGACACACGCTCAGCATGCGGACGCGCGCGCGCGCCAGGCACCA 60
QY 58 GlnGlnAlaArgGlyGlyArgPheProPheSerLeuValValCys 74
Db 61 TAGCAGCGCGCGCGCGGAGG-----TTCCCGTCGCTCGTGTGTC 105

RESULT 28
US-10-307-005-2062/c
; Sequence 2062, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/818,875
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2061
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2061

Alignment Scores:
Pred. No.:          2,44e-10      Length:      121
Score:              155.00        Matches:     34
Percent Similarity: 91.9%         Conservat:    0
Best Local Similarity: 91.9%      Mismatches:  1
Query Match:        42.1%         Indels:      2
DB:                  6            Gaps:        1

US-10-628-525A-36 (1-74) x US-10-307-005-2061 (1-121)

QY 38 SerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57
Db 121 TCGGCGCGCGGACACACGCTCAGCATGCGGACGCGCGCGCGCGCCAGGCACCA 62
QY 58 GlnGlnAlaArgGlyGlyArgPheProPheSerLeuValValCys 74
Db 61 TAGCAGCGCGCGCGCGGAGG-----TTCCCGTCGCTCGTGTGTC 17

RESULT 29
US-10-425-115-26578
; Sequence 26578, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 26578
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_124248C.1
US-10-425-115-26578

Alignment Scores:
Pred. No.:          4.13e-07      Length:      315
Score:              132.00        Matches:     29
Percent Similarity: 73.9%         Conservat:    5
Best Local Similarity: 63.0%      Mismatches: 12
Query Match:        35.9%         Indels:      0
DB:                  8            Gaps:        0

US-10-628-525A-36 (1-74) x US-10-425-115-26578 (1-315)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProApp 20
Db 178 ATGGCAGCTATGGCCACTTAGCAGCTGTTTAACGCCGCGGACTGGCGGTACATGAC 237
QY 21 AlaSerThrPheArgGlyValAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 238 GCATCCAGTTTCGACGTGGCCCTCAGAGGCCCTGAAGGGGTCAGGCATATGTGACG 297
QY 41 AlaAspThrLeuSerMet 46
Db 298 GTTGACACTCTTATTATG 315

RESULT 30
US-10-437-963-99960
; Sequence 99960, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
```

```
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/818,875
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2061
; LENGTH: 121
; TYPE: DNA
; ORGANISM: Zea mays
US-10-307-005-2061

Alignment Scores:
Pred. No.:          2,44e-10      Length:      121
Score:              155.00        Matches:     34
Percent Similarity: 91.9%         Conservat:    0
Best Local Similarity: 91.9%      Mismatches:  1
Query Match:        42.1%         Indels:      2
DB:                  6            Gaps:        1

US-10-628-525A-36 (1-74) x US-10-307-005-2062 (1-121)

QY 38 SerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGln 57
Db 121 TCGGCGCGCGGACACACGCTCAGCATGCGGACGCGCGCGCGCGCCAGGCACCA 62
QY 58 GlnGlnAlaArgGlyGlyArgPheProPheSerLeuValValCys 74
Db 61 TAGCAGCGCGCGCGCGGAGG-----TTCCCGTCGCTCGTGTGTC 17

RESULT 29
US-10-425-115-26578
; Sequence 26578, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 26578
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_124248C.1
US-10-425-115-26578

Alignment Scores:
Pred. No.:          4.13e-07      Length:      315
Score:              132.00        Matches:     29
Percent Similarity: 73.9%         Conservat:    5
Best Local Similarity: 63.0%      Mismatches: 12
Query Match:        35.9%         Indels:      0
DB:                  8            Gaps:        0

US-10-628-525A-36 (1-74) x US-10-425-115-26578 (1-315)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProApp 20
Db 178 ATGGCAGCTATGGCCACTTAGCAGCTGTTTAACGCCGCGGACTGGCGGTACATGAC 237
QY 21 AlaSerThrPheArgGlyValAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 238 GCATCCAGTTTCGACGTGGCCCTCAGAGGCCCTGAAGGGGTCAGGCATATGTGACG 297
QY 41 AlaAspThrLeuSerMet 46
Db 298 GTTGACACTCTTATTATG 315

RESULT 30
US-10-437-963-99960
; Sequence 99960, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
```





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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 01:09:48 ; Search time 231.07 Seconds  
(without alignments)  
1278.753 Million cell updates/sec

Title: US-10-628-525A-36  
Perfect score: 368  
Sequence: 1 MAALATSQLVATRAGHVPD.....RHQQARRGRPPFPLVVC 74

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abs/ABSSWEB\_spool/US10628525/runat\_31032006\_095139\_17270/app\_query.fasta.1  
-DB=Published Applications NA New -QPM=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62  
-TRANS=human40.cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
-USER=US10628525 @CGN 1.1 2249 @runat\_31032006\_095139\_17270 -NCFU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:  
1: /SIDSS5/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
2: /SIDSS5/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /SIDSS5/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
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5: /SIDSS5/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /SIDSS5/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
7: /SIDSS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
8: /SIDSS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
9: /SIDSS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
10: /SIDSS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
11: /SIDSS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
12: /SIDSS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
13: /SIDSS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
14: /SIDSS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
15: /SIDSS5/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	98.5	26.8	1714	US-11-072-512-1085
2	97.5	26.5	2886	US-10-504-599A-15
Sequence 1085, Ap				
Sequence 15, Appl				

3	82	22.3	153376	14	US-11-121-086-5	Sequence 5, Appl
c 4	80.5	21.9	1472	6	US-09-925-065A-711806	Sequence 711806,
c 5	78.5	21.3	1072	11	US-11-096-568A-13501	Sequence 13501, A
6	77.5	21.1	1239	9	US-10-330-773-285	Sequence 285, App
7	77.5	21.1	21239	9	US-10-330-773-284	Sequence 284, App
8	76.5	20.8	861	8	US-10-750-185-54914	Sequence 54914, A
9	76.5	20.8	861	8	US-10-750-623-54914	Sequence 54914, A
10	75.5	20.8	7006	8	US-10-821-234-218	Sequence 218, App
11	75	20.4	807	11	US-11-096-568A-3539	Sequence 3539, Ap
c 12	75	20.4	1069	9	US-10-921-793-57	Sequence 57, Appl
c 13	75	20.4	1069	9	US-10-931-198-57	Sequence 57, Appl
c 14	75	20.4	1069	9	US-10-942-042-57	Sequence 57, Appl
c 15	75	20.4	1534	11	US-11-096-568A-8024	Sequence 8024, Ap
c 16	75	20.4	2272	14	US-11-094-519A-12	Sequence 12, Appl
17	75	20.4	2292	8	US-10-821-234-168	Sequence 168, App
c 18	75	20.4	2294	14	US-11-094-519A-21	Sequence 21, Appl
c 19	75	20.4	2312	9	US-10-921-793-55	Sequence 55, Appl
c 20	75	20.4	2312	9	US-10-931-198-55	Sequence 55, Appl
c 21	75	20.4	2312	10	US-10-942-042-55	Sequence 91, Appl
c 22	75	20.4	2312	11	US-11-245-147-91	Sequence 240, App
c 23	75	20.4	2312	11	US-11-245-147-91	Sequence 240, App
c 24	75	20.4	88421	14	US-11-205-109-1	Sequence 1, Appl
c 25	75	20.4	153376	14	US-11-121-086-5	Sequence 5, Appl
c 26	75	20.4	172543	14	US-11-121-086-5	Sequence 6, Appl
c 27	74.5	20.2	656	6	US-09-925-065A-680636	Sequence 680636,
c 28	74.5	20.2	1781	14	US-11-091-883-18	Sequence 18, Appl
29	74.5	20.2	1781	14	US-11-091-883-164	Sequence 164, App
30	74.5	20.2	1848	11	US-11-096-568A-24055	Sequence 24055, A
31	74.5	20.2	3030	14	US-11-234-786-333	Sequence 333, App
32	73.5	20.0	361	6	US-09-925-065A-337172	Sequence 337172,
33	73.5	20.0	361	6	US-09-925-065A-337173	Sequence 337173,
34	73.5	20.0	370	10	US-10-301-480-410437	Sequence 410437,
35	73.5	20.0	370	10	US-10-301-480-410438	Sequence 410438,
36	73.5	20.0	370	10	US-10-301-480-1023846	Sequence 1023846,
37	73.5	20.0	370	10	US-10-301-480-1023847	Sequence 1023847,
c 38	73.5	20.0	635	6	US-09-925-065A-937187	Sequence 937187,
c 39	73.5	20.0	635	6	US-09-925-065A-953795	Sequence 953795,
c 40	73.5	20.0	635	6	US-09-925-065A-953796	Sequence 953796,
c 41	73.5	20.0	1181	11	US-11-096-568A-18374	Sequence 18374, A
c 42	73.5	20.0	1498	8	US-10-750-185-42352	Sequence 42352, A
43	73.5	20.0	1498	8	US-10-750-623-42352	Sequence 42352, A
44	73.5	20.0	6462	5	US-09-889-325-2	Sequence 2, Appl
45	73.5	20.0	6462	5	US-09-889-325-2	Sequence 2, Appl
46	73	19.8	600	14	US-11-136-527-7399	Sequence 7399, Ap
47	73	19.8	1295	9	US-10-978-927-25	Sequence 25, Appl
48	73	19.8	1354	11	US-11-096-568A-16245	Sequence 16245, A
49	73	19.8	1729	9	US-10-978-927-23	Sequence 23, Appl
50	73	19.8	2479	14	US-11-136-527-3303	Sequence 3303, Ap
51	73	19.8	9710	8	US-11-655-872-1	Sequence 1, Appl
52	73	19.8	12263	9	US-10-978-927-19	Sequence 19, Appl
53	73	19.8	88421	14	US-11-205-109-1	Sequence 1, Appl
c 54	72.5	19.7	556	6	US-09-925-065A-948409	Sequence 948409,
55	72.5	19.7	2092	11	US-11-096-568A-17682	Sequence 17682, A
56	72.5	19.7	6269	14	US-11-136-527-2572	Sequence 2572, Ap
57	72	19.6	1966	14	US-11-136-527-3454	Sequence 3454, Ap
58	72	19.6	3695	14	US-11-169-041-84	Sequence 84, Appl
59	72	19.6	121736	11	US-11-114-798-49	Sequence 49, Appl
60	72	19.6	318488	11	US-11-114-798-58	Sequence 58, Appl
61	71.5	19.4	656	6	US-09-925-065A-59834	Sequence 59834, A
62	71.5	19.4	656	9	US-10-301-480-161072	Sequence 161072,
63	71.5	19.4	656	10	US-10-301-480-774481	Sequence 774481,
64	71.5	19.4	943	11	US-11-096-568A-26033	Sequence 26033, A
c 65	71.5	19.4	1825	11	US-11-096-568A-21916	Sequence 21916, A
66	71.5	19.4	2561	14	US-11-127-877-26	Sequence 26, Appl
67	71.5	19.4	5679	14	US-11-075-185-36	Sequence 36, Appl
68	71.5	19.4	37507	8	US-10-522-037-2	Sequence 2, Appl
69	71.5	19.4	78869	14	US-11-075-185-1	Sequence 1, Appl
70	71.5	19.4	175023	14	US-11-121-086-18	Sequence 18, Appl
c 71	71	19.3	1202	11	US-11-096-568A-17149	Sequence 17149, A
72	71	19.3	2133	14	US-11-087-100-17	Sequence 17, Appl
73	71	19.3	2133	14	US-11-087-084-17	Sequence 17, Appl
74	71	19.3	2133	14	US-11-087-085-17	Sequence 17, Appl
c 75	71	19.3	4680	11	US-11-228-659-40	Sequence 40, Appl

149	68.5	18.6	1240	11	US-11-096-568A-20045	Sequence 20045, A
150	68.5	18.6	1283	11	US-11-096-568A-25832	Sequence 25832, A
ALIGNMENTS						
RESULT 1						
US-11-072-512-1085						
; Sequence 1085, Application US/11072512						
; Publication No. US20060029945A1						
GENERAL INFORMATION:						
; APPLICANT: ISOGAI, TAKAO						
; APPLICANT: SUGAIYAMA, TOMOYASU						
; APPLICANT: OTSUKI, TETSUJI						
; APPLICANT: WAKAMATSU, AI						
; APPLICANT: SATO, HIROYUKI						
; APPLICANT: ISHII, SHIZUKO						
; APPLICANT: YAMAMOTO, JUN-ICHI						
; APPLICANT: ISONO, YUUKO						
; APPLICANT: OTSUKA, KAORU						
; APPLICANT: NAGAI, KEIICHI						
; APPLICANT: IRIE, RYOTARO						
; APPLICANT: TAMECHIKA, ICHIRO						
; APPLICANT: SEKI, NAOHICO						
; APPLICANT: YOSHIKAWA, TSUTOMU						
; APPLICANT: OTSUKA, MOTOTYUKI						
; APPLICANT: NAGAHARI, KENJI						
; APPLICANT: MASUHO, YASUHIKO						
; TITLE OF INVENTION: Novel full length cDNA						
; FILE REFERENCE: 084335-0191						
; CURRENT APPLICATION NUMBER: US/11/072,512						
; PRIOR FILING DATE: 2005-03-07						
; PRIOR APPLICATION NUMBER: US 60/350,978						
; PRIOR FILING DATE: 2002-01-25						
; PRIOR APPLICATION NUMBER: JP 2001-379298						
; PRIOR FILING DATE: 2001-11-05						
; NUMBER OF SEQ ID NOS: 4096						
; SOFTWARE: PatentIn Ver. 2.1						
; SEQ ID NO 1085						
; LENGTH: 1714						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
US-11-072-512-1085						
Alignment Scores:						
Pred. No.: 0.279 Length: 1714						
Score: 98.50 Matches: 31						
Percent Similarity: 44.6% Conservative: 6						
Best Local Similarity: 37.3% Mismatches: 28						
Query Match: 26.8% Indels: 18						
DB: 11 Gaps: 3						
US-10-628-525A-36 (1-74) x US-11-072-512-1085 (1-1714)						
Qy	6	ThrSerGlnLeuValAla	---ThrArgAlaGlyHisGlyValProAspAlaSerThrPhe	24		
		:::		:::		
Db	784	TCCAGATGCTGGTGGCCCGGTGAGTCTGCCATTGGTGGCAGGTCCCTCTGCAC	GTGCTGCCAGGTCCCTCTGCAC	843		
Qy	25	Arg-ArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAlaAspThrLe		44		
		:::		:::		
Db	844	AGGCAGGGGAGCCAGCAGGACTTCAGGGCTGCAGAGCCCTCCCTCGAGTTTCTACCTT		903		
Qy	44	u-----	-----SerMetArgThrsAlaArgAlaAlaPr	54		
		:::		:::		
Db	904	ACAACAGGGATCTAATCCCTTAACCTGGGGTACGTGTGAGACCAACAGGGAGAGCCCTC		963		
Qy	54	oArgHisGlnGlnAlaArg	-----ArgGlyGlyArgPheProPh	68		
		:::		:::		
Db	964	GAGCATGGGCACCATGCCAGGCCCTGTAGGGCACCCTTCCTGCAGCAGCAGATCCCTT		1023		
Qy	68	eProSer	70			











Db 145 CGCAGGGGTCGGTCCGTCACAGCTCGCCAGCTCTTGGCGCAGACGGCGGAGCAGC 86  
Qy 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyArg 65  
Db 85 CGCAGCGCTCCAGCAGAGGCTCAGCGCCGCGCGGAGCGCGG 43

## RESULT 14

US-10-942-042-57/c  
; Sequence 57, Application US/10942042  
; Publication No. US20060057184A1  
; GENERAL INFORMATION:  
; APPLICANT: NYCz, Jeffrey  
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated  
; TITLE OF INVENTION: Osteoinductive Material  
; FILE REFERENCE: 64118.000087  
; CURRENT APPLICATION NUMBER: US/10/942,042  
; CURRENT FILING DATE: 2004-09-16  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 57  
; LENGTH: 1069  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-942-042-57

Alignment Scores:  
Pred. No.: 68.6 Length: 1069  
Score: 75.00 Matches: 21  
Percent Similarity: 49.1% Conservative: 6  
Best Local Similarity: 38.2% Mismatches: 27  
Query Match: 20.4% Indels: 1  
DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-942-042-57 (1-1069)

Qy 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31  
Db 205 ACACGCCGATCTTGGCGTGGCGGGAGCCGAAGTCACAGAAGAGGCCCTTGTGCGGGT 146  
Qy 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51  
Db 145 CGCAGGGGTCGGTCCGTCACAGCTCGCCAGCTCTTGGCGCAGACGGCGGAGCAGC 86  
Qy 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyArg 65  
Db 85 CGCAGCGCTCCAGCAGAGGCTCAGCGCCGCGCGGAGCGCGG 43

## RESULT 15

US-11-096-568A-8024  
; Sequence 8024, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Therby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 8024  
; LENGTH: 1534  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(1534)  
; OTHER INFORMATION: Ceres Seq. ID no. 15177270  
US-11-096-568A-8024

Alignment Scores:  
Pred. No.: 95.7 Length: 1534  
Score: 75.00 Matches: 29  
Percent Similarity: 38.8% Conservative: 4

Best Local Similarity: 34.1% Mismatches: 29  
Query Match: 20.4% Indels: 23  
DB: 11 Gaps: 3  
US-10-628-525A-36 (1-74) x US-11-096-568A-8024 (1-1534)

Qy 13 ArgAlaGlyHisGlyValProAspAla-----SerThr 23  
Db 773 CGCCGAGGAGCGCGGTCTCTCGTCAGGCAACGGCGGAGCTCGCCGCGTGTGTC 832  
Qy 24 PheArgArg-----GlyAlaAlaGlnGlyLeuArg 33  
Db 833 TACCGCGCGCGCGCGCGACCTCGGTGAGTTTCAAGATCTTTCAGCCGCGAGCAGCTCCGGCA 892  
Qy 34 GlyAlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAla 53  
Db 893 GGGTCCGGGTGTCGCTTCTCAGCGATTTCGATGCAAGTACCGCGCGCGGAGGTGCA 952  
Qy 54 ProArg-----HisGlnGlnAlaAlaArgArgGlyArgPhe-ProPheProSe 70  
Db 953 CCGCGGAGCGTGTTCATGCGGAGTGTTCGCGCGCGGGCGGTTTCGCGGAGCGGG 1012  
Qy 70 rLeuValValCys 74  
Db 1013 GCTGAGACTCTGT 1025

## RESULT 16

US-11-094-519A-12/c  
; Sequence 12, Application US/11094519A  
; Publication No. US20050281810A1  
; GENERAL INFORMATION:  
; APPLICANT: BERNSTEIN, Jeanne  
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING  
; FILE REFERENCE: 2786-0140P  
; CURRENT APPLICATION NUMBER: US/11/094,519A  
; CURRENT FILING DATE: 2005-03-31  
; PRIOR APPLICATION NUMBER: US/09/695,293  
; PRIOR FILING DATE: 2000-10-25  
; PRIOR APPLICATION NUMBER: IL 132558  
; PRIOR FILING DATE: 1999-10-25  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 2272  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-094-519A-12

Alignment Scores:  
Pred. No.: 138 Length: 2272  
Score: 75.00 Matches: 21  
Percent Similarity: 49.1% Conservative: 6  
Best Local Similarity: 38.2% Mismatches: 27  
Query Match: 20.4% Indels: 1  
DB: 14 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-094-519A-12 (1-2272)

Qy 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31  
Db 471 ACACGCCGATCTTGGCGTGGCGGGAGCCGAAGTCACAGAAGAGGCCCTTGTGCGGGT 412  
Qy 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51  
Db 411 CGCAGGGGTCGGCTCGGTGTCACAGCTCGCCAGCTTGGCGCAGACGGCGGAGCAGC 352  
Qy 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyArg 65  
Db 351 CGCAGCGCTCCAGCAGAGGCTCAGCGCCGCGCGGAGCGCGG 309

## RESULT 17

US-10-821-234-168

```
; Sequence 168, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Suan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preseclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 168
; LENGTH: 2292
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-168

Alignment Scores:
Pred. No.: 139 Length: 2292
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservative: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 8 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-821-234-168 (1-2292)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
Db 1865 ACACGCCGATCTTGGCGTGGCGGGGACCGAAGTCACAGAAGAGCCCTTGTGGCGGT 1924
QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAla 51
Db 1925 CGCAGGGTTCGGCTCGGTGCACAGCTGCCCGAGTCTTGGCGGAGCGCGGAGCAGC 1984
QY 51 gAlaAlaProArgHisGlnGlnAlaAlaArgArgGlyArg 65
Db 1985 CGCAGCGCTCCAGCAGAGGCTCACGCCCGCGGCGGCGGCGG 2027

RESULT 18
US-11-094-519A-21/c
; Sequence 21, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1993-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-094-519A-21

Alignment Scores:
Pred. No.: 139 Length: 2294
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservative: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 14 Gaps: 0

; Sequence 168, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Suan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preseclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 168
; LENGTH: 2292
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-168

Alignment Scores:
Pred. No.: 139 Length: 2292
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservative: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 8 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-821-234-168 (1-2292)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
Db 1865 ACACGCCGATCTTGGCGTGGCGGGGACCGAAGTCACAGAAGAGCCCTTGTGGCGGT 1924
QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAla 51
Db 1925 CGCAGGGTTCGGCTCGGTGCACAGCTGCCCGAGTCTTGGCGGAGCGCGGAGCAGC 1984
QY 51 gAlaAlaProArgHisGlnGlnAlaAlaArgArgGlyArg 65
Db 1985 CGCAGCGCTCCAGCAGAGGCTCACGCCCGCGGCGGCGGCGG 2027

RESULT 19
US-10-921-793-55/c
; Sequence 55, Application US/10921793
; Publication No. US20060039949A1
; GENERAL INFORMATION:
; APPLICANT: Nycz, Jeffrey
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
; FILE REFERENCE: 64118.000087
; CURRENT APPLICATION NUMBER: US/10/921,793
; CURRENT FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 2312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-921-793-55

Alignment Scores:
Pred. No.: 140 Length: 2312
Score: 75.00 Matches: 21
Percent Similarity: 49.1% Conservative: 6
Best Local Similarity: 38.2% Mismatches: 27
Query Match: 20.4% Indels: 1
DB: 9 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-921-793-55 (1-2312)
QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaAlaGlnGly 31
Db 428 ACACGCCGATCTTGGCGTGGCGGGGACCGAAGTCACAGAAGAGCCCTTGTGGCGGT 369
QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAlaAspThrLeuSerMetArgThrSerAla 51
Db 368 CGCAGGGTTCGGCTCGGTGCACAGCTGCCCGAGTCTTGGCGGAGCGCGGAGCAGC 309
QY 51 gAlaAlaProArgHisGlnGlnAlaAlaArgArgGlyArg 65
Db 308 CGCAGCGCTCCAGCAGAGGCTCACGCCCGCGGCGGCGGCGG 266

RESULT 20
US-10-931-198-55/c
; Sequence 55, Application US/10931198
; Publication No. US20060045902A1
; GENERAL INFORMATION:
; APPLICANT: Nycz, Jeffrey
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
; FILE REFERENCE: 64118.000087
; CURRENT APPLICATION NUMBER: US/10/931,198
; CURRENT FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 2312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-931-198-55
```

US-10-931-198-55

Alignment Scores:  
Pred. No.: 140 Length: 2312  
Score: 75.00 Matches: 21  
Percent Similarity: 49.1% Conservative: 6  
Best Local Similarity: 38.2% Mismatches: 27  
Query Match: 20.4% Indels: 1  
DB: 9 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-931-198-55 (1-2312)

QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgGlyAlaAlaGInGly 31  
Db 428 ACACGGCGATCTTGGCGGGGAGCGGAAGTCACAGAGAGGCCCTTGTGCGGGT 369  
QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51  
Db 368 CGCAGGGGTGCGCTCGGTGCACAGCTGCCCGAGCTGTTGGCGCAGACGCGGCGG 309  
QY 51 gAlaAlaProArgHisGInGInGlnAlaArgArgGlyArg 65  
Db 308 CGCAGCGGTCCAGCAGCAGGCTCACGCCCGCGGCGGCGGCGG 266

RESULT 21

US-10-942-042-55/c  
; Sequence 55, Application US/10942042  
; Publication No. US20060057184A1  
; GENERAL INFORMATION:  
; APPLICANT: NYCZ, Jeffrey  
; TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated  
; FILE REFERENCE: 6418.000087  
; CURRENT APPLICATION NUMBER: US/10/942,042  
; CURRENT FILING DATE: 2004-09-16  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55  
; LENGTH: 2312  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-942-042-55

Alignment Scores:  
Pred. No.: 140 Length: 2312  
Score: 75.00 Matches: 21  
Percent Similarity: 49.1% Conservative: 6  
Best Local Similarity: 38.2% Mismatches: 27  
Query Match: 20.4% Indels: 1  
DB: 9 Gaps: 0

US-10-628-525A-36 (1-74) x US-10-942-042-55 (1-2312)

QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgGlyAlaAlaGInGly 31  
Db 428 ACACGGCGATCTTGGCGGGGAGCGGAAGTCACAGAGAGGCCCTTGTGCGGGT 369  
QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51  
Db 368 CGCAGGGGTGCGCTCGGTGCACAGCTGCCCGAGCTGTTGGCGCAGACGCGGCGG 309  
QY 51 gAlaAlaProArgHisGInGInGlnAlaArgArgGlyArg 65  
Db 308 CGCAGCGGTCCAGCAGCAGGCTCACGCCCGCGGCGGCGGCGG 266

RESULT 22

US-11-245-147-91/c  
; Sequence 91, Application US/11245147  
; Publication No. US20060030541A1  
; GENERAL INFORMATION:  
; APPLICANT: GARCIA, TERESA  
; APPLICANT: ROMAN ROMAN, SERGIO  
; APPLICANT: BARON, ROLAND

; APPLICANT: CALL, KATHERINE  
; APPLICANT: THEILHABER, JOACHIM  
; APPLICANT: CONNOLLY, TIMOTHY  
; APPLICANT: JACKSON, AMANDA  
; APPLICANT: BUSHNELL, STEVEN  
; APPLICANT: RAWADI, GEORGES  
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE  
; FILE REFERENCE: 37991-0023  
; CURRENT APPLICATION NUMBER: US/11/245,147  
; CURRENT FILING DATE: 2005-10-07  
; PRIOR APPLICATION NUMBER: PCT/IB02/02211  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/281,400  
; PRIOR FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 91  
; LENGTH: 2312  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-245-147-91

Alignment Scores:  
Pred. No.: 140 Length: 2312  
Score: 75.00 Matches: 21  
Percent Similarity: 49.1% Conservative: 6  
Best Local Similarity: 38.2% Mismatches: 27  
Query Match: 20.4% Indels: 1  
DB: 11 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-245-147-91 (1-2312)

QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgGlyAlaAlaGInGly 31  
Db 428 ACACGGCGATCTTGGCGGGGAGCGGAAGTCACAGAGAGGCCCTTGTGCGGGT 369  
QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaAr 51  
Db 368 CGCAGGGGTGCGCTCGGTGCACAGCTGCCCGAGCTGTTGGCGCAGACGCGGCGG 309  
QY 51 gAlaAlaProArgHisGInGInGlnAlaArgArgGlyArg 65  
Db 308 CGCAGCGGTCCAGCAGCAGGCTCACGCCCGCGGCGGCGGCGG 266

RESULT 23

US-11-245-147-240/c  
; Sequence 240, Application US/11245147  
; Publication No. US20060030541A1  
; GENERAL INFORMATION:  
; APPLICANT: GARCIA, TERESA  
; APPLICANT: ROMAN ROMAN, SERGIO  
; APPLICANT: BARON, ROLAND  
; APPLICANT: CALL, KATHERINE  
; APPLICANT: THEILHABER, JOACHIM  
; APPLICANT: CONNOLLY, TIMOTHY  
; APPLICANT: JACKSON, AMANDA  
; APPLICANT: BUSHNELL, STEVEN  
; APPLICANT: RAWADI, GEORGES  
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE  
; FILE REFERENCE: 37991-0023  
; CURRENT APPLICATION NUMBER: US/11/245,147  
; CURRENT FILING DATE: 2005-10-07  
; PRIOR APPLICATION NUMBER: PCT/IB02/02211  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/281,400  
; PRIOR FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 240  
; LENGTH: 2312  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; OTHER INFORMATION: Homo sapiens connective tissue growth factor  
; OTHER INFORMATION: (CTGF), mRNA  
US-11-245-147-240

Alignment Scores:                      140                      Length:                      2312  
Pred. No.:                      75.00                      Matches:                      21  
Score:                      49.1%                      Conservative:                      6  
Percent Similarity:                      38.2%                      Mismatches:                      27  
Best Local Similarity:                      20.4%                      Indels:                      1  
Query Match:                      11                      Gaps:                      0  
DB:

US-10-628-525A-36 (1-74) x US-11-245-147-240 (1-2312)

QY 12 ThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArgGlyAlaalaGIndgly 31  
Db                      |||||                      |||||                      ::                      |||||                      |||||  
428 ACACGCCGATCTTGGCGTGGCGGGAGCCGAAGTCACAGAAGAGCCCTTGTGCGG 369  
QY 32 LeuArgGly-AlaArgAlaSerAlaAlaAlaSerThrLeuSerMetArgThr-SerAlaAr 51  
Db                      |||||                      |||||                      ::                      |||||                      |||||  
368 CGCAGGGTCTCGCTCGTGGTGCACAGCTGCCCGAGCTGTGGCGCAGACGCCGACGACG 309  
QY 51 gAlaAlaProArgHisGlnGlnAlaArgArgGlyGlyArg 65  
Db                      |||||                      |||||                      ::                      |||||                      |||||  
308 CGCAGCGGTCCAGCAGCGCTCACGCCGCCGCCGCCGCGCGG 266

RESULT 24

US-11-205-109-1  
; Sequence 1, Application US/11205109  
; Publication NO. US20050287641A1  
; GENERAL INFORMATION:  
; APPLICANT: Farnet, Chris  
; APPLICANT: Zazopoulos, Emmanuel  
; APPLICANT: Stafira, Alfredo  
; TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS  
; FILE REFERENCE: 3002-2US  
; CURRENT APPLICATION NUMBER: US/11/205,109  
; PRIOR FILING DATE: 2005-08-17  
; PRIOR APPLICATION NUMBER: US/09/976,059  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/239,924  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 88421  
; TYPE: DNA  
; ORGANISM: Actinoplanes sp.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2077)..(3078)  
; OTHER INFORMATION: ORF 1; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (3118)..(4032)  
; OTHER INFORMATION: ORF 2; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4038)..(5048)  
; OTHER INFORMATION: ORF 3; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5665)..(5814)  
; OTHER INFORMATION: ORF 4; negative strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (7703)..(6693)  
; OTHER INFORMATION: ORF 5; negative strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9464)..(8130)  
; OTHER INFORMATION: ORF 6; negative strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9691)..(10761)  
; OTHER INFORMATION: ORF 7; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (12751)..(10829)  
; OTHER INFORMATION: ORF 8; negative strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (13617)..(12802)  
; OTHER INFORMATION: ORF 9; negative strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (15203)..(13614)  
; OTHER INFORMATION: ORF 10; negative strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (15591)..(15863)  
; OTHER INFORMATION: ORF 11; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (15880)..(19035)  
; OTHER INFORMATION: ORF 12; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (19032)..(39713)  
; OTHER INFORMATION: ORF 13; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (39713)..(65800)  
; OTHER INFORMATION: ORF 14; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (65826)..(66530)  
; OTHER INFORMATION: ORF 15; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (66546)..(67370)  
; OTHER INFORMATION: ORF 16; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (67384)..(70059)  
; OTHER INFORMATION: ORF 17; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (70059)..(70662)  
; OTHER INFORMATION: ORF 18; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (70659)..(71906)  
; OTHER INFORMATION: ORF 19; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (73439)..(71964)  
; OTHER INFORMATION: ORF 20; negative strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (74216)..(73563)  
; OTHER INFORMATION: ORF 21; negative strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (75424)..(74213)  
; OTHER INFORMATION: ORF 22; negative strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (75535)..(76464)  
; OTHER INFORMATION: ORF 23; positive strandedness  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (78110)..(76449)  
; OTHER INFORMATION: ORF 24; negative strandedness  
; FEATURE:  
; NAME/KEY: misc feature

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; LOCATION: (79864)..(78107)
; OTHER INFORMATION: ORF 25; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81624)..(79861)
; OTHER INFORMATION: ORF 26; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81909)..(81682)
; OTHER INFORMATION: ORF 27; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82346)..(82062)
; OTHER INFORMATION: ORF 28; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82587)..(84446)
; OTHER INFORMATION: ORF 29; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (84481)..(85548)
; OTHER INFORMATION: ORF 30; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (85556)..(86845)
; OTHER INFORMATION: ORF 31; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (87372)..(86803)
; OTHER INFORMATION: ORF 32; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-11-205-109-1

Alignment Scores:
Pred. No.: 4.05e+03 Length: 88421
Score: 75.00 Matches: 28
Percent Similarity: 44.1% Conservative: 2
Best Local Similarity: 41.2% Mismatches: 26
Query Match: 20.4% Indels: 12
DB: 14 Gaps: 3

US-10-628-525A-36 (1-74) x US-11-205-109-1 (1-88421)
QY 5 AlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPhe 24
Db 57238 GCTCGATCCGGTATCCGGCGCCCGCTGGC-----CCGGATGTCGAGGAGCG 57288
QY 25 ArgArgGlyAlaAlaGlnGly-----LeuArgGlyAlaAlaAlaAlaAla 41
Db 57289 CGCGCGGCGCTGCTGTGCCACGCGCGCACCGGAGCGCGTGCCTCCCGCGCGCA 57348
QY 42 AspThrLeuSerMetArgThrSerAlaAlaAlaAlaAlaAlaAlaAlaAlaArg 61
Db 57349 GCGACT-----GCTGTGGACGACCGCGCACCGCGCGCGGAGTGGC 57390
QY 62 ArgGlyGlyArgPheProPhePro 69
Db 57391 CCGGTGGACGGCGACCGGATCCG 57414

RESULT 25
US-11-121-086-5/c
; Sequence 5, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 172543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-6

Alignment Scores:
Pred. No.: 7.51e+03 Length: 172543
Score: 75.00 Matches: 27
Percent Similarity: 49.2% Conservative: 5
Best Local Similarity: 41.5% Mismatches: 18
Query Match: 20.4% Indels: 15
DB: 14 Gaps: 3

US-10-628-525A-36 (1-74) x US-11-121-086-6 (1-172543)
QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26
Db 3395 ACCAGTTCAAGTTCACCGCGTGAAGGGGAGTGGCC-----CGG 3354
QY 27 GlyAlaAlaGlnGlyLeuArgGly-AlaArgAlaSerAlaAlaAlaAspThrLeuSerMe 46
Db 3395 ACCAGTTCAAGTTCACCGCGTGAAGGGGAGTGGCC-----CGG 3354

; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 153376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-5

Alignment Scores:
Pred. No.: 6.74e+03 Length: 153376
Score: 75.00 Matches: 27
Percent Similarity: 49.2% Conservative: 5
Best Local Similarity: 41.5% Mismatches: 18
Query Match: 20.4% Indels: 15
DB: 14 Gaps: 3

US-10-628-525A-36 (1-74) x US-11-121-086-5 (1-153376)
QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26
Db 99969 AACCAATTCAAGTTCACCGCGTGAAGGGGAGTGGCC-----CGG 99928
QY 27 GlyAlaAlaGlnGlyLeuArgGly-AlaArgAlaSerAlaAlaAlaAspThrLeuSerMe 46
Db 99927 GGGCGGGCGGGGGCTGAGTCCGCCAGGGCGGCTGGCTGCG-----99882
QY 46 tangThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAlaArgGlyArgPh 66
Db 99881 -CGGAGCCCTTCCACCCCGCCAGCGGGGGGGTTCCTCCAGACCGG-----AGGCT 99832
QY 66 eProPheProSer 70
Db 99831 CCCCAGTCCCTCC 99819

RESULT 26
US-11-121-086-6/c
; Sequence 6, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 172543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-6

Alignment Scores:
Pred. No.: 7.51e+03 Length: 172543
Score: 75.00 Matches: 27
Percent Similarity: 49.2% Conservative: 5
Best Local Similarity: 41.5% Mismatches: 18
Query Match: 20.4% Indels: 15
DB: 14 Gaps: 3

US-10-628-525A-36 (1-74) x US-11-121-086-6 (1-172543)
QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26
Db 3395 ACCAGTTCAAGTTCACCGCGTGAAGGGGAGTGGCC-----CGG 3354
QY 27 GlyAlaAlaGlnGlyLeuArgGly-AlaArgAlaSerAlaAlaAlaAspThrLeuSerMe 46
Db 3395 ACCAGTTCAAGTTCACCGCGTGAAGGGGAGTGGCC-----CGG 3354
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Db 3353 GGGGGGGGGGGGGGGTGGTCCGCCAGGGGGGGTGGTGGC----- 3308
Qy 46 tArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAlaArgGlyGlyArgPh 66
Db 3307 -CGAGCCCTCCACCCCGCCAGCCCGGGGGGCTTCCAGGACCG-AGGCT 3258
Qy 66 eProPheProSer 70
Db 3257 CCCCAGTCCCTCC 3245

RESULT 27
US-09-925-065A-680636/c
; Sequence 680636, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 680636
; LENGTH: 656
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-680636

Alignment Scores:
Pred. No.: 49.6 Length: 656
Score: 74.50 Matches: 21
Percent Similarity: 44.6% Conservatives: 8
Best Local Similarity: 32.3% Mismatches: 31
Query Match: 20.2% Indels: 5
DB: 6 Gaps: 2

US-10-628-525A-36 (1-74) x US-09-925-065A-680636 (1-656)
Qy 4 LeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThr 23
Db 621 GTGGGAACTCCGGGGCTCCGGGACCCGACATCAGCGACTGCGCTGACCGCGG 562
Qy 24 PheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAlaAlaSerThr 43
Db 561 CTGCGGGCGAGTGTAGGAACGGCTTCTGTCG-----AGGAGTGGAGATG 514
Qy 44 LeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAlaArgGly 63
Db 513 ATCACAACAACTCCCGCGCCCGGGCTCCACCCGCCCGGAGTGGAGCTTTCCCGGG 454
Qy 64 Gly---ArgPhePro 67
Db 453 GGTGAGCTTTCCTCC 439

RESULT 28
US-11-091-883-18
; Sequence 18, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; FILE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
; FILE REFERENCE: 5394205
; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 164
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-091-883-164

Alignment Scores:
Pred. No.: 125 Length: 1781
Score: 74.50 Matches: 29

```

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; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; FILE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
; FILE REFERENCE: 5394205
; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-091-883-18

Alignment Scores:
Pred. No.: 125 Length: 1781
Score: 74.50 Matches: 29
Percent Similarity: 44.6% Conservatives: 4
Best Local Similarity: 39.2% Mismatches: 20
Query Match: 20.2% Indels: 21
DB: 14 Gaps: 4

US-10-628-525A-36 (1-74) x US-11-091-883-18 (1-1781)
Qy 9 LeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgGlyAla 28
Db 535 CTGCCAGCTGGCGCTGCGCAGGCTGAGTG-----GCTGCACGACGACGCGGGGAGCC 588
Qy 29 AlaGlnGlyLeu-----ArgGly 34
Db 589 GGGCGGGGACCCCTACTCTCCGTGGACCTGCCCGCGCGGTGAGGAGCGGTGACGTGGG 648
Qy 35 AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaPro 54
Db 649 GGGCGTGGGGGAGGCGCTGCTGGATGAGTCCCG-----GCCGCTCTTCGAGGATACCG 702
Qy 55 ArgHis-----GlnGlnGlnAlaArgArgGlyGlyArg 65
Db 703 CGCCATGTTTCCCTGCGCCTGCGCAACGCGGAGCGGAGGAGGCGCGC 744

RESULT 29
US-11-091-883-164
; Sequence 164, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; FILE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
; FILE REFERENCE: 5394205
; CURRENT APPLICATION NUMBER: US/11/091,883
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 164
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-091-883-164

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Score: 74.50 Matches: 29

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US-10-628-525A-36 (1-74) x US-11-091-883-164 (1-1781)

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QY 29 AlaGlnGlyLeu-----ArgGly 34  
DB 589 GCGCGGGGACCTTACTCTCCGTGGACCTGCCCCCGCTGAGGAGCGTGACGTGGG 648  
QY 35 AlaArgAlaSerAlaAlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaPro 54  
DB 649 GCGCTGGCGGAGGCGCTGCTGGATGATGCCG-----GCCGCTCTTCGAGCGATACCG 702  
QY 55 ArgHis-----GlnGlnGlnAlaArgArgGlyArg 65  
DB 703 CGCATGTTCGCCCTCGCAACGCGGAGGCGAGGCGCGC 744

## RESULT 30

US-11-096-568A-24055  
; Sequence 24055, Application US/11096568A  
; Publication No. US2006048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
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; TYPE: DNA  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(1848)  
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US-11-096-568A-24055

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US-10-628-525A-36 (1-74) x US-11-096-568A-24055 (1-1848)

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QY 31 -----GlyLeuArg----- 33  
DB 393 CCGCGCTACACGACGAGGAGTTCGAGTTTACCTCTCCGACTCGGAGCGCGCTCCT 452  
QY 34 -----GlyAlaArgAlaSerAlaAlaAspThrLeuSerMetArgThr 48  
DB 453 CGTCACCAACGCGGAGGCGCAACGCGGAGCGAGGCTGC-----CGCTGC 497  
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DB 498 CAAGCTCGGGCTGCGCCAGCCACCGCCCTCCACGACGCGCGCGCTGTCCA 554

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GenCore version 5.1.7  
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# SUMMARIES

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9	333	90.5	1818	3	PCT-US04-20582-2	Sequence 2, Appli	82	288	78.3	400	28	US-09-619-643-16655	Sequence 16655, A
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66	314	85.3	408	28	US-09-619-643-19289	Sequence 19289, A	139	160	43.5	369	23	US-09-304-517A-89175	Sequence 89175, A
67	314	85.3	408	75	US-60-145-148-2849	Sequence 2849, Ap	140	160	43.5	369	23	US-09-371-146A-89175	Sequence 89175, A
68	313.5	85.2	1170	3	PCT-US04-07182A-77	Sequence 77, Appl	141	160	43.5	369	27	US-09-553-094-1751	Sequence 1751, Ap
69	313.5	85.2	1425	3	PCT-US04-07182A-77	Sequence 105, App	142	160	43.5	369	29	US-09-654-617-292592	Sequence 292592, A
70	306.5	83.3	1863	3	PCT-US04-20582-11	Sequence 11, Appl	143	160	43.5	369	29	US-09-684-016-292592	Sequence 292592, A
71	306.5	83.3	1863	62	US-10-877-645-11	Sequence 11, Appl	144	160	43.5	369	39	US-09-985-678-89175	Sequence 89175, A
72	306.5	83.3	4470	3	PCT-US04-20582-1	Sequence 1, Appli	145	160	43.5	369	51	US-10-425-115-148056	Sequence 148056, A
73	306.5	83.3	4470	62	US-10-877-645-1	Sequence 1, Appli	146	160	43.5	369	75	US-60-130-180-1968	Sequence 1968, Ap
74	302	82.1	386	28	US-09-619-643-20077	Sequence 20077, A	147	159	43.2	121	1	PCT-US03-31862-2057	Sequence 2057, Ap
75	302	82.1	386	75	US-60-145-148-3657	Sequence 3657, Ap	148	159	43.2	121	1	PCT-US03-31862-2058	Sequence 2058, Ap
76	295	80.2	431	27	US-09-394-745-22672	Sequence 22672, A	149	159	43.2	121	48	US-10-307-005-2057	Sequence 2057, Ap
77	295	80.2	431	27	US-09-565-306-45136	Sequence 45136, A	150	159	43.2	121	48	US-10-307-005-2058	Sequence 2058, Ap
78	293	78.6	1101	72	US-11-218-305-19766	Sequence 19766, A	151	159	43.2	121	48	US-10-307-005-2058	Sequence 2058, Ap
79	289	78.5	2267	13	US-08-300-726-1	Sequence 1, Appli	152	159	43.2	121	48	US-10-307-005-2058	Sequence 2058, Ap
80	289	78.5	2267	13	US-08-300-726A-1	Sequence 1, Appli	153	159	43.2	121	48	US-10-307-005-2058	Sequence 2058, Ap

## RESULT 1

```

US-09-304-517A-87805
; Sequence 87805, Application US/99304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Pla
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,5
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 87805
; LENGTH: 414
; TYPE: DNA
; ORGANISM: zea mays
US-09-304-517A-87805

```

Alignment Scores:		
Pred. No.:	3.6e-33	Length:
Score:	333.00	Matches:
Percent Similarity:	95.9%	Conservative:
Best Local Similarity:	95.9%	Mismatches:
Query Match:	90.5%	Indels:
DB:	23	Gaps:
		414

US-10-628-525A-36 (1-74) x US-09-304-517A-87805 (1-414)

Qy	1	MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp	20
Db	169	ATGGCGGCTCTGGCCACGCTCGCAGCTCGTCGACCGCGCGCTGGCGGC	228
Qy	21	AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla	40
Db	229	GGGTCCACGTTCCGCGCGCGCCCGCAGGGCTTGAGGGGGGCGCGGGCG	288
Qy	41	AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla	60
Db	289	GCGGCACGCTCAGCATCGGACACGCGCGCGCGCGGCCACGACGACGCG	348
Qy	61	ArgArgGlyGlyArgPheProPheProSerLeuValValCys	74
Db	349	CGCCGCGGTGGCAGG-----TTCCGTCGCTCGCTCGTGTGC	384

## RESULT 2

```

US-09-371-146A-87805
; Sequence 87805, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordin
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371,146A
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 87805
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-146A-87805

```

Alignment Scores:		
Pred. No.:	3.6e-33	414
Score:	33.00	71
Percent Similarity:	95.9%	Conservative: 0
Best Local Similarity:	95.9%	Mismatches: 1
Query Match:	90.5%	Indels: 2
DB:	23	Gaps: 1

US-10-628-525A-36 (1-74) x US-09-371-146A-87805 (1-414)

Qy	1	MetAla	Ala	Leu	Ala	Leu	Ala	Thr	Ser	Gln	Leu	Val	Ala	Thr	Arg	Ala	Gly	His	Gly	Val	Pro	Asp	20
Db	169	ATG	CGG	CTG	TGG	CAC	GTG	CG	AGT	CGT	CGC	ACG	CGC	GGC	GGC	GTG	GCG	CGT	CGC	GGAC		228	
Qy	21	Ala	Ser	Thr	Phe	Arg	Arg	Gly	Val	Ala	Gln	Gly	Leu	Arg	Gly	Val	Ala	Arg	Ala	Ser	Ala	Ala	40
Db	229	CGT	TCC	AGT	TCC	GCG	CGG	CGG	CGC	CGC	GAG	GCC	CTG	AGG	GGG	GCC	CGG	CGC	GTG	CGG	CGCG	288	
Qy	41	Ala	Asp	Thr	Leu	Ser	Met	Arg	Thr	Ser	Ala	Arg	Ala	Ala	Pro	Arg	His	Gln	Gln	Gln	Ala	60	
Db	289	GCG	GAC	ACG	CTC	AGC	ATG	CGG	ACC	CAG	CGC	GCG	GCG	GCG	CGC	CGC	CAG	CAC	CAG	CAG	CGCG	348	
Qy	61	Arg	Arg	Gly	Gly	Arg	Phe	Phe	Pro	Phe	Pro	Ser	Leu	Val	Val	Cys						74	
Db	349	CGC	CGC	GGT	GGC	AGG	-----	TT	CCC	GT	CGT	CGT	CGT	GTG								384	

## RESULT 3

```

US-09-553-094-4757
; SEQUENCE 4757, Application US/09553094
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21 (15503) B
; CURRENT APPLICATION NUMBER: US/09/553
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 18831
; SEQ ID NO 4757
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: Lib3061
US-09-553-094-4757

```

Alignment Scores:		
Pred. No.:	3.6e-33	Length:
Score:	33.00	Matches:
Percent Similarity:	95.9%	Conservative:
Best Local Similarity:	95.9%	Mismatches:
Query Match:	90.5%	Indels:
DB:	27	Gaps:
		414

US-10-628-525A-36 (1-74) x US-09-553-094-4757 (1-414)

Qy	Qy	Qy	Qy	Qy	Qy
1	MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp	20	21	AlaSerThrPheArgArgGlyValAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla	40
169	ATGGGGGCTCTGGCCACGCTCGTCGCAACGGCGCGCGCTGGGGCTCCGGAC	238	229	GGGTCCACGTTCCTCGCGCGCGCGCGCGAGGGCTTAGGGGGGGCGCCGGGGCGCG	288
			41	AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla	60
			289	GGGGACAGCTCAGATCGGAGACAGAGCGCGCGCGCGCCACAGGACACAGACAGAGCG	348
			61	ArgArgGlyGlyArgPheProPheProSerLeuValValCys	74
			349	CGCCCGCGGTGGCAGG-----TTCCCGTCGTCGTGCTGTGC	384

## RESULT 4

```

US/09-985-678-87805
; Sequence 87805, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 1517.255/38-21(15037)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US/09/304,517
; PRIOR FILING DATE: 1999-05-06

```

; NUMBER OF SEQ ID NOS: 295529  
; SEQ ID NO 87805  
; LENGTH: 414  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-985-678-87805

Alignment Scores:  
Pred. No.: 3.6e-33 Length: 414  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 39 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-985-678-87805 (1-414)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20  
DB 169 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCCAAACGCGCGCGCTGGCGCTCCCGGAC 228  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 229 GCGTCCACGTTCCGCGCGCGCGCGCGCGAGGCGCTGAGGGGGCGCGCGCGCTCCCGGAC 288  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60  
DB 289 GCGGACACGCTAGCATGTGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 349 CGCGCGGCTGGCAGG-----TTCCGTCGCTCGTCTGTGTC 384

RESULT 5

US-60-130-180-74  
; Sequence 74, Application US/60130180  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; TITLE REFERENCE: 38-21(15503)A  
; CURRENT APPLICATION NUMBER: US/60/130,180  
; PRIOR FILING DATE: 1999-04-22  
; NUMBER OF SEQ ID NOS: 5164  
; SEQ ID NO 74  
; LENGTH: 414  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3061-001-Q1-K2-E5  
US-60-130-180-74

Alignment Scores:  
Pred. No.: 3.6e-33 Length: 414  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 75 Gaps: 1

US-10-628-525A-36 (1-74) x US-60-130-180-74 (1-414)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20  
DB 169 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCCAAACGCGCGCGCTGGCGCTCCCGGAC 228  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 229 GCGTCCACGTTCCGCGCGCGCGCGCGCGAGGCGCTGAGGGGGCGCGCGCGCTCCCGGAC 288  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60

DB 289 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 349 CGCGCGGCTGGCAGG-----TTCCGTCGCTCGTCTGTGTC 384

RESULT 6

US-09-865-419A-36190  
; Sequence 36190, Application US/09865419A  
; GENERAL INFORMATION:  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(51935)B  
; CURRENT APPLICATION NUMBER: US/09/865,419A  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 60/208,063  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 54020  
; SEQ ID NO 36190  
; LENGTH: 609  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3600-059-Q1-K6-B7  
US-09-865-419A-36190

Alignment Scores:  
Pred. No.: 6.44e-33 Length: 609  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 33 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-865-419A-36190 (1-609)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProApp 20  
DB 36 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCCAAACGCGCGCGCTGGCGCTCCCGGAC 95  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 96 GCGTCCACGTTCCGCGCGCGCGCGCGAGGCGCTGAGGGGGCGCGCGCGCTCCCGGAC 155  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaThrArgAlaAlaProArgHisGlnGlnAla 60  
DB 156 GCGGACACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 215  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 216 CGCGCGGCGGCGAGG-----TTCCGTCGCTCGTCTGTGTC 251

RESULT 7

US-60-208-063-19249  
; Sequence 19249, Application US/60208063  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Lalquid, Raghunath V.  
; APPLICANT: Ruff, Thomas G.  
; APPLICANT: Shukla, Hridayabhiranjan  
; APPLICANT: Wu, Kunsheng  
; APPLICANT: Xu, Nanfei  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(51935)A  
; CURRENT APPLICATION NUMBER: US/60/208,063  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 25021  
; SEQ ID NO 19249

; LENGTH: 609  
; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: LIB3600-059-Q1-K6-B7  
US-60-208-063-19249

## Alignment Scores:

Pred. No.: 6.44e-33 Length: 609  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 76 Gaps: 1

US-10-628-525A-36 (1-74) x US-60-208-063-19249 (1-609)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 36 ATGGCGGCTCTGGCCACGTCGACGCTGTCGAACGCGCGCGGCTGGCGCTCCGGAC 95  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 96 GCGTCCACGTTCCG 155  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 156 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 215  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 216 CGCGCGCGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 251

## RESULT 8

US-09-553-094-11949  
; Sequence 11949, Application US/09553094  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: Plants  
; CURRENT APPLICATION NUMBER: US/09/553,094  
; CURRENT FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18331  
; SEQ ID NO 11949  
; LENGTH: 634  
; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: LIB3061-091-Q1-K6-G11  
US-09-553-094-11949

## Alignment Scores:

Pred. No.: 6.84e-33 Length: 634  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 27 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-553-094-11949 (1-634)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 150 ATGGCGGCTCTGGCCACGTCGACGCTGTCGAACGCGCGCGGCTGGCGCTCCGGAC 209  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 210 GCGTCCACGTTCCG 269  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 270 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 329

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 330 CGCGCGGGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 365

## RESULT 9

PCT-US04-20582-2  
; Sequence 2, Application PC/TUS0420582  
; GENERAL INFORMATION:  
; APPLICANT: Ravanello, Monica P  
; APPLICANT: Foley, Terry J  
; APPLICANT: LeDeaux, John R  
; APPLICANT: Wyrick, Annette E  
; APPLICANT: Savage, Thomas J  
; TITLE OF INVENTION: Elevation of Oil Levels in Plants  
; FILE REFERENCE: REN-00-119  
; CURRENT APPLICATION NUMBER: PCT/US04/20582  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Zea mays  
PCT-US04-20582-2

Alignment Scores:  
Pred. No.: 3.34e-32 Length: 1818  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 3 Gaps: 1

US-10-628-525A-36 (1-74) x PCT-US04-20582-2 (1-1818)

QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 1 ATGGCGGCTCTGGCCACGTCGACGCTGTCGAACGCGCGCGGCTGGCGCTCCGGAC 60  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 61 GCGTCCACGTTCCG 120  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 121 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 181 CGCGCGGGGGGAGG-----TTCCCGTCGCTCGTGTGTGC 216

## RESULT 10

US-10-877-645-2  
; Sequence 2, Application US/10877645  
; GENERAL INFORMATION:  
; APPLICANT: Ravanello, Monica P  
; APPLICANT: Foley, Terry J  
; APPLICANT: LeDeaux, John R  
; APPLICANT: Wyrick, Annette E  
; APPLICANT: Savage, Thomas J  
; TITLE OF INVENTION: Elevation of Oil Levels in Plants  
; FILE REFERENCE: REN-00-119  
; CURRENT APPLICATION NUMBER: US/10/877,645  
; CURRENT FILING DATE: 2004-06-25  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2  
; LENGTH: 1818  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-10-877-645-2

Alignment Scores:

Pred. No.: 3.34e-32 Length: 1818  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 62 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-877-645-2 (1-1818)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 DB 1 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCGCTGGCGCGTCCCGGAC 60  
 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValAlaArgAlaSerAlaAla 40  
 DB 61 GGTCCACGCTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGTCCGCGGCG 120  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
 DB 121 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 DB 181 CGCCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 216

RESULT 11  
 ; US-10-425-115-155307  
 ; Sequence 155307, Application US/10425115  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; FILE REFERENCE: 38-21(53222)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,115  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 155307  
 ; LENGTH: 2111  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: M74577\_7321C.1  
 ; US-10-425-115-155307

Alignment Scores:  
 Pred. No.: 4.19e-32 Length: 2111  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 51 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-425-115-155307 (1-2111)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 DB 1 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCGCTGGCGCGTCCCGGAC 60  
 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValAlaArgAlaSerAlaAla 40  
 DB 61 GGTCCACGCTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGTCCGCGGCG 120  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
 DB 121 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 DB 181 CGCCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 216

RESULT 12  
 PCT-US02-33122-1  
 ; Sequence 1, Application PC/TUS0233122  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ExSeed Genetics  
 ; TITLE OF INVENTION: Starch  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: PCT/US02/33122  
 ; CURRENT FILING DATE: 2002-10-17  
 ; PRIOR APPLICATION NUMBER: 60/329,525  
 ; PRIOR FILING DATE: 2001-10-01  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 2263  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Wild type sequence EX385  
 ; PCT-US02-33122-1

Alignment Scores:  
 Pred. No.: 4.65e-32 Length: 2263  
 Score: 333.00 Matches: 71  
 Percent Similarity: 95.9% Conservative: 0  
 Best Local Similarity: 95.9% Mismatches: 1  
 Query Match: 90.5% Indels: 2  
 DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x PCT-US02-33122-1 (1-2263)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
 DB 194 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCGCGCGCTGGCGCGTCCCGGAC 253  
 QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyValAlaArgAlaSerAlaAla 40  
 DB 254 GGTCCACGCTCCGCGCGCGCGCGCGCGCTGAGGGGGCGCGCGCGTCCGCGGCG 313  
 QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArgAlaAlaProArgHisGlnGlnAla 60  
 DB 314 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373  
 QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
 DB 374 CGCCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 409

RESULT 13  
 PCT-US02-33122-2  
 ; Sequence 2, Application PC/TUS0233122  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ExSeed Genetics  
 ; TITLE OF INVENTION: Starch  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: PCT/US02/33122  
 ; CURRENT FILING DATE: 2002-10-17  
 ; PRIOR APPLICATION NUMBER: 60/329,525  
 ; PRIOR FILING DATE: 2001-10-01  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 2263  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: mutation  
 ; LOCATION: (1643)  
 ; OTHER INFORMATION: The mutation is at position 1643 in the sequence,  
 ; OTHER INFORMATION: 1450 bp after the start codon.  
 ; FEATURE:  
 ; NAME/KEY: mutation  
 ; LOCATION: (1643)  
 ; OTHER INFORMATION: The change is a "G" in the wild type (EX385) to an

```
; OTHER INFORMATION: "A" in the mutant
PCT-US02-33122-2

Alignment Scores:
Pred. No.: 4.65e-32 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x PCT-US02-33122-2 (1-2263)
QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 194 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCGCTGGGGCGTCCCGGAC 253
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 254 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCCCGCGCGCGCG 313
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 314 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCCAGGACACGAGCGGCG 373
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 374 CGCGCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 409

RESULT 14
US-10-628-525A-36 (1-74) x PCT-US02-33122-2 (1-2263)
; Sequence 1, Application US/10272291
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The mutation is at position 1643 in the sequence,
; OTHER INFORMATION: 1450 bp after the start codon.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The change is a "G" in the wild type (EX385) to an
; OTHER INFORMATION: "A" in the mutant
US-10-628-525A-36 (1-74) x US-10-628-525A-36 (1-2263)
Alignment Scores:
Pred. No.: 4.65e-32 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-628-525A-36 (1-2263)
QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 194 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCGCTGGGGCGTCCCGGAC 253
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 254 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCCCGCGCGCGCG 313
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 314 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCCAGGACACGAGCGGCG 373
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 374 CGCGCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 409

; OTHER INFORMATION: Wild type sequence EX385
US-10-628-525A-36 (1-74) x US-10-628-525A-36 (1-2263)
Alignment Scores:
Pred. No.: 4.65e-32 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-628-525A-36 (1-2263)
QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 194 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCGCTGGGGCGTCCCGGAC 253
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 254 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCCCGCGCGCGCG 313
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 314 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCCAGGACACGAGCGGCG 373
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 374 CGCGCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 409
```

```
Db 374 CGCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 409

RESULT 15
US-10-628-525A-36 (1-74) x US-10-628-525A-36 (1-2263)
; Sequence 2, Application US/10272291
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/272,291
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The mutation is at position 1643 in the sequence,
; OTHER INFORMATION: 1450 bp after the start codon.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1643)
; OTHER INFORMATION: The change is a "G" in the wild type (EX385) to an
; OTHER INFORMATION: "A" in the mutant
US-10-628-525A-36 (1-74) x US-10-628-525A-36 (1-2263)
Alignment Scores:
Pred. No.: 4.65e-32 Length: 2263
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x US-10-628-525A-36 (1-2263)
QY 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 194 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCGCTGGGGCGTCCCGGAC 253
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
DB 254 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGCGCCCGCGCGCGCG 313
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
DB 314 GCGGACACGCTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCCAGGACACGAGCGGCG 373
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
DB 374 CGCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 409

; OTHER INFORMATION: PC/TUS0233122
; GENERAL INFORMATION:
; APPLICANT: ExSeed Genetics
; TITLE OF INVENTION: Starch
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US02/33122
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/329,525
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4800
```

```

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1233)..(1448)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1554)..(1684)
; OTHER INFORMATION: number 2
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1766)..(1859)
; OTHER INFORMATION: number 3
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1959)..(2054)
; OTHER INFORMATION: number 4
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2145)..(2225)
; OTHER INFORMATION: number 5
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2290)..(2412)
; OTHER INFORMATION: number 6
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2514)..(2650)
; OTHER INFORMATION: number 7
; FEATURE:
; NAME/KEY: intron
; LOCATION: (2761)..(2857)
; OTHER INFORMATION: number 8
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3102)..(3211)
; OTHER INFORMATION: number 9
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3395)..(3489)
; OTHER INFORMATION: number 10
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3682)..(3792)
; OTHER INFORMATION: number 11
; FEATURE:
; NAME/KEY: intron
; LOCATION: (3880)..(3976)
; OTHER INFORMATION: number 12
; FEATURE:
; NAME/KEY: intron
; LOCATION: (4106)..(4226)
; OTHER INFORMATION: number 13
PCT-US02-33122-5

Alignment Scores:
Pred. No.: 1 44e-31 Length: 4800
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x PCT-US02-33122-5 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAep 20
Db 1233 ATGGCGGCTCTGGCCAGCTCGCTCGCAACGCGCGCGCTGGCGCTCCCGGAC 1292

Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 1293 GCGTCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGGCGCGCGCGCTCCCGGAC 1352

TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: transit_peptide
LOCATION: (1233)..(1448)
FEATURE:
NAME/KEY: intron
LOCATION: (1554)..(1684)
OTHER INFORMATION: number 2
FEATURE:
NAME/KEY: intron
LOCATION: (1766)..(1859)
OTHER INFORMATION: number 3
FEATURE:
NAME/KEY: intron
LOCATION: (1959)..(2054)
OTHER INFORMATION: number 4
FEATURE:
NAME/KEY: intron
LOCATION: (2145)..(2225)
OTHER INFORMATION: number 5
FEATURE:
NAME/KEY: intron
LOCATION: (2290)..(2412)
OTHER INFORMATION: number 6
FEATURE:
NAME/KEY: intron
LOCATION: (2514)..(2650)
OTHER INFORMATION: number 7
FEATURE:
NAME/KEY: intron
LOCATION: (2761)..(2857)
OTHER INFORMATION: number 8
FEATURE:
NAME/KEY: intron
LOCATION: (3102)..(3211)
OTHER INFORMATION: number 9
FEATURE:
NAME/KEY: intron
LOCATION: (3395)..(3489)
OTHER INFORMATION: number 10
FEATURE:
NAME/KEY: intron
LOCATION: (3682)..(3792)
OTHER INFORMATION: number 11
FEATURE:
NAME/KEY: intron
LOCATION: (3880)..(3976)
OTHER INFORMATION: number 12
FEATURE:
NAME/KEY: intron
LOCATION: (4106)..(4226)
OTHER INFORMATION: number 13
PCT-US02-33122-5

Alignment Scores:
Pred. No.: 1 44e-31 Length: 4800
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x PCT-US02-33122-5 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAep 20
Db 1233 ATGGCGGCTCTGGCCAGCTCGCTCGCAACGCGCGCGCTGGCGCTCCCGGAC 1292

Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 1293 GCGTCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGGCGCGCGCGCTCCCGGAC 1352

Qy 41 AlaSerThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 1353 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412

Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 1413 CGCGCGCGGGGCGAGG-----TTCCCGTGGCTGGTGGTGGC 1448

RESULT 17
US-09-625-406-4
; Sequence 4, Application US/09625406
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Greenlee, Winner and Sullivan, P.C.
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,406
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/941,445
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1449..1553, 1685..1765, 1860..1958, 2055
; LOCATION: ..2144, 2226..2289, 2413..2513, 2651..2760, 2858
; LOCATION: ..3101, 3212..3394, 3490..3681, 3793..3879, 3977
; LOCATION: ..4105, 4227..4343)
; US-09-625-406-4

Alignment Scores:
Pred. No.: 1 44e-31 Length: 4800
Score: 333.00 Matches: 71
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 1
Query Match: 90.5% Indels: 2
DB: 1 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-625-406-4 (1-4800)

Qy 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAep 20
Db 1233 ATGGCGGCTCTGGCCAGCTCGCTCGCAACGCGCGCGCTGGCGCTCCCGGAC 1292
```



QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 1293 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1352  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 1353 GCGGACACGCTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 1413 CG 1448

## RESULT 18

US-10-109-048-1141  
; Sequence 1141, Application US/10109048  
; GENERAL INFORMATION:  
; APPLICANT: COMMURI, PADMA  
; APPLICANT: KEELING, PETER L.  
; APPLICANT: RAMIREZ, NONA  
; APPLICANT: MCKEAN, ANGELA  
; APPLICANT: GAO, ZHONG  
; APPLICANT: GUAN, HANPING  
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS  
; FILE REFERENCE: 2461-76  
; CURRENT APPLICATION NUMBER: US/10/109,048  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: 60/279,720  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 1154  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1141  
; LENGTH: 4800  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-10-109-048-1141

Alignment Scores:  
Pred. No.: 1.44e-31 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 42 Gaps: 1

US-10-628-525a-36 (1-74) x US-10-109-048-1141 (1-4800)

QY 1 MetaAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 1233 ATGGCGGCTCTGGCCACGTCGCAGCTCGTCGCAACGCGCGCGCGCGCGCGCGCGCGCGCG 1292  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 1293 GCGTCCACGTTCCG 1352  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 1353 GCGGACACGCTCAGCATGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 1413 CG 1448

## RESULT 19

US-10-272-291-5  
; Sequence 5, Application US/10272291  
; GENERAL INFORMATION:  
; APPLICANT: Exseed Genetics  
; TITLE OF INVENTION: Starch  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/272,291  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 60/329,525

; PRIOR FILING DATE: 2001-10-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 4800  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: transit\_peptide  
; LOCATION: (1233)..(1448)  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1554)..(1684)  
; OTHER INFORMATION: number 2  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1766)..(1859)  
; OTHER INFORMATION: number 3  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1959)..(2054)  
; OTHER INFORMATION: number 4  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2145)..(2225)  
; OTHER INFORMATION: number 5  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2290)..(2412)  
; OTHER INFORMATION: number 6  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2514)..(2650)  
; OTHER INFORMATION: number 7  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2761)..(2857)  
; OTHER INFORMATION: number 8  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (3102)..(3211)  
; OTHER INFORMATION: number 9  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (3395)..(3489)  
; OTHER INFORMATION: number 10  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (3682)..(3792)  
; OTHER INFORMATION: number 11  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (3880)..(3976)  
; OTHER INFORMATION: number 12  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (4106)..(4226)  
; OTHER INFORMATION: number 13  
US-10-272-291-5

Alignment Scores:  
Pred. No.: 1.44e-31 Length: 4800  
Score: 333.00 Matches: 71  
Percent Similarity: 95.9% Conservative: 0  
Best Local Similarity: 95.9% Mismatches: 1  
Query Match: 90.5% Indels: 2  
DB: 43 Gaps: 1

US-10-628-525a-36 (1-74) x US-10-272-291-5 (1-4800)

QY 1 MetaAlaAlaLeuAlaThrSerGlnLeuValAlaAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 1233 ATGGCGGCTCTGGCCACGTCGCAGCTCGTCGCAACGCGCGCGCGCGCGCGCGCGCGCGCG 1292



```
DB: 53 Gaps: 1
US-10-628-525A-36 (1-74) x US-10-628-525A-4 (1-4800)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 1233 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCTGGCGCTCCCGGAC 1292
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 1293 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCGCTGAGGGGGGCCCGCGCGCG 1352
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 1353 GCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1412
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 1413 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 1448

RESULT 22
US-09-304-517A-91115
; Sequence 91115, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304, 517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 91115
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Zea mays
US-09-304-517A-91115

Alignment Scores:
Pred. No.: 1.68e-32 Length: 418
Score: 328.00 Matches: 70
Percent Similarity: 94.6% Conservative: 0
Best Local Similarity: 94.6% Mismatches: 2
Query Match: 89.1% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-304-517A-91115 (1-418)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 179 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCTGGCGCTCCCGGAC 238
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 239 GCGTCCACGTTCCGCGCGCGCGCGCGCGCGCTGAGGGGGGCCCGCGCGCG 298
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 299 GCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCG 358
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 359 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 394

RESULT 23
US-09-371-146A-91115
; Sequence 91115, Application US/09371146A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)C
; CURRENT APPLICATION NUMBER: US/09/371, 146A
; CURRENT FILING DATE: 1999-08-09
```

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; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 294310
; SEQ ID NO 91115
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-146A-91115

Alignment Scores:
Pred. No.: 1.68e-32 Length: 418
Score: 328.00 Matches: 70
Percent Similarity: 94.6% Conservative: 0
Best Local Similarity: 94.6% Mismatches: 2
Query Match: 89.1% Indels: 2
DB: 23 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-371-146A-91115 (1-418)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 179 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCTGGCGCTCCCGGAC 238
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 239 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGGCCCGCGCGCG 298
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
Db 299 GCGGACACGCTCAGCATGCGGACACGCGCGCGCGCGCGCGCGCGCGCGCG 358
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 359 CGCGCGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 394

RESULT 24
US-09-553-094-1278
; Sequence 1278, Application US/09553094
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15503)B
; CURRENT APPLICATION NUMBER: US/09/553,094
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 18831
; SEQ ID NO 1278
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3061-052-Q1-K1-F7
US-09-553-094-1278

Alignment Scores:
Pred. No.: 1.68e-32 Length: 418
Score: 328.00 Matches: 70
Percent Similarity: 94.6% Conservative: 0
Best Local Similarity: 94.6% Mismatches: 2
Query Match: 89.1% Indels: 2
DB: 27 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-553-094-1278 (1-418)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 179 ATGGCGGCTCTGGCCACGTCGCAGCTCGTGCACACGCGCGCGCTGGCGCTCCCGGAC 238
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 239 GCGTCCACGTTCCGCGCGCGCGCGCGCGCTGAGGGGGGCCCGCGCGCG 298
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60
```

Db  
299 GCGGACACGCTCAGCATGCGGCACCAGCGCGCGCGGCCACGACGACGCGCG 358

Qy  
61 ArgAtqGdlyGlyArgPheProPheSerIeuValValCys 74

Db  
359 CGCCGGCGGTGGCAGG-----TTCCCCTCGTTCGTCTGTGTC 394

```

RESULT 25
US-09-985-678-91115
; Sequence 91115, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 91115
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Zea mays
US-09-985-678-91115

```

Alignment Scores:	1.68e-32	Length:	418
Pred. No.:	Score:	Matches:	70
	328.00	Conservative:	0
Percent Similarity:	94.6%	Mismatches:	2
Best Local Similarity:	94.6%	Indels:	2
Query Match:	89.1%	Gaps:	1
DB:	39		

US-10-628-525A-36 (1-74) x US-09-985-678-91115 (1-418)

Qy	1	MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp	20
Db	179	ATGGGGGCTCTGGCCACCTCGCAGCTGTCGCAACGGCGCCGGCCTGGGGCTCCGGAC	238
Qy	21	AlaSerThrPheAcqArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla	40
Db	239	GGGTCACGTTCCGCGGGCGCGCGATGGCTGAGGGGGGCGCGGGCGCTCGCGGGCG	298
Qy	41	AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla	60
Db	299	GGGGACAAGCTCAGCATCGGACACAGCGGGCGCGCGGCCCGACAGGACACAGGCG	358
Qy	61	ArgArgGlyArgPheProPheProSerLeuValValCys	74
Db	359	CGCCCGGGTGGCAGG-----TTCCGCTCGCTCGCTGCTGTC	394

```

RESULT 26
US-60-130-180-4602
; Sequence 4602, Application US/60130180
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Mole
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15503)A
; CURRENT APPLICATION NUMBER: US/60/130,180
; CURRENT FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 5164
; SEQ ID NO 4602
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: L183061-052-Q1-K1-F7
US-60-130-180-4602

```

**Alignment Scores:**

Pred. No.:	1.68e-32	Length:	418
Score:	328.00	Matches:	70
Percent Similarity:	94.6%	Conservative:	0
Best Local Similarity:	94.6%	Mismatches:	2
Query Match:	89.1%	Indels:	2
DB:	75	Gaps:	1

US-10-628-525A-36 (1-74) x US-60-130-180-4602 (1-418)

Qy	1	MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp	20
Db	179	ATGGCGGCTCTTCGGCACGTCGCGAGCTCGTCACACGGCGCGCGGCTCGGGCGTCCCGGAC	238
Qy	21	AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla	40
Db	239	GGTCCACGTTCCGGCGGCGCGCCGCGCATGGCTCTGAGGGGGGCGCCGGCGGTGCGCGGCG	298
Qy	41	AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla	60
Db	299	GCGGACAGCTCAGCATCGGACCAGCGCGCGCGCGGCCCGCCAGGCACACGACGAGCGCG	358
Qy	61	ArgArgGlyGlyArgPheProPheProSerLeuValValCys	74
Db	359	CGCCGCGGTGGCAGG-----TTCCGTCGCTCGCTCGTGTGC	394

## RESULT 27

```

US-09-619-643-19435
; Sequence 19435, Application US/09619643
; GENERAL INFORMATION:
; APPLICANT: Lalqudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Mo
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51230)B
; CURRENT APPLICATION NUMBER: US/09/619,643
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 19435
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3151-045
US-09-619-643-19435

```

Alignment Scores:		
Pred. No.:	2.25e-32	339
Score:	326.00	70
Percent Similarity:	94.6%	Conservative: 0
Best Local Similarity:	94.6%	Mismatches: 2
Query Match:	98.6%	Indels: 2
DB:	28	Gaps: 1

US-10-628-525A-36 (1-74) x US-09-619-643-19435 (1-339)

Qy	1	MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp	20
Db	65	ATGGCGGCTCTGGCCACGCTCGCAGCTGTCGCAACGCCCGCGCGCTGGCGCTCCGGAC	124
Qy	21	AlaSerThrPheArgArgGlyAlaAlaGlnClyLeuArgGlyAlaArgAlaSerAlaAla	40
Db	125	GGGTCCAGTTCCTCCGCGCGCGCGCGCGAGGGCTGAGGGGGGCGCGCGGCTCGCGGGCG	184
Qy	41	AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAla	60
Db	185	GGGGACACGCTCAGCATGGGACCAGCGCGCGCGCGGCCCGCCAGGCACAGCAGCAGGGCG	244
Qy	61	ArgArgGlyGlyArgPheProPheProSerLeuValValCys	74
Db	245	CGCCCGCGGGGGCAGG-----TTCCCGTCGCTCGTCGTGTGC	280

RESULT 28

US-60-145-148-3000  
; Sequence 3000, Application US/60145148

GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Deng, Mollan  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Miller, Philip W.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 38-21(51230)A  
; CURRENT APPLICATION NUMBER: US/60/145,148  
; CURRENT FILING DATE: 1999-07-22  
; SEQ ID NO 3000  
; LENGTH: 339  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-045-Q1-K1-D7  
US-60-145-148-3000

Alignment Scores:  
Pred. No.: 2,25e-32 Length: 339  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 75 Gaps: 1

US-10-628-525A-36 (1-74) x US-60-145-148-3000 (1-339)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 65 ATGGGGCTCTGGCCACGCTCGAGCTCGTGCACACGCCCGCCGCTGGGGCTCCCGGAC 124  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 125 GCGTCCACGTTCCCGCGCGCGCGCGAGCGCTGAGGGGGCGCCGCGGGCTGGGGCG 184  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 185 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCCAGGACACGAGCAGCGCG 244  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 245 CGCCGGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 280

RESULT 29  
US-09-619-643-19534  
; Sequence 19534, Application US/09619643  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(51230)B  
; CURRENT APPLICATION NUMBER: US/09/619,643  
; CURRENT FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 19534  
; LENGTH: 386  
; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: LIB3151-046-Q1-K1-F12  
US-09-619-643-19534

Alignment Scores:  
Pred. No.: 2,74e-32 Length: 386  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 28 Gaps: 1

US-10-628-525A-36 (1-74) x US-09-619-643-19534 (1-386)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 146 ATGGGGCTCTGGCCACGCTCGAGCTCGTGCACACGCCCGCCGCTGGGGCTCCCGGAC 205  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 206 GCGTCCACGTTCCCGCGCGCGCGAGGCGCTGAGGGGGCGCCGCGGGCTCGCGGGCG 265  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 266 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCCAGGACACGAGCAGCGCG 325  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 326 CGCCGGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 361

#### RESULT 30

US-60-145-148-3100  
; Sequence 3100, Application US/60145148  
; GENERAL INFORMATION:  
; APPLICANT: Cheikh, Nordine  
; APPLICANT: Deng, Mollan  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Miller, Philip W.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 38-21(51230)A  
; CURRENT APPLICATION NUMBER: US/60/145,148  
; CURRENT FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 3994  
; SEQ ID NO 3100  
; LENGTH: 386  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-046-Q1-K1-F12  
US-60-145-148-3100

Alignment Scores:  
Pred. No.: 2,74e-32 Length: 386  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 75 Gaps: 1

US-10-628-525A-36 (1-74) x US-60-145-148-3100 (1-386)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 146 ATGGGGCTCTGGCCACGCTCGAGCTCGTGCACACGCCCGCCGCTGGGGCTCCCGGAC 205  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 206 GCGTCCACGTTCCCGCGCGCGCGAGGCGCTGAGGGGGCGCCGCGGGCTCGCGGGCG 265  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 266 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCCAGGACACGAGCAGCGCG 325  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 326 CGCCGGGGGGCAGG-----TTCCCGTCGCTCGTGTGTGC 361

Search completed: April 2, 2006, 03:25:50  
Job time : 2029.88 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 21:21:57 ; Search time 138.391 Seconds  
(without alignments)  
1603.719 Million cell updates/sec

Title: US-10-628-525A-36

Perfect score: 368

Sequence: 1 MAALATSQLVTRAGHGVPD.....RHQQQARRGRRFPFSLVVC 74

Scoring table:

BLOSUM62	Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 6698573 seqs, 1499593917 residues

Total number of hits satisfying chosen parameters: 13397146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-DB=Pending Patents NA.New -QFMT=fastap -SUPPFX=p2n.rpn -MINMATCH=0.1  
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-MAXLEN=2000000000 -HOST=abes06h  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA New:\*

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2:	/SID55/ptodata/2/pna/US06 NEW COMB.seq:*
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12:	/SID55/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	90.5	414	8	US-11-329-388-4757 Sequence 4757, Ap
2	333	90.5	634	8	US-11-329-388-11949 Sequence 11949, A
3	328	89.1	418	8	US-11-329-388-1278 Sequence 1278, Ap
4	326	88.6	339	10	US-11-227-183A-19435 Sequence 19435, A
5	326	88.6	386	10	US-11-227-183A-19534 Sequence 19534, A

326	88.6	415	10	US-11-227-183A-18500	Sequence 18500, A
326	88.6	428	8	US-11-353-150-45112	Sequence 45112, A
326	88.6	449	10	US-11-227-183A-17085	Sequence 17085, A
326	88.6	561	10	US-11-227-183A-20738	Sequence 20738, A
326	88.6	1409	8	US-11-398-234A-9	Sequence 9, Appli
324	88.0	1915	8	US-11-330-822-50	Sequence 50, Appli
323	87.8	408	10	US-11-227-183A-19022	Sequence 19022, A
323	87.8	420	10	US-11-227-183A-19076	Sequence 19076, A
314	85.3	408	10	US-11-227-183A-19289	Sequence 19289, A
302	82.1	386	10	US-11-227-183A-20077	Sequence 20077, A
295	80.2	431	8	US-11-353-150-45136	Sequence 45136, A
288	78.3	400	10	US-11-227-183A-16655	Sequence 16655, A
285	77.4	388	10	US-11-227-183A-18495	Sequence 18495, A
278	75.5	625	8	US-11-329-388-8047	Sequence 8047, Ap
278	75.5	649	8	US-11-329-388-8026	Sequence 8026, Ap
276	75.0	432	8	US-11-329-388-1754	Sequence 1754, Ap
268	72.8	422	10	US-11-227-183A-17758	Sequence 17758, A
266	72.3	354	10	US-11-227-183A-19448	Sequence 19448, A
263	71.5	363	8	US-11-329-388-3077	Sequence 3077, Ap
263	71.5	365	10	US-11-227-183A-18014	Sequence 18014, A
221	60.1	371	10	US-11-227-183A-18823	Sequence 18823, A
221	60.1	338	10	US-11-227-183A-32098	Sequence 32098, A
208	56.5	203	10	US-11-227-183A-18999	Sequence 18999, A
208	56.5	519	10	US-11-227-183A-20737	Sequence 20737, A
162	44.0	360	10	US-11-227-183A-18231	Sequence 18231, A
160	43.5	369	8	US-11-329-388-1751	Sequence 1751, Ap
150	40.8	297	10	US-11-227-183A-28810	Sequence 28810, A
139	37.8	283	10	US-11-227-183A-18478	Sequence 18478, A
132	35.9	304	10	US-11-227-183A-17248	Sequence 17248, A
132	35.9	315	8	US-11-353-150-62704	Sequence 62704, A
116	31.5	291	10	US-11-227-183A-17794	Sequence 17794, A
111	30.2	283	10	US-11-227-183A-20080	Sequence 20080, A
110	29.9	360	10	US-11-227-183A-18826	Sequence 18826, A
96	26.1	266	10	US-11-227-183A-26235	Sequence 26235, A
94	25.5	150	10	US-11-227-183A-20693	Sequence 20693, A
93	25.3	241	10	US-11-227-183A-26412	Sequence 26412, A
93	25.3	251	10	US-11-227-183A-20324	Sequence 20324, A
91	24.7	146	8	US-11-329-388-4836	Sequence 4836, Ap
91	24.7	275	10	US-11-227-183A-17503	Sequence 17503, A
88	23.9	1000	10	US-11-266-748A-205192	Sequence 205192, A
88	23.9	2300	12	US-60-762-056-37460	Sequence 37460, A
87	23.6	2580	7	US-10-276-817B-2668	Sequence 2668, Ap
87	23.6	2622	7	US-10-276-817B-2314	Sequence 2314, Ap
84.5	23.0	1379	10	US-11-266-748A-162166	Sequence 162166, A
84.5	23.0	1819	8	US-11-174-307B-3253	Sequence 3253, Ap
84	22.8	237	10	US-11-227-183A-18998	Sequence 18998, A
83.5	22.7	2300	12	US-60-762-056-31257	Sequence 31257, A
82	22.3	2300	12	US-60-762-056-20206	Sequence 20206, A
82	22.3	2300	12	US-60-762-056-20207	Sequence 20207, A
82	22.3	2501	1	PCT-US04-20336-36	Sequence 36, Appli
82	22.3	2501	10	US-11-317-798-36	Sequence 36, Appli
82	22.3	2778	7	US-10-461-673-5700	Sequence 5700, Ap
82	22.3	3286	12	US-60-751-420-3381	Sequence 3381, Ap
82	22.3	16842	7	US-10-506-111-30	Sequence 30, Appli
80.5	21.9	2300	12	US-60-762-056-4634	Sequence 4634, Ap
80.5	21.9	2300	12	US-60-762-056-16509	Sequence 16509, A
79.5	21.6	460	8	US-11-353-150-65596	Sequence 65596, A
79.5	21.6	576	10	US-11-266-748A-90641	Sequence 90641, A
79.5	21.6	576	10	US-11-266-748A-143452	Sequence 143452, A
79.5	21.6	1031	10	US-11-266-748A-98299	Sequence 98299, A
79.5	21.6	1031	10	US-11-266-748A-151110	Sequence 151110, A
79.5	21.6	2300	12	US-60-762-056-20106	Sequence 20106, A
79.5	21.6	3523	7	US-10-567-867-1152	Sequence 1152, Ap
79.5	21.6	3686	7	US-10-567-867-1150	Sequence 1150, Ap
79.5	21.6	11000	12	US-60-740-736-57	Sequence 57, Appli
79	21.5	838	10	US-11-266-748A-370877	Sequence 370877, A
79	21.5	838	10	US-11-266-748A-454256	Sequence 454256, A
79	21.5	4631	10	US-11-266-748A-23775	Sequence 23775, A
78.5	21.3	852	7	US-10-526-468-1	Sequence 1, Appli
78.5	21.3	1072	8	US-11-056-355B-67001	Sequence 67001, A
78	21.2	1632	7	US-10-953-343-28425	Sequence 28425, A
78	21.2	2300	12	US-60-762-056-27646	Sequence 27646, A
77.5	21.1	467	8	US-11-360-355-52941	Sequence 52941, A

79	77.5	21.1	975	7	US-10-533-232A-103	Sequence 103, App
80	77.5	21.1	1239	7	US-10-540-898-285	Sequence 285, App
C 81	77.5	21.1	2182	8	US-11-360-355-22269	Sequence 22269, A
C 82	77.5	21.1	2300	12	US-60-762-056-16197	Sequence 16197, A
C 83	77.5	21.1	21239	8	US-10-540-898-284	Sequence 284, App
C 84	77.5	21.1	84428	8	US-11-330-363-1	Sequence 1, Appl
C 85	77	20.9	291	8	US-11-239-625A-1671	Sequence 1671, Ap
C 86	77	20.9	2300	12	US-60-762-056-23276	Sequence 23276, A
C 87	76.5	20.8	373	10	US-11-227-183A-28897	Sequence 28897, A
C 88	76.5	20.8	1522	8	US-11-174-307B-1097	Sequence 1097, Ap
C 89	76.5	20.8	1522	8	US-11-056-355B-10007	Sequence 10007, A
C 90	76.5	20.8	70782	6	US-10-526-572-47	Sequence 47, Appl
C 91	76.5	20.8	82868	6	US-10-526-572-1	Sequence 1, Appl
C 92	76.5	20.8	82868	6	US-10-526-572-18	Sequence 18, Appl
C 93	76.5	20.8	402	10	US-11-227-183A-16939	Sequence 16939, A
C 94	75.5	20.5	413	8	US-11-353-150-44264	Sequence 44264, A
C 95	75.5	20.5	421	8	US-11-353-150-64448	Sequence 64448, A
C 96	75.5	20.5	1552	8	US-11-174-307B-5185	Sequence 5185, Ap
C 97	75.5	20.5	2300	12	US-60-762-056-28190	Sequence 28190, A
C 98	75.5	20.5	2300	12	US-60-762-056-29256	Sequence 29256, A
C 99	75.5	20.5	2300	12	US-60-762-056-29257	Sequence 29257, A
C 100	75.5	20.5	4763	7	US-10-529-348-184	Sequence 184, App
C 101	75.5	20.5	4763	10	US-11-266-748A-29652	Sequence 29652, A
C 102	75.5	20.5	15203	10	US-11-214-063A-1619	Sequence 1619, Ap
C 103	75	20.4	613	7	US-10-953-349-37623	Sequence 37623, A
C 104	75	20.4	908	10	US-11-266-748A-184390	Sequence 184390, A
C 105	75	20.4	908	10	US-11-266-748A-191895	Sequence 191895, A
C 106	75	20.4	922	10	US-11-266-748A-184386	Sequence 184386, A
C 107	75	20.4	977	7	US-10-461-673-3209	Sequence 3209, Ap
C 108	75	20.4	1000	10	US-11-266-748A-406913	Sequence 406913, A
C 109	75	20.4	1000	10	US-11-266-748A-477959	Sequence 477959, A
C 110	75	20.4	1047	12	US-60-763-373-372	Sequence 372, App
C 111	75	20.4	1047	12	US-60-781-308-180	Sequence 180, App
C 112	75	20.4	1388	8	US-11-360-355-76095	Sequence 76095, A
C 113	75	20.4	1534	8	US-11-056-355B-51703	Sequence 51703, A
C 114	75	20.4	1854	8	US-11-056-355B-66119	Sequence 66119, A
C 115	75	20.4	2300	12	US-60-762-056-20212	Sequence 20212, A
C 116	75	20.4	2300	12	US-60-762-056-26111	Sequence 26111, A
C 117	75	20.4	2312	1	PC7-US05-46084-1	Sequence 1, Appl
C 118	75	20.4	2312	7	US-10-529-348-769	Sequence 769, App
C 119	75	20.4	2312	8	US-11-342-366-1204	Sequence 1204, Ap
C 120	75	20.4	2312	8	US-11-342-367-1204	Sequence 1204, Ap
C 121	75	20.4	2312	10	US-11-313-200-1	Sequence 1, Appl
C 122	75	20.4	2312	12	US-60-751-420-1585	Sequence 1585, Ap
C 123	75	20.4	2473	10	US-11-266-748A-73797	Sequence 73797, A
C 124	75	20.4	2473	10	US-11-266-748A-108013	Sequence 108013, A
C 125	75	20.4	2473	10	US-11-266-748A-126608	Sequence 126608, A
C 126	75	20.4	2956	8	US-11-360-355-12464	Sequence 12464, A
C 127	75	20.4	3363	1	PC7-US05-45818-51	Sequence 51, Appl
C 128	75	20.4	3778	10	US-11-266-748A-29168	Sequence 29168, A
C 129	75	20.4	3889	10	US-11-266-748A-27035	Sequence 27035, A
C 130	75	20.4	90573	1	PC7-US05-45818-151	Sequence 151, App
C 131	74.5	20.2	426	8	US-11-329-388-18655	Sequence 18655, A
C 132	74.5	20.2	1270	8	US-11-089-097-6	Sequence 6, Appl
C 133	74.5	20.2	1316	7	US-10-240-851A-76	Sequence 76, Appl
C 134	74.5	20.2	1356	8	US-11-089-097-7	Sequence 7, Appl
C 135	74.5	20.2	1356	8	US-11-342-366-1804	Sequence 1804, Ap
C 136	74.5	20.2	1356	8	US-11-342-367-1804	Sequence 1804, Ap
C 137	74.5	20.2	1363	10	US-11-266-748A-186709	Sequence 186709, A
C 138	74.5	20.2	1363	10	US-11-266-748A-241491	Sequence 241491, A
C 139	74.5	20.2	1700	10	US-11-266-748A-81026	Sequence 81026, A
C 140	74.5	20.2	1700	10	US-11-266-748A-133837	Sequence 133837, A
C 141	74.5	20.2	1740	7	US-10-531-147-312	Sequence 312, App
C 142	74.5	20.2	1740	7	US-10-531-147-2447	Sequence 2447, Ap
C 143	74.5	20.2	1772	10	US-11-266-748A-56645	Sequence 56645, A
C 144	74.5	20.2	1848	8	US-11-056-355B-20264	Sequence 20264, A
C 145	74.5	20.2	1956	7	US-10-461-673-5468	Sequence 5468, Ap
C 146	74.5	20.2	2300	12	US-60-762-056-16025	Sequence 16025, A
C 147	74.5	20.2	2300	12	US-60-762-056-40627	Sequence 40627, A
C 148	74.5	20.2	2300	12	US-60-762-056-43992	Sequence 43992, A
C 149	74.5	20.2	2300	12	US-60-762-056-44619	Sequence 44619, A
C 150	74.5	20.2	3030	8	US-11-344-932-333	Sequence 333, App

ALIGNMENTS

RESULT 1

US-11-329-388-4757

Sequence 4757, Application US/11329388

GENERAL INFORMATION:

APPLICANT: Andersen, Scott E.

APPLICANT: Fisher, Dane K.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 16517.357 - 38-21(15503)C/US

CURRENT APPLICATION NUMBER: US/11/329,388

CURRENT FILING DATE: 2006-01-11

PRIOR APPLICATION NUMBER: 09/553,094

PRIOR FILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 18831

SEQ ID NO 4757

LENGTH: 414

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

US-11-329-388-4757

Alignment Scores:

Pred. No.: 5,01e-29

Length: 414

Score: 333.00

Matches: 71

Percent Similarity: 95.9%

Conservative: 0

Best Local Similarity: 95.9%

Mismatches: 1

Query Match: 90.5%

Indels: 2

DB: 8

Gaps: 1

US-10-628-525A-36 (1-74) x US-11-329-388-4757 (1-414)

Qy 1 MetAlaLaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAep 20

169 ATGGCGGCTCTGGCCACGTCGACGCTCGCGAGCGCGCGCGCGCGCGCGCGCGCG 228

Db

Qy 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaLa 40

229 GCGTCACGCTTCGGCCACGTCGACGCTCGCGAGCGCGCGCGCGCGCGCGCGCGCG 288

Db

Qy 41 AlaSerThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnGlnAla 60

289 GCGGACGCTCAGCATCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348

Db

Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74

349 CGCGCGGCTGGCAGG-----TTCCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 384

Db

RESULT 2

US-11-329-388-11949

Sequence 11949, Application US/11329388

GENERAL INFORMATION:

APPLICANT: Andersen, Scott E.

APPLICANT: Fisher, Dane K.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 16517.357 - 38-21(15503)C/US

CURRENT APPLICATION NUMBER: US/11/329,388

CURRENT FILING DATE: 2006-01-11

PRIOR APPLICATION NUMBER: 09/553,094

PRIOR FILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 18831

SEQ ID NO 11949

LENGTH: 634

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

US-11-329-388-11949





Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-19534 (1-386)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 146 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCGCAACGCCCGCGGCTGGCGCTCCGGAC 205  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 206 GGTCCACGTTCCGCGCGCGCGCGCAGGAGGCTGAGGGGGCCCGGCGTCGCGCGGCG 265  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 266 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 325  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 326 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 361

## RESULT 6

US-11-227-183A-18500  
; Sequence 18500, Application US/11227183A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalquidi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 18500  
; LENGTH: 415  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-029-Q1-K1-E4  
US-11-227-183A-18500

Alignment Scores:  
Pred. No.: 3,238-28 Length: 415  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-18500 (1-415)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 146 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCGCAACGCCCGCGGCTGGCGCTCCGGAC 205  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 206 GGTCCACGTTCCGCGCGCGCGCGCAGGAGGCTGAGGGGGCCCGGCGTCGCGCGGCG 265  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 266 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 325  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 326 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 361

## RESULT 7

US-11-353-150-45112  
; Sequence 45112, Application US/11353150  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Lalquidi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US  
; CURRENT FILING DATE: 2006-02-14  
; PRIOR APPLICATION NUMBER: 09/565,386  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/132,860  
; PRIOR FILING DATE: 1999-05-07  
; NUMBER OF SEQ ID NOS: 83523  
; SEQ ID NO 45112  
; LENGTH: 428  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3066-030-Q1-K1-A8  
US-11-353-150-45112

Alignment Scores:  
Pred. No.: 3,378-28 Length: 428  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-353-150-45112 (1-428)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 187 ATGGCGGCTCTGGCCACGTCGCGAGCTCGTCGCAACGCCCGCGGCTGGCGCTCCGGAC 246  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 247 GGTCCACGTTCCGCGCGCGCGCGCAGGAGGCTGAGGGGGCCCGGCGTCGCGCGGCG 306  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 307 GCGGACACGCTCAGCATGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 366  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 367 CGCCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 402

## RESULT 8

US-11-227-183A-17085  
; Sequence 17085, Application US/11227183A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalquidi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 17085  
; LENGTH: 449  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-008-Q1-K1-G3  
US-11-227-183A-17085

## Alignment Scores:

Pred. No.: 3,59e-28 Length: 449  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-17085 (1-449)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 177 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCCGCCGCGCTGGCGGTACCGGAC 236  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 237 GCCTCCACGTTCCGCCG 236  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 297 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 356  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 357 CGCGCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 392

RESULT 9  
US-11-227-183A-20738  
; Sequence 20738, Application US/11227183A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated with  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT APPLICATION NUMBER: US/11/227,183A  
; PRIOR FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 20738  
; LENGTH: 561  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-022-Q1-K1-D3-R2  
US-11-227-183A-20738

Alignment Scores:  
Pred. No.: 4,87e-28 Length: 561  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-20738 (1-561)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 173 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCCGCCGCGCTGGCGGTACCGGAC 232  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 233 GCCTCCACGTTCCGCCG 232  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 293 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 352  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 353 CGCGCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 388

RESULT 10  
US-11-298-234A-9  
; Sequence 9, Application US/11298234A  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fenggao  
; APPLICANT: Hauge, Brian M.  
; APPLICANT: Oggero, Christopher M  
; TITLE OF INVENTION: Methods for Ligation Independent Cloning of DNA  
; FILE REFERENCE: 53344  
; CURRENT APPLICATION NUMBER: US/11/298,234A  
; PRIOR FILING DATE: 2005-12-09  
; PRIOR APPLICATION NUMBER: 60634779  
; PRIOR FILING DATE: 2004-12-09  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 9  
; LENGTH: 1409  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-11-298-234A-9

Alignment Scores:  
Pred. No.: 1,71e-27 Length: 1409  
Score: 326.00 Matches: 70  
Percent Similarity: 94.6% Conservative: 0  
Best Local Similarity: 94.6% Mismatches: 2  
Query Match: 88.6% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-298-234A-9 (1-1409)

Qy 1 MetAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
Db 175 ATGGCGGCTCTGGCCACGTCGACGTCGTCGCAACGCCGCCGCGCTGGCGGTACCGGAC 234  
Qy 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
Db 235 GCCTCCACGTTCCGCCG 294  
Qy 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
Db 295 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 354  
Qy 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
Db 355 CGCGCGCGGGGCGAGG-----TTCCCGTCGCTCGTGTGTGC 390

RESULT 11  
US-11-330-822-50  
; Sequence 50, Application US/11330822  
; GENERAL INFORMATION:  
; APPLICANT: GUAN, HANPING  
; APPLICANT: KEELING, PETER L.  
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN  
; TITLE OF INVENTION: HOSTS  
; FILE REFERENCE: 15053-04  
; CURRENT APPLICATION NUMBER: US/11/330,822  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: PCT/US98/06660  
; PRIOR FILING DATE: 1998-04-03  
; PRIOR APPLICATION NUMBER: 60/042,939  
; PRIOR FILING DATE: 1997-04-04  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 50  
; LENGTH: 1915  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) .. (1815)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1819) .. (1914)



## US-11-227-183A-19289

Alignment Scores:  
Pred. No.: 7.65e-27 Length: 408  
Score: 314.00 Matches: 68  
Percent Similarity: 91.9% Conservative: 0  
Best Local Similarity: 91.9% Mismatches: 4  
Query Match: 85.3% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-19289 (1-408)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 163 ATGGCGGCTCTGGCCACGTCGACGTCGTCACACGCCCGCGGCTGGGGCGTCCGGAC 222  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 223 GCGTCCACGTTCCGCGCGGCGCGCGCANGGCTGAGGGGGGCCCGGGGTCCGGCGG 282  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 283 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCGCCANGCACCAGCAGCAAGCG 342  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 343 CGCGCGGGGGCAGG-----TTCCTGCTGCTGCTGCTGTCG 378

## RESULT 15

US-11-227-183A-20077  
; Sequence 20077, Application US/11227183A  
; GENERAL INFORMATION:

; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalgudi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR FILING DATE: 2005-09-16  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 20077  
; LENGTH: 386  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-057-Q1-K1-F6  
US-11-227-183A-20077

Alignment Scores:  
Pred. No.: 1.72e-25 Length: 386  
Score: 302.00 Matches: 66  
Percent Similarity: 91.8% Conservative: 1  
Best Local Similarity: 90.4% Mismatches: 4  
Query Match: 82.1% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-20077 (1-386)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 173 ATGGCGGCTCTGGCCACGTCGACGTCGTCACACGCCCGCGGCTGGGGCGTCCGGAC 232  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 233 GCGTCCACGTTCCGCGCGGCGCGCGCATGCGCTGAGGGGGGCCCGGGGTCCGGCGG 292  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 293 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCGCCAGGACCAGCAGCAAGCG 352

QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValVal 73  
DB 353 CGCGCGGGGGCAAG-----GTCCCGTCTGCTGCTG 385

## RESULT 16

US-11-353-150-45136  
; Sequence 45136, Application US/11353150  
; GENERAL INFORMATION:

; APPLICANT: Andersen, Scott E.  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Lalgudi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US  
; CURRENT FILING DATE: 2006-02-14  
; PRIOR FILING DATE: 2006-02-14  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR FILING DATE: 1999-05-07  
; NUMBER OF SEQ ID NOS: 83523  
; SEQ ID NO 45136  
; LENGTH: 431  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3066-030-Q1-E1-H5  
US-11-353-150-45136

Alignment Scores:  
Pred. No.: 1.28e-24 Length: 431  
Score: 295.00 Matches: 64  
Percent Similarity: 87.8% Conservative: 1  
Best Local Similarity: 86.5% Mismatches: 7  
Query Match: 80.2% Indels: 2  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-353-150-45136 (1-431)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20  
DB 202 ATGGCGGCTCTGGCCACGTCGACGTCGTCACACGCCCGCGGCTGGGGCGTCCGGAC 261  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 262 GCGTCCACGTTCCGCGCGGCGCGCGCATGCGCTGAGGGGGGCCCGGGGTCCGGCGG 321  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 322 GCGGACACGCTCAGCATGCGGACGAGCGCGCGCGCCCAATCACCATCAACAAGCG 381  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 382 CGCGCGGGGGCAAG-----TTCCTGCTGCTGCTGTCG 417

## RESULT 17

US-11-227-183A-16655  
; Sequence 16655, Application US/11227183A  
; GENERAL INFORMATION:

; APPLICANT: Fisher, Dane K.  
; APPLICANT: Lalgudi, Raghunath V.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR FILING DATE: 2005-09-16  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 16655  
; LENGTH: 400  
; TYPE: DNA

; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-003-Q1-K1-B3  
US-11-227-183A-16655

Alignment Scores:  
Pred. No.: 7.45e-24 Length: 400  
Score: 288.00 Matches: 63  
Percent Similarity: 86.5% Conservative: 1  
Best Local Similarity: 85.1% Mismatches: 8  
Query Match: 78.3% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-16655 (1-400)

QY 1 MetAlaLeuAlaLeuSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20  
DB 169 ATGGCGGCTTCGCCACGTTGCAGCTAGTCCGAACGCCCGCGGCTGGCGCTCCCGGAC 228  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyValaAlaSerAlaAla 40  
DB 229 GGGTCCAGCTTCGCCGAGCGCCACGACGCGCTGAGGGGGCGCGCTCGGGCGG 288  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 289 GTGGACACGCTTAACATGCGGACCGCGCGCTGCGCCAGGACCAGCAGCAGCGG 348  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 349 CGCCGCGGTGCAGG-----TTCCGCTCGCTCGACGTGTC 384

## RESULT 18

US-11-227-183A-18495  
; Sequence 18495, Application US/11227183A  
; GENERAL INFORMATION:

; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517-336 - 38-21(15230)C/US  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 18495  
; LENGTH: 388  
; TYPE: DNA  
; ORGANISM: Zea mays

; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-029-Q1-K1-E1

US-11-227-183A-18495

Alignment Scores:  
Pred. No.: 1.59e-23 Length: 388  
Score: 285.00 Matches: 60  
Percent Similarity: 89.6% Conservative: 0  
Best Local Similarity: 89.6% Mismatches: 7  
Query Match: 77.4% Indels: 0  
DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-227-183A-18495 (1-388)

QY 1 MetAlaLeuAlaLeuSerGlnLeuValAlaThrArgAlaGlyHisGlyValProasp 20  
DB 174 ATGGCGGCTTCGCCACGTTGCAGCTAGTCCGAACGCCCGCGGCTGGCGCTCCCGGAC 233  
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyValaAlaSerAlaAla 40  
DB 234 GGGTCCAGCTTCGCCGCTGGCGCGGACGCGCTGAGGGGGCGCGCTCGGCTGG 293  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60

DB 294 GCGGACACGCTCAGCATGCCGACGCGCGCGCGGCGCTTAGGCACCATCATCATGCG 353  
QY 61 ArgArgGlyGlyArgPhePro 67  
DB 354 CGCCGAGGAGGAGGTTCGCG 374

## RESULT 19

US-11-329-388-8047  
; Sequence 8047, Application US/11329388  
; GENERAL INFORMATION:

; APPLICANT: Andersen, Scott E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US  
; CURRENT APPLICATION NUMBER: US/11/329,388  
; PRIOR FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: 09/553,094  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18831  
; SEQ ID NO 8047  
; LENGTH: 625  
; TYPE: DNA  
; ORGANISM: Zea mays

; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(625)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3061-084-Q1-K6-E9  
US-11-329-388-8047

## Alignment Scores:

Pred. No.: 1.95e-22 Length: 625  
Score: 278.00 Matches: 63  
Percent Similarity: 92.6% Conservative: 0  
Best Local Similarity: 92.6% Mismatches: 3  
Query Match: 75.5% Indels: 3  
DB: 8 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-329-388-8047 (1-625)

QY 7 SerGlnLeuValAlaThrArgAlaGlyHisGlyValProAspAlaSerThrPheArgArg 26  
DB 5 TCGCAGCTCGTCGC-ACGCGCGCGCGCTGGCGCTCCCGCGCGCTCCAGCTTCGCGCGC 63  
QY 27 GlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAlaAlaAspThrLeuSerMet 46  
DB 64 GCGCGCGCGCAGGGCTGAGGGGGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCATG 123  
QY 47 ArgThrSerAlaAlaAlaProArgHisGlnGlnAlaAlaArgGlyGlyArgPhe 66  
DB 124 CGGACG 180  
QY 67 PropheProSerLeuValValCys 74  
DB 181 ---TTCCGCTCGCTCGTGTGTC 201

## RESULT 20

US-11-329-388-8026  
; Sequence 8026, Application US/11329388  
; GENERAL INFORMATION:

; APPLICANT: Andersen, Scott E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US  
; CURRENT APPLICATION NUMBER: US/11/329,388  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: 09/553,094  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18831  
; SEQ ID NO 8026  
; LENGTH: 649



NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 19448  
; LENGTH: 354  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-045-Q1-K1-F11  
US-11-227-183A-19448

Alignment Scores:  
Pred. No.: 2,18e-21 Length: 354  
Score: 266.00 Matches: 57  
Percent Similarity: 95.0% Conservative: 0  
Best Local Similarity: 95.0% Mismatches: 3  
Query Match: 72.3% Indels: 0  
DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-227-183A-19448 (1-354)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
DB 173 ATGGCGGCTCTGGCCACGCTCGAGCTCGTGCACACGCCCGCGGCTGGCGCTCCGGAC 232  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 233 GGCTCCAGTTTCGGCGCGCGCGCGCGCAAGSCCTGAGGGGGCGCGGCTCGCGGGCG 292  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60  
DB 293 GCGGACACGCTCAGCATGGGACCGAGCGCGCGCGCGGCCCGCCANGCACCAGCAGCGCG 352

## RESULT 24

US-11-329-388-3077  
; Sequence 3077, Application US/11329388  
; GENERAL INFORMATION:  
; APPLICANT: Andersen, Scott E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 16517.357 - 38-21(15503)C/US  
; CURRENT APPLICATION NUMBER: US/11/329,388  
; CURRENT FILING DATE: 2006-01-11  
; PRIOR APPLICATION NUMBER: 09/553,094  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 18831  
; SEQ ID NO 3077  
; LENGTH: 363  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3061-033-Q1-K1-C5  
US-11-329-388-3077

Alignment Scores:  
Pred. No.: 5,01e-21 Length: 363  
Score: 263.00 Matches: 55  
Percent Similarity: 96.6% Conservative: 2  
Best Local Similarity: 93.2% Mismatches: 2  
Query Match: 71.5% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-329-388-3077 (1-363)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
DB 185 ATGGCGGCTCTGGCCACGCTCGAGCTCGTGCACACGCCCGCGGCTGGCGCTACCGAC 244  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 245 GCGTCCAGTTCCCGCGCGCGCGCGCGAGGCCCTGAGGGGGCGCGGCTCGTGGCGCGCG 304

QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGln 59  
DB 305 GCGGACACGCTCAGCATGGGACCGAGCTCGCGCGCTGGCCCGGACCGAGCGAG 361

## RESULT 25

US-11-227-183A-18014  
; Sequence 18014, Application US/11227183A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT APPLICATION NUMBER: US/11/227,183A  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 18014  
; LENGTH: 365  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-022-Q1-K1-D3  
US-11-227-183A-18014

Alignment Scores:  
Pred. No.: 5,05e-21 Length: 365  
Score: 263.00 Matches: 58  
Percent Similarity: 92.4% Conservative: 3  
Best Local Similarity: 78.4% Mismatches: 11  
Query Match: 71.5% Indels: 2  
DB: 10 Gaps: 1

US-10-628-525A-36 (1-74) x US-11-227-183A-18014 (1-365)

QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAap 20  
DB 126 ATGTGGGCTCTGTGCACATGTCAGATCTGTCAACGCCCGCGGCTGTGGTTCGGAC 185  
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40  
DB 186 GCGTGTACATTTCCGCGCGCGCGCGCGCGCGCTGTGGGGCGCGCGGCTGTGGCGCG 245  
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAla 60  
DB 246 GCGGACACACTCAGCATGCGGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 305  
QY 61 ArgArgGlyGlyArgPheProPheProSerLeuValValCys 74  
DB 306 CGCGCGGGGGGCGAGG-----TTCCCGTCTCGTCTGTGTGC 341

## RESULT 26

US-11-227-183A-18823  
; Sequence 18823, Application US/11227183A  
; GENERAL INFORMATION:  
; APPLICANT: Fisher, Dane K.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US  
; CURRENT APPLICATION NUMBER: US/11/227,183A  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: US 09/619,643  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 32236  
; SEQ ID NO 18823  
; LENGTH: 371  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3151-037-Q1-K1-D3  
US-11-227-183A-18823



```
Alignment Scores:
Pred. No.: 3,63e-16 Length: 371
Score: 221.00 Matches: 49
Percent Similarity: 80.0% Conservative: 3
Best Local Similarity: 75.4% Mismatches: 13
Query Match: 60.1% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-227-183A-18823 (1-371)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 176 ATGGGGCTCTGGCCAGCTGCGAGCTGTCGCAACGCCCGCCGCGCTGGCGGCTCCCGGAC 235
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAa 40
DB 236 GCGTCCACGTTCCGCGCGCGCGCGCGAGGGCTGAGGGGGCGCGCGCGCTGGCGGGCG 295
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaAlaProArgHisGlnGlnAla 60
DB 296 GCGGCCACCTTAAGATGCGGCAACAGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 355
QY 61 ArgArgGlyGlyArg 65
DB 356 CCGCGGGGGCCAGG 370

RESULT 27
US-11-227-183A-32098
; Sequence 32098, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; PRIOR FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 32098
; LENGTH: 338
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3182-014-P2-M1-P5
US-11-227-183A-32098
Alignment Scores:
Pred. No.: 2,05e-15 Length: 338
Score: 214.00 Matches: 46
Percent Similarity: 87.0% Conservative: 1
Best Local Similarity: 85.2% Mismatches: 7
Query Match: 58.2% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-36 (1-74) x US-11-227-183A-32098 (1-338)
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 175 ATGGCGGCTCTGGCCAGCTGCGAGCTGTCGCAACGCCCGCCGCGCTGGCGGCTCCCGGAC 234
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAa 40
DB 235 GCGTCCACGTTCCGCGCGCGCGCGAGGGCTGAGGGGGCGCGCGCTGCTGTGTG 294
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaPro 54
DB 295 GTGGACACGCTTAGCATGCTGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 336

RESULT 28
US-11-227-183A-18999
```

```
; Sequence 18999, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; PRIOR FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 18999
; LENGTH: 203
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-039-Q1-K1-G5
US-11-227-183A-18999
```

```
Alignment Scores:
Pred. No.: 5,04e-15 Length: 203
Score: 208.00 Matches: 45
Percent Similarity: 92.2% Conservative: 2
Best Local Similarity: 88.2% Mismatches: 4
Query Match: 56.5% Indels: 0
DB: 10 Gaps: 0
```

US-10-628-525A-36 (1-74) x US-11-227-183A-18999 (1-203)

```
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
DB 50 ATGGCGGCTCTGGCCAGCTGCGAGCTGTCGCAACGCCCGCCGCGCTGGCGGCTCCCGGAC 109
QY 21 AlaSerThrPheArgArgGlyAlaAlaGlnGlyLeuArgGlyAlaAlaSerAlaAa 40
DB 110 GCGTCCACGTTCCGCGCGCGCGCGAGGGCTGAGGGGGCGCGCGCGCTGAGCGGCG 169
QY 41 AlaAspThrLeuSerMetArgThrSerAlaArg 51
DB 170 GCGGACCTCTCAGCATGCGGACCAACGCGCGC 202
```

## RESULT 29

```
US-11-227-183A-20737
; Sequence 20737, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; PRIOR FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 20737
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-022-Q1-K1-D3.R1
US-11-227-183A-20737
```

```
Alignment Scores:
Pred. No.: 1,81e-14 Length: 519
Score: 208.00 Matches: 60
Percent Similarity: 82.7% Conservative: 2
Best Local Similarity: 80.0% Mismatches: 8
Query Match: 56.5% Indels: 7
DB: 10 Gaps: 3
```

US-10-628-525A-36 (1-74) x US-11-227-183A-20737 (1-519)

```
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 168 ATGGCGGCTCTGGCCACGTCGACGCTCGTCGACAGCCC-GCCGGCTGGGCGTCCCGGAC 226
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 227 CGGTCCACGTTCCGCGCGCGCGGCA---GGGCTGAGGGGGCGGCGGTCGGCGGG 283
QY 41 AlaAspThrLeuSerMetArgThrSerAlaAlaArg-AlaAlaProArgHisGlnGlnAl 60
Db 284 GCGGACACCTC-AGCATGCGGACCGCGCGCTCCGCC---AGGCACACGACGAGGC 339
QY 60 aArgArgGlyGlyArgPheProPheProSerLeuValValCys 74
Db 340 GCGCGCGGGGCGAGG-----TTCCGTCGCTCGTGTGTGC 376
```

## RESULT 30

```
US-11-227-183A-18231
; Sequence 18231, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Jagudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 18231
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-025-Q1-K1-C12
US-11-227-183A-18231
```

## Alignment Scores:

Pred. No.:	2,248-09	Length:	360
Score:	162.00	Matches:	41
Percent Similarity:	69.4%	Conservative:	2
Best Local Similarity:	66.1%	Mismatches:	18
Query Match:	44.0%	Indels:	1
DB:	10	Gaps:	0

US-10-628-525A-36 (1-74) x US-11-227-183A-18231 (1-360)

```
QY 1 MetAlaAlaLeuAlaThrSerGlnLeuValAlaThrArgAlaGlyHisGlyValProAsp 20
Db 170 ATGGCGGCTCTGGCCACGTCACATCTCGACGGCATCGCCCTCGGCGTCCCGGAC 229
QY 21 AlaSerThrPheArgGlyAlaAlaGlnGlyLeuArgGlyAlaArgAlaSerAlaAla 40
Db 230 GGGTTACATTTCCGACGAGCGCGCTGCAAGGACTGAGGTGGGCCCTATCATATGAGGTA 289
QY 41 -AlaAspThrLeuSerMetArgThrSerAlaArgAlaAlaProArgHisGlnGlnAl 60
Db 290 CGCTGACACGCTCATTAATCGGACCGAGCATGCGCGCACGACATACACCAACATCAGGC 349
QY 60 aArg 61
Db 350 ACGC 353
```

Search completed: April 2, 2006, 03:51:38  
Job time : 143.391 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: April 1, 2006, 04:29:01 ; Search time 776.782 Seconds  
(without alignments)  
2853.949 Million cell updates/sec

Title: US-10-628-525a-37

Perfect score: 191

Sequence: 1 MATPSAVGACLLARXAMPVAVGDRPRLQRLVLR 39

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abs/ABSSWEB spool/US10628525/runat\_31032006\_095113\_16622/app\_query.fasta\_1  
-DB=GenEmbl -QPM=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=150  
-DOCALLIGN=200 -THR\_SCORE=pcp -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcp -NORM=ext -HEADSIZE=500 -MINLEN=2000000000 -HOST=abs06h  
-USER=US10628525 @CGN\_1.1\_4375 @runat\_31032006\_095113\_16622 -NCFU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*  
1: gb.ba.\*  
2: gb.in.\*  
3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	100.0	153	6	AR106497
2	191	100.0	153	6	BD071190
3	191	100.0	1415	6	BD249565

4	191	100.0	1415	6	AR340013
5	191	100.0	2008	6	BD249566
6	191	100.0	2008	6	AR340014
7	191	100.0	2357	15	AF036891
8	191	100.0	2383	6	A93359
9	191	100.0	2383	6	AR174874
10	191	100.0	2383	6	AR411327
11	191	100.0	2491	6	BD249559
12	191	100.0	2491	6	AR340007
13	190	99.5	2992	6	A63308
14	168	88.0	2990	6	AR049919
15	139.5	73.0	2592	15	AF168786
16	74.5	39.0	110000	14	AP006500_07
17	74	38.7	53583	14	AC013160
18	71.5	37.4	110000	15	AP008212_269
19	71.5	37.4	165270	15	AP004744
20	71	37.2	2182	2	AY310711
21	71	37.2	19791	1	SPFXBAD
22	71	37.2	110000	1	BA000012_29
23	70.5	36.9	3741	1	AB091437
24	70.5	36.9	25768	1	AY327575
25	70	36.6	2115	2	AY310707
26	70	36.6	2146	2	AY310691
27	70	36.6	2171	2	AY310683
28	70	36.6	2171	2	AY310693
29	70	36.6	2175	2	AY310679
30	70	36.6	2175	2	AY310679
31	70	36.6	2175	2	AY310682
32	70	36.6	2176	2	AY310684
33	70	36.6	2176	2	AY310686
34	70	36.6	2176	2	AY310712
35	70	36.6	140953	14	AC159112
36	69	36.1	2144	2	AY310696
37	69	36.1	2175	2	AY310677
38	69	36.1	2177	2	AY310697
39	69	36.1	2178	2	AY310673
40	69	36.1	2178	2	AY310675
41	69	36.1	2178	2	AY310687
42	69	36.1	2178	2	AY310689
43	69	36.1	2178	2	AY310714
44	69	36.1	2179	2	AY310685
45	68.5	35.9	168278	9	AC126246
46	68.5	35.9	187977	9	AL672229
47	68.5	35.9	211386	9	AC153418
48	68	35.6	2184	2	AY310709
49	68	35.6	2185	2	AY310713
50	68	35.6	2206	2	AY310702
51	68	35.6	18270	1	AF148496
52	68	35.6	62630	14	AC101139
53	68	35.6	110000	1	AB017282_02
54	68	35.6	110000	1	AB017282_03
55	68	35.6	110000	15	AP008210_099
56	68	35.6	120640	15	OSJN00113
57	68	35.6	195700	14	AC162574
58	68	35.6	210614	1	AB088224
59	67.5	35.3	835	15	AK105139
60	67.5	35.3	2000	6	AX655130
61	67.5	35.3	9754	1	AE012077
62	67.5	35.3	10873	1	AE012494
63	67.5	35.3	67480	7	AY129334
64	67.5	35.3	110000	1	CR555306_20
65	67.5	35.3	110000	1	AP006840_11
66	67.5	35.3	110000	1	AP006840_20
67	67.5	35.3	110000	1	CP000050_44
68	67.5	35.3	110000	1	CP000050_45
69	67.5	35.3	110000	15	AP008209_000
70	67.5	35.3	125217	15	AC097627
71	67.5	35.3	134431	13	AY386265
72	67.5	35.3	156933	15	AK125411
73	67.5	35.3	274762	1	BX664015
74	67	35.1	692	10	BV640012
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AR340013 Sequence  
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AR340014 Sequence  
AF036891 Zsa mayas  
A93359 Sequence 1  
AR174874 Sequence  
AR411327 Sequence  
BD249559 Modificat  
AR340007 Sequence  
A63308 Sequence 1  
AR049919 Sequence  
AF168786 Sorghum b  
Continuation (8 of  
AC013160 Drosophil  
Continuation (270  
AP004744 Oryza sat  
AY310711 Saccomorp  
Y10438 Streptomyce  
Continuation (30 o  
AB091437 Burkholde  
AY327575 Delftia a  
AY310707 Episcaphu  
AY310691 Mycotretu  
AY310683 Lybas sp.  
AY310693 Lybas sp.  
AY310679 Mycotretu  
AY310679 Mycotretu  
AY310682 Mycotretu  
AY310684 Peelaphac  
AY310686 Peelaphac  
AY310712 Peelaphac  
AC159112 Pan trogl  
AY310696 Megalodac  
AY310677 Iphiclus  
AY310697 Megalodac  
AY310673 Iphiclus  
AY310675 Iphiclus  
AY310687 Iphiclus  
AY310689 Prepophar  
AY310714 Prepophar  
AY310685 Iphiclus  
AC126246 Mus muscu  
AL672229 Mouse DNA  
AC153418 Mus muscu  
AY310709 Asgithus  
AY310713 Nitridulin  
AY310702 Encaustes  
AF148496 Pseudomon  
AC101139 Mus muscu  
Continuation (3 of  
Continuation (4 of  
Continuation (100  
AL606991 Oryza sat  
AC162574 Bos tauru  
AB088224 Streptomy  
AK105139 Oryza sat  
AX655130 Sequence  
AE012077 Xanthomon  
AE012494 Xanthomon  
AY129334 Mycobacte  
Continuation (21 o  
Continuation (12 o  
Continuation (21 o  
Continuation (45 o  
Continuation (46 o  
AP008209 Oryza sat  
AC097627 Genomic s  
AY386265 Bovine pa  
AK125411 Genomic s  
BX664015 Serratia  
BV640012 S215P6132  
AC008570 Homo sapi  
AC145149 Homo sapi



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1. .153
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/mol_type="genomic DNA"
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ORIGIN
Alignment Scores:
Pred. No.: 2,21e-11 Length: 153
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x BD071190 (1-153)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
Db 1 ATGGCGAGCCCTCGGCGCGTGGCGCGCGTGCCTCTCTCGCGCGGCGCGCTGGCCG 60

Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 61 GCCGCGCTCGCGACCGCGCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGCG 117

RESULT 3
BD249565 1415 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
Modification of starch biosynthesis enzyme gene expression for
ACCESSION
BD249565
VERSION
BD249565.1 GI:33059335
KEYWORDS
JP 2002525029-A/11.
SOURCE
Zea mays
ORGANISM
Zea mays

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1415)
Brogliie,K.E. and Lightner,J.E.
Modifcation of starch biosynthesis enzyme gene expression for
Patent: JP 2002525029-A 11 13-AUG-2002;
E1 DU PONT DE NEMOURS AND CO
Query Match: 100.0%
Indels: 0
Gaps: 0

FEATURES
source
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ORIGIN
Alignment Scores:
Pred. No.: 1,64e-10 Length: 1415
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x AR340013 (1-1415)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
Db 2 ATGGCGAGCCCTCGGCGCGTGGCGCGCGTGCCTCTCTCGCGCGGCGCGCTGGCCG 61

Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 62 GCCGCGCTCGCGACCGCGCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGCG 118

RESULT 5
BD249566 2008 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
Modification of starch biosynthesis enzyme gene expression for
production of starch in grain crops.
ACCESSION
BD249566
VERSION
BD249566.1 GI:33059336
KEYWORDS
JP 2002525029-A/12.
SOURCE
Zea mays
ORGANISM
Zea mays

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2008)
Brogliie,K.E. and Lightner,J.E.
Modifcation of starch biosynthesis enzyme gene expression for
production of starch in grain crops
Patent: JP 2002525029-A 12 13-AUG-2002;
E1 DU PONT DE NEMOURS AND CO
Query Match: 100.0%
Indels: 0
Gaps: 0

FEATURES
source
1. .1415
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/db_xref="taxon:4577"

ORIGIN
Alignment Scores:
Pred. No.: 1,64e-10 Length: 1415
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x BD249565 (1-1415)

```

PI KAREN E BROGLIE, JONATHAN EDWARD LIGHTNER  
PC A01H5/00, A01H1/00, C08B33/00, C12N15/09, C12N15/00 CC  
Modification of starch biosynthesis enzyme  
gene expression for  
CC of starch in grain crops  
FH Key Location/Qualifiers  
FT source 1..2008  
FT Location/Qualifiers  
FT /organism='Zea mays (maize)'.  
FT /organism='Zea mays'  
FT /mol\_type='genomic DNA'  
FT /db\_xref='taxon:4577'

FEATURES  
source

ORIGIN

Alignment Scores:

Pred. No.: 2,25e-10 Length: 2008  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x BD249566 (1-2008)

Qy 1 MetaLThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 2 ATGGGACGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 61  
Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
Db 62 GCCGCGGTGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 118

RESULT 6

AR340014 2008 bp DNA linear PAT 17-AUG-2003  
LOCUS Sequence 12 from patent US 6570008.  
DEFINITION AR340014  
ACCESSION AR340014  
VERSION AR340014.1 GI:33731308  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE 1 (bases 1 to 2008)  
AUTHORS Broglie, K.E. and Lightner, J.E.  
TITLE Modification of starch biosynthetic enzyme gene expression to  
produce starches in grain crops  
JOURNAL Patent: US 6570008-A 12 27-MAY-2003;  
E. I. du Pont de Nemours and Company; Wilmington, DE  
FEATURES  
source  
1..2008  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 2,25e-10 Length: 2008  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x AR340014 (1-2008)

Qy 1 MetaLThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 2 ATGGGACGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 61  
Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
Db 62 GCCGCGGTGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 118

RESULT 7

AR340014

LOCUS

DEFINITION

AR340014

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Zea mays

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

FEATURES

source

1..2357

/organism="Zea mays"

/mol\_type="mRNA"

/strain="W64A"

/db\_xref="taxon:4577"

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/EC number="2.4.1.21"

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/protein\_id="AAB99957.2"

/db\_xref="GI:51832613"

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FVDHPSVHRPGNLVCDKFGARDNQFRVTLACYACEAPLILLEGGLYVGNQCMFVNV  
DWHASLVPLLAAKRTPYGVYKDSRIIVNENLAHQGVPEASTYPDLGLPFWYGALE  
WVFPENARRHALDKEAVNFKGAVTADRIVTVSKYSWEVTTAAGGGGLNELLSRR  
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GFIGRLDYQKIGIDILQIIPDLMRDQVFMVLDGSDPELDMWRSTESI FKDKFRGWV  
GFSVPVSHRITAGCDLILMPRFPCGLNQLVAMQYGVVTVVTHATGGLRDTVENPNP  
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/product="plastid starch synthase I"

ORIGIN

Alignment Scores:

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Pred. No.: 2.6e-10 Length: 2357
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 15 Gaps: 0

US-10-628-525A-37 (1-39) x AF036891 (1-2357)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg**AlaTrpPro 20
Db 55 ATGCGAGCCCTCGGCGTGGCGCGCGCTCTCTCTCGCGCGCGCGCTGGCGG 114

Qy 21 AlaAlaValGlyAapArgAlaAArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 115 GCCCGCGTGGCGAGCGGCGCGCGCGCGCGCGCTCCAGCGCGTGTGCGCGCGCGG 171

RESULT 8
LOCUS A93359 2383 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1 from Patent WO9744472.
ACCESSION A93359
VERSION A93359.1 GI:6741623
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2383)
Kossmann,J. and Froberg,C.
NUCLEIC ACID MOLECULES CODING SOLUBLE MAIZE STARCH SYNTHASES
Patent: WO 9744472-A 1 27-NOV-1997;
KOSSMANN JENS (DE); FROBERG CLAUS (DE)
FEATURES
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/codon_start=1
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/db_xref="GI:6741624"
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DVCSFVALLAARGHVRVMPRYLNGTSDKNANAFYTEKHIRIPCGGEHEVTFPH
EYRSVDVDFVDPHSVHRPCNLVGDKFQADNQFRVTLACYACEAPLVLEGGVLY
GONCFVVDNDHASLVPLLAAKRYPGVYKDSRSILVINHLAQGVPEPASTVPDGLI
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FKDFKDFVGFSPVSHRIYAGCDIILMPSRFPCLGNLYAMQYGTVPVPHATGGYLR
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ORIGIN

Alignment Scores:
Pred. No.: 2.62e-10 Length: 2383
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x A93359 (1-2383)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg**AlaTrpPro 20
Db 29 ATGCGAGCCCTCGGCGTGGCGCGCGCGCTCTCTCTCGCGCGCGCGCTGGCGG 88

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US-10-628-525A-37 (1-39) x AR411327 (1-2383)

QY 1 MetaLThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 29 ATGGCGACCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCCCTGGCG 88  
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
Db 89 GCCCGCGTGGCGACCGCGCGCGCGCGCGCGCTCCAGCGGTGTGTGGCGCGCG 145

RESULT 11  
BD249559  
LOCUS BD249559 2491 bp DNA linear PAT 17-JUL-2003  
DEFINITION Modification of starch biosynthesis enzyme gene expression for  
production of starch in grain crops.

ACCESSION BD249559

VERSION BD249559.1 GI:33059329

KEYWORDS JP 2002525029-A/5.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 2491)

Brogliie,K.E. and Lightner,J.E.

Modification of starch biosynthesis enzyme gene expression for

Production of starch in grain crops

Patent: JP 2002525029-A 5 13-AUG-2002;

E1 DU PONT DE NEMOURS AND CO

OS Zea mays (maize)

PN JP 2002525029-A/5

PD 13-AUG-2002

PP 26-JUL-1999 JP 2000562537

PR 28-JUL-1998 US 60/094436

PI KAREN E BROGLIE, JONATHAN EDWARD LIGHTNER

PC A01H5/00,A01H1/00,C08B33/00,C12N15/09,C12N15/00 CC

Modification of starch biosynthesis enzyme

gene expression for

CC production

CC of starch in grain crops

FH Key Location/Qualifiers

FT source 1..2491

FT /organism='Zea mays (maize)'. .

FEATURES

source

1..2491

/organism="Zea mays"

/mol\_type="genomic DNA"

/db\_xref="taxon:4577"

ORIGIN

Alignment Scores:

Pred. No.: 2,73e-10 Length: 2491

Score: 191.00 Matches: 38

Percent Similarity: 97.4% Conservative: 0

Best Local Similarity: 97.4% Mismatches: 1

Query Match: 100.0% Indels: 0

DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x BD249559 (1-2491)

QY 1 MetaLThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 145 ATGGCGACCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCCCTGGCG 204

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
Db 205 GCCCGCGTGGCGACCGCGCGCGCGCGCGCTCCAGCGGTGTGTGGCGCGCG 261

RESULT 12  
AR340007  
LOCUS AR340007 2491 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 5 from patent US 6570008.  
ACCESSION AR340007

VERSION AR340007.1 GI:33731301

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2491)

AUTHORS Broglie,K.E. and Lightner,J.E.

TITLE Modification of starch biosynthesis enzyme gene expression to

produce starches in grain crops

Patent: US 6570008-A 5 27-MAY-2003;

E. I. du Pont de Nemours and Company; Wilmington, DE

JOURNAL Location/Qualifiers

FEATURES source

1..2491

/organism="unknown"

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ORIGIN

Alignment Scores:

Pred. No.: 2,73e-10 Length: 2491

Score: 191.00 Matches: 38

Percent Similarity: 97.4% Conservative: 0

Best Local Similarity: 97.4% Mismatches: 1

Query Match: 100.0% Indels: 0

DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x AR340007 (1-2491)

QY 1 MetaLThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 145 ATGGCGACCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCCCTGGCG 204

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
Db 205 GCCCGCGTGGCGACCGCGCGCGCGCGCTCCAGCGGTGTGTGGCGCGCG 261

RESULT 13

AR3308

LOCUS A63308 2992 bp DNA linear PAT 12-MAR-1998

DEFINITION Sequence 1 from Patent WO9720936.

ACCESSION A63308

VERSION A63308.1 GI:3717138

KEYWORDS unidentified

SOURCE unidentified

ORGANISM unclassified sequences.

REFERENCE 1

AUTHORS Keeling,P.L. and Knight,M.E.

TITLE MODIFICATION OF STARCH SYNTHESIS IN PLANTS

Patent: WO 9720936-A 1 12-JUN-1997;

JOURNAL ZENECA LTD (GB)

COMMENT Other publication AU 1037197 19970627.

FEATURES source

1..2992

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/clone="NUMBER 1"

ORIGIN

Alignment Scores:

Pred. No.: 4.08e-10 Length: 2992

Score: 190.00 Matches: 39

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 99.5% Indels: 0

DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x A63308 (1-2992)

QY 1 MetaLThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 602 ATGGCGACCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCCCTGGCG 661



QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
Db 662 GCCCCGTCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 718

RESULT 14  
LOCUS AR049919 2990 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 1 from patent US 5824790.  
ACCESSION AR049919  
VERSION AR049919.1 GI:5971911  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2990)  
AUTHORS Keeling, P. Lewis., Knight, M. E. and Guan, H.  
TITLE Modification of starch synthesis in plants  
JOURNAL Patent: US 5824790-A 1 20-OCT-1998;  
FEATURES Location/Qualifiers  
source 1..2990  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 7,24e-08 Length: 2990  
Score: 168.00 Matches: 38  
Percent Similarity: 97.4% Conservatives: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 88.0% Indels: 1  
DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x AR049919 (1-2990)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 602 ATGGCGACGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
Db 661 GCCCGCGTCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 717

RESULT 15  
AF168786  
LOCUS Sorghum bicolor (sorghum)  
DEFINITION Sorghum bicolor soluble starch synthase mRNA, complete cds.  
ACCESSION AF168786  
VERSION AF168786.2 GI:12019655  
KEYWORDS  
SOURCE Sorghum bicolor (sorghum)  
ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 2592)  
Hsieh, J.S., Chen, M.R. and Hsing, Y.I.C.  
TITLE Molecular cloning of a Sorghum cDNA encoding the soluble starch  
synthase SBSS  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2592)  
AUTHORS Hsieh, J.S., Chen, M.R. and Hsing, Y.I.C.  
TITLE Direct Submission  
JOURNAL Submitted (14-JUL-1999) Agronomy, National Taiwan University, No.  
1, Sec. 4, Roosevelt Rd., Taipei 10617, Taiwan  
3 (bases 1 to 2592)  
Hsieh, J.S., Chen, M.R. and Hsing, Y.I.C.  
TITLE Direct Submission  
JOURNAL Submitted (03-JAN-2001) Agronomy, National Taiwan University, No.  
1, Sec. 4, Roosevelt Rd., Taipei 10617, Taiwan  
REMARK Sequence update by submitter  
COMMENT On Jan 3, 2001 this sequence version replaced gi:5616514.  
FEATURES Location/Qualifiers  
source 1..2592

## CDS

/organism="Sorghum bicolor"  
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/strain="Kafir 5765-6-1-11-3"  
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/product="soluble starch synthase"  
/protein\_id="AAD45815.2"  
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/translation="MATPSAVGAACLVARAAAGLGPGRGGDRARPRFORVRRR  
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CGSLPVALAARGHRVMVMPRYLNGTSDKNYANAFYTERHIRPCFGEHEVTFPHE  
RDSVDVFDHPSYRPGNLYGDKFAGDNGQRYTLCLCYAACAPLVLGLGYIYQ  
NCMFVNDWHSILVPLLAATKPYGVYKDSRSLIVHNLAHQGVBPASTYDGLGLPP  
EWYGALEWVPEWARHDLKGEAVNFKGAVTADRI VTVSKGYSWEVTTASGGGL  
NELLSRSKSLVINGIDINWNPATDKICPCHYSVDLSSGAKKCSALQKBLGLPI  
RREVELLIGTIGRLDYQGLDLQLIIPHLMRDDVQVMLGSGDFELEDMMRSTSDPK  
DKFRGWGFSVPVSHRITAGCDLILMPSRPEPCGLNQLYAMQYGTVPVVAHAGLRDT  
VENFNPFGENGEGTGWAFAPLTTEMNFVDIANCFDIQGAQIFLGRAHEGHVKRLH  
VGPCR"

## ORIGIN

Alignment Scores:  
Pred. No.: 5,23e-05 Length: 2592  
Score: 139.50 Matches: 31  
Percent Similarity: 75.0% Conservatives: 2  
Best Local Similarity: 70.5% Mismatches: 6  
Query Match: 73.0% Indels: 5  
DB: 15 Gaps: 1

US-10-628-525A-37 (1-39) x AF168786 (1-2592)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*Ala----- 18  
Db 59 ATGGCGACGCCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 118

QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35  
Db 119 CTTGGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 178

QY 36 LeuArgArgArg 39  
Db 179 GTGCGCAGCGCG 190

RESULT 16  
AP006500.07  
WPCOMMENT

Sequence split into 13 fragments LOCUS AP006500 Accession AP006500

Fragment Name	Begin	End
AP006500_00	1	110000
AP006500_01	100001	210000
AP006500_02	200001	310000
AP006500_03	300001	410000
AP006500_04	400001	510000
AP006500_05	500001	610000
AP006500_06	600001	710000
AP006500_07	700001	810000
AP006500_08	800001	910000
AP006500_09	900001	1010000
AP006500_10	1000001	1110000
AP006500_11	1100001	1210000
AP006500_12	1200001	1254097

Continuation (8 of 13) of AP006500 from base 700001 (AP006500 Cyanidioschyzon merolae str.

Alignment Scores:  
Pred. No.: 6.82e+03 Length: 110000  
Score: 74.50 Matches: 19  
Percent Similarity: 56.4% Conservatives: 3  
Best Local Similarity: 48.7% Mismatches: 16  
Query Match: 39.0% Indels: 1  
DB: 14 Gaps: 1

US-10-628-525A-37 (1-39) x AP006500\_07 (1-110000)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 93954 ATGGCAACAAAGTCCCTTGGCGGCTGCTGCTCTTGGGAGATTGTTTCGGA 94013  
Qy 21 AlaAlaValGlyAspArgAlaArg---ProArgArgLeuGlnArgValLeuArgArg 38  
Db 94014 CAACGCAGCAGCATCGCGCGGCGCTCGNAGGCCATCAGTCGCAATTCGACG 94070

RESULT 17

AC013160 53583 bp DNA linear HTG 03-NOV-1999  
LOCUS Drosophila melanogaster, \*\*\* SEQUENCING IN PROGRESS \*\*\*.  
DEFINITION AC013160  
AC013160 HTG; HTGS\_PHASE2.  
VERSION AC013160.1 GI:6223171  
KEYWORDS Drosophila melanogaster (fruit fly)  
SOURCE Drosophila melanogaster  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 53583)  
Adams,M. and Venter,J.C.  
Direct Submission  
TITLE Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,  
Rockville, MD, USA  
COMMENT This sequence was identified as CD1:10213792 by the submitter.  
For further information on this sequence you may e-mail to  
fly@celera.com.

REFERENCE

AUTHORS \* NOTE: This is a 'working draft' sequence.  
TITLE \* This sequence will be replaced.  
JOURNAL \* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
Rockville, MD, USA  
Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,  
Rockville, MD, USA  
This sequence was identified as CD1:10213792 by the submitter.  
For further information on this sequence you may e-mail to  
fly@celera.com.

FEATURES

source  
1..53583  
Location/Qualifiers  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"

ORIGIN

Alignment Scores:  
Pred. No.: 4,01e+03 Length: 53583  
Score: 74.00 Matches: 16  
Percent Similarity: 56.8% Conservative: 5  
Best Local Similarity: 43.2% Mismatches: 16  
Query Match: 38.7% Indels: 0  
DB: 14 Gaps: 0

US-10-628-525A-37 (1-39) x AC013160 (1-53583)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 37623 ATGGGCACCAAGCAGCTTGGGCAAAATAGTATTGACCGCATCGCGGAAGCCATGGCG 37682  
Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37  
Db 37683 GCTGTGGTCAGATAGCGCTAAAGACGAGGATTTTAGTAGAATCTTCGC 37733

RESULT 18

AP008212.269/c

WPCOMMENT

Sequence split into 308 fragments LOCUS AP008212 Accession AP008212

Fragment Name	Begin	End
AP008212_000	1	110000
AP008212_001	100001	210000
AP008212_002	200001	310000
AP008212_003	300001	410000
AP008212_004	400001	510000
AP008212_005	500001	610000
AP008212_006	600001	710000
AP008212_007	700001	810000
AP008212_008	800001	910000

AP008212\_009 900001 1010000  
AP008212\_010 1000001 1110000  
AP008212\_011 1100001 1210000  
AP008212\_012 1200001 1310000  
AP008212\_013 1300001 1410000  
AP008212\_014 1400001 1510000  
AP008212\_015 1500001 1610000  
AP008212\_016 1600001 1710000  
AP008212\_017 1700001 1810000  
AP008212\_018 1800001 1910000  
AP008212\_019 1900001 2010000  
AP008212\_020 2000001 2110000  
AP008212\_021 2100001 2210000  
AP008212\_022 2200001 2310000  
AP008212\_023 2300001 2410000  
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AP008212\_025 2500001 2610000  
AP008212\_026 2600001 2710000  
AP008212\_027 2700001 2810000  
AP008212\_028 2800001 2910000  
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AP008212\_030 3000001 3110000  
AP008212\_031 3100001 3210000  
AP008212\_032 3200001 3310000  
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 AP008212\_196 1960001 19710000

Alignment Scores:

Pred. No.: 1.38e+04 Length: 110000  
 Score: 71.50 Matches: 20  
 Percent Similarity: 60.0% Conservative: 1  
 Best Local Similarity: 57.1% Mismatches: 13  
 Query Match: 37.4% Indels: 1  
 DB: 15 Gaps: 1

US-10-628-525A-37 (1-39) x AP008212\_269 (1-110000)

Qy 5 SerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaAlaValGly 24  
 Db 48647 GCGGCGAGGCGCGCGCGGCTGAGTGGAGCGGCGGCTGCGCAGCG---GGA 48591  
 Qy 25 AspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
 Db 48590 GGCAGAGCTCGCCCGCGCAGGTTGCGTGCAGGTTGAGCGCGCG 48546

RESULT 19

AP004744/c 165270 bp DNA linear PLN 16-SEP-2004  
 LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,  
 DEFINITION BAC clone: OSUNBB0065C04.  
 ACCESSION AP004744  
 VERSION AP004744.2 GI:47169781  
 KEYWORDS  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE AUTHORS TITLE	Ehrhartoideae; Oryzae; Oryza. 1 Sasaki, T., Matsuoto, T. and Yamamoto, K. Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC clone:OSJNBb0065C04
JOURNAL REFERENCE AUTHORS TITLE	Published Only in Database (2002) 2 (bases 1 to 165270) Sasaki, T., Matsuoto, T. and Yamamoto, K. Direct Submission Submitted (13-FEB-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kanonndai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT	On May 13, 2004 this sequence version replaced gi:18656390. Genes were predicted from the integrated results of the following: GENSCAN (http://ccr-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://opal.biology.gatech.edu/GeneMark/), GlimmerM (http://www.tigr.org/tcb/glimmer/glmr form.html), RiceHMM (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4 (http://globin.cse.psu.edu/html/docs/sim4.html), gap2 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to RGP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from M13rev to -21M13 of the BAC clone. This sequence of OSJNBb0065C04 clone has an overlap with OSJNBa0051002 (DDBJ: AP005769) clone at 5' end and with F0473H04 (DDBJ: AP003628) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/genomeSeq.html. Location/Qualifiers 1. 165270 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="genomic DNA" /cultivar="Nipponbare" /db_xref="taxon:39947" /chromosome="6" /clone="OSJNBb0065C04" complement(1420..2703) /gene="OSJNBb0065C04.2" complement(join(1420..1704,2159..2703)) /gene="OSJNBb0065C04.2" /note="supported by full-length cDNA(s): AK099401" /gene="OSJNBb0065C04.2" /note="contains full-length cDNA(s): AK099401" /codon_start=1 /product="unknown protein" /protein_id="BAD45845.1" /db_xref="GI:52075899" /translation="MSASSRSLRAGFLRGGIGILAARCGHYTRRLPLTAEVY EGGSAAGAGHSTEEAGSSSARWEEAIDGAMRMSEPEWAPRPQGSYIAPP RPGAARGLLALVSHAAARMGVPRLASDAEARVDAASRGFPCTTYFDGHFDEVE RSDVTPAEDE"
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Percent Similarity: 60.0%      Conservative: 1
Best Local Similarity: 57.1%      Mismatches: 13
Query Match:      37.4%      Indels:      1
DB:              15        Gaps:         1

US-10-628-525A-37 (1-39) x AP004744 (1-165270)

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Qy      25 AspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39
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RESULT 20
AV310711/c      2182 bp      DNA      linear      INV 15-APR-2004
LOCUS      Saccomorphus sp. JAR-2003 28S ribosomal RNA gene, partial sequence.
DEFINITION      AY310711
ACCESSION      AY310711.1 GI:37223334
VERSION      1
KEYWORDS      Saccomorphus sp. JAR-2003
SOURCE      Saccomorphus sp. JAR-2003
ORGANISM      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Strotylidae; Saccomorphus.
1 (bases 1 to 2182)
Robertson,J.A., McHugh,J.V. and Whiting,M.F.
A molecular phylogenetic analysis of the Pleasing Fungus Beetles
(Coleoptera: Strotylidae): evolution of color patterns,
gregariousness and mycophagy
Syst. Entomol. 29 (2), 173-187 (2004)
2 (bases 1 to 2182)
Robertson,J.A., McHugh,J.V. and Whiting,M.F.
Direct Submission
Submitted (02-JUN-2003) Integrative Biology, Brigham Young
University, 401 WIDB, Provo, UT 84602, USA
Location/Qualifiers
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Alignment Scores:
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DB:              2        Gaps:         1

US-10-628-525A-37 (1-39) x AV310711 (1-2182)

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Qy      22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39
Db      1612 TCGGTA-----AGAAAGACAGACCGCACATGCGCTGACCG 1577

RESULT 21
SPFKBAD      19791 bp      DNA      linear      BCT 18-APR-2005
LOCUS      Streptomyces sp. MA6548 fkbA gene and partial fkbD gene encoding
DEFINITION      FK506 polyketide synthase and cytochrome P-450-9-deoxo-FK506
hydroxylase, respectively.
ACCESSION      Y10438
VERSION      Y10438.1 GI:1781343
KEYWORDS      acyl carrier protein; acyltransferase; beta-ketoacyl-ACP-synthase;
beta-ketoreductase; cytochrome P-450-9-deoxo-FK506 hydroxylase;
dehydratase; enoyl reductase; FK506 polyketide synthase; fkbA gene;
fkbD gene.
SOURCE      Streptomyces sp. MA6548
ORGANISM      Streptomyces sp. MA6548
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
1
REFERENCE      Motamedi,H., Cai,S.J., Shafiee,A. and Elliston,K.O.
AUTHORS      Structural organization of a multifunctional polyketide synthase
TITLE      involved in the biosynthesis of the macrolide immunosuppressant
FK506
JOURNAL      Eur. J. Biochem. 244 (1), 74-80 (1997)
PUBMED      9063448
2 (bases 1 to 19791)
Motamedi,H.
Direct Submission
Submitted (08-JAN-1997) H. Motamedi, Merck Research Labs, P.O.Box
2000, Bldg. RY80X-225, Rayway, NJ 07065, USA
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ADVSALTAKLTDADRGRIRRGFPPLSAADGMRLFDSAARTSRSSRRSPSDVRLDG
VAPLRLGVHARSQSPVAVARNADDEPLAARLAGHTAEOQRVMOEVVLRQAALVA
YGLGEVAAADPRFDLGFDSLITAVDLNRLEAETGLRLPTTVVFSHTAEALATHLE
LDDPAALTGAPLAVTAAPGTAADQDEPIAIVAMACRLPGVTSPEELMRLVESG
TDATITPDGRGMDLDALYDPPDPAVGKAYSLRGFLGEGAAEFDAFDFISPRELGM
DQORLLILETWEAIEERGINPASLHGREIGVYVGAAGQYGLGAEDETNATIGST
SLLSRLAYLLEGEPAVTVDTACSSSILVALHACQRLGELCELALAGGVSLSPAS
AFVFSRORGLAADGRCKSGSGADGTTWAGVGVLVLEQLSDAELGHTVLAVRGS
AVTSDGASGLITAPNGLAQQRVIRKALAAAGLTAADVLVEGHGTCGLRGLDPEADAL
LATYQNGRGEVPLGSLKSNIGHATAAGAVAGVITVQAIGATMPTRLHADPESPAV
DWTAGQVSLLTGNERPWPMTSPGERSPRSGAGTTLTSLNSTVSPWRDRLARNP
CRCLGCPGRLPPLPCRRPPVCAIWRPSGPDLDIGYAQATSRHQFTHRAABEASAP
DGRFAGLDVADGAEPASSABPPRSARRFLPDQGOAQRVGMRLHGRFVFAAAMD
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CHSVGEVTAAYAGVLTILADATTLIVARGRLRALPGAMTAVESGPAEVGAPTDLDI
AAVNGPSAVLTGAPDDVDAAFEREWAAAGRAKRLDVGHFHSRHDGALDDGVLE
SLAFGAARLPVSTTGTGDAAGDLATPEHRLHARRPVLAYADARELADGLGMFVAV
PGSALASANTGSSAGTYHVARLARTGESALTAELHAGAPVLAALVLAGG
RPVLDVPVYFOHRSVWLAPAVGSGSPATVPTGRTPEPDPTLVAEIVRRRAAALLG
IADPGVDADDTFFALGFDLSLAVORLNQLTAACTLDLPTAVLPHDPTPSALTLEB
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domain of module 7"
1609..2413
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/function="approx. span of dehydratase domain of module 7"
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misc\_feature

misc\_feature

misc\_feature

misc\_feature



[illegible]



REFERENCE	Environmental Research, Permoserstrasse 15, Leipzig 04318, Germany
AUTHORS	4 (bases 1 to 25768)
TITLE	Schleinitz, K.M.
JOURNAL	Direct Submissions
REMARK	Submitted (20-JUN-2003) Environmental Microbiology, UFZ Centre for
COMMENT	Environmental Research, Permoserstrasse 15, Leipzig 04318, Germany
	Nucleotide sequence updated by submitter
	On or before Sep 8, 2004 this sequence version replaced
FEATURES	gi:22087562, gi:22087559.
source	Location/Qualifiers
	1. .25768
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	/mol_type="genomic DNA"
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CDS	574. .966
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	/protein_id="AAP88271.1"
	/db_xref="GI:32815754"
	/translation="MDNERVREGWAKLKEVDQAGENVDSLGIAPDPARLLIEPPP
	GDLYTPGDLDTRELATVAALTAMGTAGPQLRVHLHGARNVGCSEQEIYEVLMQAV
	YAGFPALNGLLAKSEVFCQKQSDGFQ"
	complement (2236. .2799)
CDS	/notes="putative"
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	LIVPLLAAVAFIAPPALDAQAVVPSR"
	3018. .3494
CDS	/notes="putative"
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	/protein_id="AAP88273.1"
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	/translation="MQGNPQVVDYFDKLLRGLAARDQVFIHSRIYEDQGFKLVTRL
	DEMOBETHOALLRLRIFLGCMRPKAFTPGTVPDMRLTDLATEYAVRGALQQ
	GMALCESVDYVSRDLLLAQLDTEHDHAYWLEKQIGLIDKVGLENYLSQMGSTA"
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CDS	/notes="putative"
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	/product="LysR type regulator"
	/protein_id="AAP88274.1"
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	VSTVGEQLEPVAWRAFRVHPQVALVELVATGDVQLQALERGEIDAGLMLHSPGAPP
	GLAHLQVLEPLVLAHPAHHAELAEHPAPVAPLPLVPRRTVPSLHDAVFLGYP
	RAGCLPVVPEQAIQMCTIWNLSAGIYAWVPESVMQPRRQGVVTRVPTRRKQQR
	ATPVCELSLWRAQPDGSGVAPALAFVDFVRAQGG"
	4745. .6124
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	/protein_id="AAP88275.1"
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	/translation="METKPIQINRSANITEKSRAPNRSFYAMGYBEGDFKPMVG
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	GODLNAVSVFAVQNAAGNLSDELTOIERRAIPGTSCGCGNTANTHSSAFELGM
	SIFPSTSWPHDENKSNKSVLLIEAKIKDLPRDITVTKKANAVAVIMATGGS
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/protein_id="AAP88280.1"
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## CDS

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Score: 70.50 Matches: 16  
Percent Similarity: 51.5% Conservative: 1  
Best Local Similarity: 48.5% Mismatches: 11  
Query Match: 36.9% Indels: 5  
DB: 1 Gaps: 1

US-10-628-525A-37 (1-39) x AY327575 (1-25768)

QY 4 ProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaAArg\*\*\*Ala 18  
Db 10987 CGCGCCGCTTGGAGAGAGGTGCCGCGGTGCTGATGCTACGTGGCGCGCTGCG 10928  
QY 19 TrpProAlaAlaValGlyAspArgAlaArgProArgArg 31  
Db 10927 TGGCTGCGGTGCGCGGTGATGCGCGCATCCACGACGA 10889

RESULT 25  
AY310707/c  
LOCUS Episcaphula sp. 2-JAR-2003 2115 bp DNA linear INV 15-APR-2004  
DEFINITION Episcaphula sp. 2-JAR-2003 28S ribosomal RNA gene, partial  
sequence.  
ACCESSION AY310707  
VERSION AY310707.1 GI:37223330  
KEYWORDS  
SOURCE Episcaphula sp. 2-JAR-2003  
ORGANISM Episcaphula sp. 2-JAR-2003  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
Erotylidae; Episcaphula.

REFERENCE 1 (bases 1 to 2115)  
AUTHORS Robertson,J.A., McHugh,J.V. and Whiting,M.F.  
TITLE A molecular phylogenetic analysis of the Pleasing Fungus Beetles  
(Coleoptera: Erotylidae): evolution of color patterns,  
gregariousness and mycophagy  
JOURNAL Syst. Entomol. 29 (2), 173-187 (2004)  
REFERENCE 2 (bases 1 to 2115)  
AUTHORS Robertson,J.A., McHugh,J.V. and Whiting,M.F.  
TITLE Direct Submission

JOURNAL Submitted (02-JUN-2003) Integrative Biology, Brigham Young  
University, 401 WIDB, Provo, UT 84602, USA  
FEATURES  
Location/Qualifiers

source  
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/mol\_type="genomic DNA"  
/isolate="Ce86"  
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Pred. No.: 558 Length: 2115

Score: 70.00 Matches: 19  
Percent Similarity: 59.0% Conservative: 4  
Best Local Similarity: 48.7% Mismatches: 10  
Query Match: 36.6% Indels: 6  
DB: 2 Gaps: 2

US-10-628-525A-37 (1-39) x AY310707 (1-2115)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaAArg\*\*\*AlaTrpProAla 21  
Db 1605 GCCAGCCCTTCTGCGCTACCGCCGCGACCTCTACTCGTCAGGCTTCATGGCGGTCC 1546  
QY 22 AlaValGlyAspArgAla-----ArgPro-----ArgArgLeuGlnArg 34  
Db 1545 CGAGAGACAGACCGACATGCGCTGACGGCGGAGTATTAAGCAGCAGCTTCAGCGC 1489

RESULT 26  
AY310691/c  
LOCUS MYCOTRETUS sp. 2-JAR-2003 2146 bp DNA linear INV 15-APR-2004  
DEFINITION MYCOTRETUS sp. 2-JAR-2003 28S ribosomal RNA gene, partial sequence.  
ACCESSION AY310691  
VERSION AY310691.1 GI:37223314  
KEYWORDS  
SOURCE MYCOTRETUS sp. 2-JAR-2003  
ORGANISM MYCOTRETUS sp. 2-JAR-2003  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
Erotylidae; MYCOTRETUS.

REFERENCE 1 (bases 1 to 2146)  
AUTHORS Robertson,J.A., McHugh,J.V. and Whiting,M.F.  
TITLE A molecular phylogenetic analysis of the Pleasing Fungus Beetles  
(Coleoptera: Erotylidae): evolution of color patterns,  
gregariousness and mycophagy  
JOURNAL Syst. Entomol. 29 (2), 173-187 (2004)  
REFERENCE 2 (bases 1 to 2146)  
AUTHORS Robertson,J.A., McHugh,J.V. and Whiting,M.F.  
TITLE Direct Submission

JOURNAL Submitted (02-JUN-2003) Integrative Biology, Brigham Young  
University, 401 WIDB, Provo, UT 84602, USA  
FEATURES  
Location/Qualifiers

source  
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## rRNA

## ORIGIN

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Query Match: 36.6% Indels: 6  
DB: 2 Gaps: 2

US-10-628-525A-37 (1-39) x AY310691 (1-2146)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaAArg\*\*\*AlaTrpProAla 21  
Db 1636 GCCAGCCCTTCTGCGCTACCGCCGCGACCTCTACTCGTCAGGCTTCATGGCGGTCC 1577  
QY 22 AlaValGlyAspArgAla-----ArgPro-----ArgArgLeuGlnArg 34  
Db 1576 CGAAAGACAGACCGCACATGCGCTGACGGCGGAGTATTAAGCAGCAGCTTCAGCGC 1520

## RESULT 27

## AY310683/c

LOCUS LYBAS sp. 1-JAR-2003 2171 bp DNA linear INV 15-APR-2004  
DEFINITION LYBAS sp. 1-JAR-2003 28S ribosomal RNA gene, partial sequence.  
ACCESSION AY310683  
VERSION AY310683.1 GI:37223306

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KEYWORDS
SOURCE
ORGANISM
  Lybas sp. 1-JAR-2003
  Lybas sp. 1-JAR-2003
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
  Erotylidae; Lybas.
REFERENCE
AUTHORS
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
TITLE
  A molecular phylogenetic analysis of the Pleasing Fungus Beetles
  (Coleoptera: Erotylidae): evolution of color patterns,
  gregariousness and mycophagy
JOURNAL
  Syst. Entomol. 29 (2), 173-187 (2004)
REFERENCE
AUTHORS
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
TITLE
  Direct Submission
JOURNAL
  Submitted (02-JUN-2003) Integrative Biology, Brigham Young
  University, 401 WIDB, Provo, UT 84602, USA
FEATURES
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  Query Match: 36.6% Indels: 6
  DB: 2 Gaps: 2
US-10-628-525A-37 (1-39) x AY310693 (1-2171)
QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
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Db 1666 GCCAGCCCTTCGCGCTCACCAGCGGCGACCTCTCTACTGTCAGGGCTTCATGCCGTC 1607
QY 22 AlaValGlyAspArgAla-----ArgPro-----ArgArgLeuGlnArg 34
  |||||
Db 1606 CGAAAGACAGACCGCACATGCCGCTGACGCGCGAGTATAGCAGCAGCTTCAGCGC 1550
RESULT 28
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LOCUS
  Mycotretus sp. 1-JAR-2003 2175 bp DNA linear INV 15-APR-2004
DEFINITION
  Mycotretus sp. 1-JAR-2003 28S ribosomal RNA gene, partial sequence.
ACCESSION
  AY310678
VERSION
  AY310678.1 GI:37223301
KEYWORDS
  Mycotretus sp. 1-JAR-2003
SOURCE
  Mycotretus sp. 1-JAR-2003
ORGANISM
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
  Erotylidae; Mycotretus.
REFERENCE
  1 (bases 1 to 2175)
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
  A molecular phylogenetic analysis of the Pleasing Fungus Beetles
  (Coleoptera: Erotylidae): evolution of color patterns,
  gregariousness and mycophagy
JOURNAL
  Syst. Entomol. 29 (2), 173-187 (2004)
REFERENCE
AUTHORS
  Robertson, J.A., McHugh, J.V. and Whiting, M.F.
TITLE
  Direct Submission
JOURNAL
  Submitted (02-JUN-2003) Integrative Biology, Brigham Young
  University, 401 WIDB, Provo, UT 84602, USA
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  Percent Similarity: 59.0% Conservative: 4
  Best Local Similarity: 48.7% Mismatches: 10
  Query Match: 36.6% Indels: 6
  DB: 2 Gaps: 2
US-10-628-525A-37 (1-39) x AY310678 (1-2175)
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  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1665 GCCAGCCCTTCGCGCTCACCAGCGGCGACCTCTCTACTGTCAGGGCTTCATGCCGTC 1606
QY 22 AlaValGlyAspArgAla-----ArgPro-----ArgArgLeuGlnArg 34
  |||||
Db 1605 CGAAAGACAGACCGCACATGCCGCTGACGCGCGAGTATAGCAGCAGCTTCAGCGC 1549
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RESULT 30  
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LOCUS MYCOTRETUS SCITULUS isolate Cel07 28S ribosomal RNA gene, partial  
DEFINITION sequence.  
ACCESSION AY310679  
VERSION AY310679  
KEYWORDS  
SOURCE MYCOTRETUS SCITULUS  
ORGANISM  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
Erotylidae; Mycotretus.  
REFERENCE 1 (bases 1 to 2175)  
ROBERTSON, J.A., McHugh, J.V. and Whiting, M.F.  
A molecular phylogenetic analysis of the Pleasing Fungus Beetles  
(Coleoptera: Erotylidae): evolution of color patterns,  
gregariousness and mycophagy  
Syst. Entomol. 29 (2), 173-187 (2004)  
REFERENCE 2 (bases 1 to 2175)  
ROBERTSON, J.A., McHugh, J.V. and Whiting, M.F.  
Direct Submission  
Submitted (02-JUN-2003) Integrative Biology, Brigham Young  
University, 401 WIDB, Provo, UT 84602, USA  
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rRNA  
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Pred. No.: 572 Length: 2175  
Score: 70.00 Matches: 19  
Percent Similarity: 59.0% Conservatives: 4  
Best Local Similarity: 48.7% Mismatches: 10  
Query Match: 36.6% Indels: 6  
DB: 2 Gaps: 2  
US-10-628-525A-37 (1-39) x AV310679 (1-2175)  
QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpProAla 21  
Db 1665 GCCAGCCCTTCTGCGCTCACCGCGGACCCCTCTACTCGTCAGGGCTTCATGGCGGTCC 1606  
QY 22 AlaValGlyAspArgAla-----ArgPro-----ArgArgLeuGlnArg 34  
Db 1605 CGAAGACGGACCGCACATGCCGCTGACGGCGGAGTATAGCAGCAGCGCTTCAGCGC 1549

Search completed: April 1, 2006, 15:18:17  
Job time : 818.782 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 00:15:06 ; Search time 91.8204 Seconds  
(without alignments)  
2830.777 Million cell updates/sec

Title: US-10-628-525A-37

Perfect score: 191

Sequence: 1 MATPSAVGACILLARXAWPAVGDRAPRRLQRLRR 39

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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-DB=N Geneseq -QPMT=fastcap -SUPPIX=p2n.rng -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0  
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-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pcio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs06h  
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-WARN TIMOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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13: Geneseqn2004bs:\*  
14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	191	100.0	2383	2	Aat95785

5	191	100.0	2491	3	Aaz50636
6	191	100.0	2991	8	Abx09932
7	190	99.5	2992	2	Aat67285
8	168	88.0	2990	2	Aav66832
9	74	38.7	1531	11	ACL26080
10	71	37.2	1569	13	AD60020
11	69.5	36.4	1013	11	ACN91862
12	68	35.6	249	6	ABQ90655
13	68	35.6	507	6	ABQ91048
14	67.5	35.3	2000	8	ADA71676
15	67	35.1	778	6	ABQ28522
16	67	35.1	778	6	ABQ28523
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19	66.5	34.8	960	11	ADJ11419
20	66.5	34.8	1011	11	ADJ11653
21	66.5	34.8	1012	13	ADT18986
22	66.5	34.8	1284	14	ASB67003
23	66.5	34.8	6297	10	AAD54236
24	66.5	34.8	50543	10	AAD54230
25	66	34.6	1437	10	ADF50282
26	65.5	34.3	365	6	AAD42748
27	65.5	34.3	365	9	ACA05145
28	65.5	34.3	365	14	ABE11213
29	65.5	34.3	365	14	ABE48334
30	65.5	34.3	815	13	ADX33610
31	65	34.0	702	5	ABL57895
32	65	34.0	1035	2	AAT49316
33	65	34.0	1035	2	AAV36430
34	65	34.0	1035	2	AAV39975
35	65	34.0	1035	2	AAV54609
36	65	34.0	1035	2	AAV83991
37	65	34.0	1035	3	AA006674
38	65	34.0	1035	3	AAA14944
39	65	34.0	1035	4	AA012808
40	65	34.0	1035	6	AA411136
41	65	34.0	1035	6	AA029128
42	65	34.0	1035	6	AA027021
43	65	34.0	1035	6	ABL51714
44	65	34.0	1035	13	AD082191
45	65	34.0	19849	14	AD213007
46	64.5	33.8	400	8	ACC58118
47	64.5	33.8	1973	8	ACC58114
48	64.5	33.8	2073	8	ACC58112
49	64.5	33.8	2502	14	ACL68217
50	64.5	33.8	3554	8	ACC58113
51	64.5	33.8	3654	8	ACC58111
52	64.5	33.8	3811	6	AA028061
53	64.5	33.8	24754	14	ACL64767
54	64.5	33.8	76994	12	ADP64454
55	64	33.5	36063	10	ADB74391
56	64	33.5	174155	14	AEA07466
57	63.5	33.2	2530	14	AEA47619
58	63.5	33.2	5710	4	ABL18813
59	63.5	33.2	5922	4	ABL18812
60	63.5	33.2	24379	2	AAT93095
61	63.5	33.2	24379	2	AAV25925
62	63.5	33.2	69300	6	AA038804
63	63	33.0	829	13	ADX36796
64	63	33.0	846	13	ADU58501
65	63	33.0	1338	13	ADT43083
66	63	33.0	2904	3	AA076178
67	63	33.0	8705	5	ABA82624
68	63	33.0	8705	8	ACC45365
69	63	33.0	8705	10	ADU98065
70	63	33.0	8705	10	ADU82434
71	63	33.0	8705	13	ADR16928
72	63	33.0	8705	13	ADR47579
73	63	33.0	8705	14	ABR69308
74	63	33.0	36305	6	ABR32783
75	63	33.0	156843	11	ACN44786
76	62.5	32.7	909	11	ABD04642
77	62.5	32.7	1197	14	ACL70309

Aaz50636	Corn solu
Abx09932	DNA encod
Aat67285	Soluble s
Aav66832	Zea maye
ACL26080	Rice abio
AD60020	Bacterial
ACN91862	Breast ca
ABQ90655	M. capaul
ABQ91048	M. capaul
ADA71676	Rice gene
ABQ28522	Oligonuc
ABQ28523	Oligonuc
AD082611	Plant ful
ADJ11765	Rice cDNA
ADJ11419	Rice DNA
ADJ11653	Rice DNA
ADT18986	Plant cDN
ASB67003	Rice geno
AAD54236	Streptomy
AAD54230	Streptomy
ADF50282	Human PFM
AAD42748	Corn GGGP
ACA05145	Corn gera
ABE11213	Maize GGP
ABE48334	Corn GGGP
ADX33610	Plant ful
ABL57895	Partial h
AAT49316	Hypereens
AAV36430	Hypereens
AAV39975	Pseudomon
AAV54609	Pseudomon
AAV83991	DNA encod
AA006674	Pseudomon
AAA14944	DNA encod
AA012808	Pseudomon
AA411136	Hypereens
AA029128	Pseudomon
AA027021	P. solana
ABL51714	P. solana
AD082191	Ralstonia
AD213007	Human can
ACC58118	Human typ
ACC58114	Human typ
ACC58112	Human typ
ACL68217	M. xanthu
ACC58113	Human typ
ACC58111	Human typ
AA028061	Human ade
ACL64767	M. xanthu
ADP64454	Sorangium
ADB74391	Mycobacte
AEA07466	M. ulcera
AEA47619	Nucleotid
ABL18813	Drosophil
ABL18812	Drosophil
AAT93095	Streptomy
AAV25925	Streptomy
AA038804	BAC clone
ADX36796	Plant ful
ADU58501	Bacterial
ADT43083	Bacterial
AA076178	Human ORF
ABA82624	Human HBM
ACC45365	Human HBM
ADU98065	HBM-relat
ADU82434	Human DNA
ADR16928	BAC clone
ADR47579	BAC clone
ABR69308	Human HBM
ABR32783	Human HBM
ACN44786	Human gen
ABD04642	Pseudomon
ACL70309	M. xanthu

c	78	62.5	32.7	1995	11	ABD04718	Abd04718 Pseudomon
	79	62.5	32.7	4607	6	ABK46540	Abk46540 DNA encod
	80	62.5	32.7	4801	10	ADD78275	Add78275 Human CGD
	81	62.5	32.7	4884	9	AAD57243	Aad57243 Human CGD
	82	62.5	32.7	4933	8	ACD13338	Acd13338 Human DNA
	83	62.5	32.7	5079	9	AAD57244	Aad57244 Human CGD
	84	62.5	32.7	5139	10	ABV72514	Abv72514 Nucleotid
	85	62.5	32.7	5153	12	ADO34015	Ado34015 Human WBC
	86	62.5	32.7	9501	4	AAS59550	Aas59550 Propionib
	87	62.5	32.7	9501	8	ACF64479	Acf64479 Propionib
	88	62.5	32.7	15271	14	ACL64588	Act64588 M. xanthu
	89	62	32.5	894	11	ABD13132	Abd13132 Pseudomon
	90	62	32.5	894	11	ABD13132	Abd13132 Pseudomon
	91	62	32.5	1035	13	ADT42241	Adt42241 Bacterial
	92	62	32.5	1035	13	ADT42241	Adt42241 Bacterial
	93	62	32.5	1035	13	ADT42241	Adt42241 Bacterial
	94	62	32.5	1482	13	ADT18764	Act18764 Plant CDN
	95	62	32.5	1560	10	ADC08230	Adc08230 Rice DNA
	96	62	32.5	1560	10	ADC07849	Adc07849 Rice DNA
	97	62	32.5	2000	8	ADA71962	Aad71962 Rice gene
	98	62	32.5	3112	4	AAS06753	Aas06753 Polynucle
	99	62	32.5	3112	4	AAS06753	Aas06753 Polynucle
	100	62	32.5	3261	12	ADH41718	Adh41718 Novel hum
	101	62	32.5	3694	2	AAQ36930	Aaq36930 Human KA-
	102	62	32.5	4800	14	ACL64099	Act64099 M. xanthu
	103	62	32.5	16671	8	ABQ76670	Abq76670 Androgen
	104	62	32.5	54000	8	AAD52261	Aad52261 Human int
	105	62	32.5	79467	9	ADAO2717	Ada2717 Mouse Nfa
	106	62	32.5	79467	10	ADB72455	Adb72455 Mouse Nfa
	107	62	32.5	79467	10	ADB72455	Adb72455 Mouse Nfa
	108	61.5	32.2	1164	8	ACA37786	Aca37786 Prokaryot
	109	61.5	32.2	1224	13	ADX47573	Adx47573 Plant ful
	110	61.5	32.2	1255	8	ABS58052	Ab58052 Gene enco
	111	61.5	32.2	1255	8	ABS58052	Ab58052 Gene enco
	112	61.5	32.2	1348	14	ACC00853	Acc00853 Oryza sat
	113	61.5	32.2	1356	11	ACL26756	Act26756 Rice gene
	114	61.5	32.2	1356	11	ACL26756	Act26756 Rice gene
	115	61.5	32.2	2397	12	ADM99263	Adm99263 Environme
	116	61.5	32.2	2742	8	AAU61191	Aal61191 Actinosyn
	117	61.5	32.2	75839	11	ACN43958	Acn43958 Human gen
	118	61.5	32.2	82746	8	AAU61224	Aal61224 Actinosyn
	119	61	31.9	453	9	ACH35388	Ach35388 Human end
	120	61	31.9	472	9	ACH33745	Ach33745 Human end
	121	61	31.9	573	11	ABD05682	Abd05682 Pseudomon
	122	61	31.9	609	12	ADJ43098	Adj43098 Plant CDN
	123	61	31.9	1173	4	ABU29397	Abu29397 Drosophil
	124	61	31.9	1375	13	ADX48635	Adx48635 Plant ful
	125	61	31.9	1785	4	AAI20590	Aai20590 Probe #10
	126	61	31.9	1785	4	ABA65633	Ab65633 Human foe
	127	61	31.9	1785	4	AAI45799	Aai45799 Probe #14
	128	61	31.9	1785	4	ABA47739	Ab47739 Human bre
	129	61	31.9	1785	4	ABA32720	Ab32720 Probe #11
	130	61	31.9	1785	4	AAK39782	Aak39782 Human bon
	131	61	31.9	1785	4	AAK14036	Aak14036 Human bon
	132	61	31.9	1785	4	ABS39370	Ab39370 Human liv
	133	61	31.9	1785	5	AAI06289	Aai06289 Probe #62
	134	61	31.9	1785	6	ABS13877	Ab13877 Human gen
	135	61	31.9	1967	13	ADT19819	Adt19819 Plant CDN
	136	61	31.9	2133	8	ACA37962	Act37962 Prokaryot
	137	61	31.9	2428	6	ABK34868	Abk34868 Human CDN
	138	61	31.9	2673	6	ABV72118	Abv72118 Nucleotid
	139	61	31.9	3356	4	ABL29396	Ab129396 Drosophil
	140	61	31.9	3628	3	AAZ88923	Aaz88923 Human wml
	141	61	31.9	3640	10	ADF68183	Adf68183 Human WPS
	142	61	31.9	3640	13	ADR25366	Adr25366 Breast ca
	143	61	31.9	3640	14	ADZ67421	Adz67421 Different
	144	61	31.9	3673	3	AAA08994	Aaa08994 Human WPS
	145	61	31.9	3686	3	AAA08993	Aaa08993 Human WPS
	146	61	31.9	3688	3	AAA09002	Aaa09002 Human WPS
	147	61	31.9	3688	3	AAA08998	Aaa08998 Human WPS
	148	61	31.9	3688	3	AAA09004	Aaa09004 Human WPS
	149	61	31.9	3688	3	AAA08997	Aaa08997 Human WPS
	150	61	31.9	3688	3	AAA09003	Aaa09003 Human WPS

ALIGNMENTS

RESULT 1

AAV70963

ID AAV70963 standard; DNA; 153 BP.

XX

AC AAV70963;

XX

DT 23-AUG-1999 (first entry)

XX

DE DNA encoding transit peptide of maize starch soluble synthase I.

XX

KW Non-glycogen-like polysaccharide production; fermentation;

KW starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;

KW non-starch branching gene; amylopectin; amylose; plant-like starch;

KW maize starch soluble synthase I; transit peptide; ss.

XX

OS Zea mays.

XX

XX WO9844780-A1.

PN 15-OCT-1998.

PD

XX

PF 03-APR-1998; 98WO-US006660.

XX

PR 04-APR-1997; 97US-0042939P.

XX

(EXSE-) EXSEED GENETICS LLC.

PI Guan H, Keeling PL;

XX

DR WPI; 1998-568285/48.

DR P-PSDB; AAW70897.

XX

PT Producing non-glycogen-like polysaccharides in bacteria, fungi or plants

PT - transformed with genes for enzymes involved in starch or glycogen

PT synthesis allows fermentative production of starches with engineered

PT properties.

XX

XX Disclosure; Fig 55; 150pp; English.

CC The specification describes a method for the production of non-glycogen-

CC like polysaccharides in a host. The method comprises transforming a host,

CC suitable for fermentation, with genes encoding starch- or glycogen-

CC synthesis enzymes, and fermenting the transformants. The specification

CC also describes hosts transformed with a gene active in glycogen synthesis

CC and at least one non-starch branching gene, involved in production of

CC amylopectin or amylose in its original host. The method is used to

CC produce plant-like starches by fermentation and new starches in plants.

CC These starches are useful for all food and non-food applications of

CC starch. The present sequence is used in the course of the invention

XX

SQ Sequence 153 BP; 10 A; 62 C; 64 G; 17 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,93e-15 Length: 153

Score: 191.00 Matches: 38

Percent Similarity: 97.4% Conservative: 0

Best Local Similarity: 97.4% Mismatches: 1

Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0

US-10-628-525A-37 (1-39) x AAV70963 (1-153)

QY 1 MetalArProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20

DB 1 ATGGCGACGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGGCGCCCTGGCGG 60

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39

DB 61 GCGCGCGTGGCGACCGCGCGCGCGCGCGCGCGTCCAGCGCGTGTGCGCGCGCGG 117

## RESULT 2

AAZ50642  
ID AAZ50642 standard; cDNA; 1415 BP.  
XX  
AC AAZ50642;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Corn soluble starch synthase gene fragment inserted in pSS64-C5.  
XX  
KW Soluble starch synthase; starch fine structure; corn; transgenic plant;  
KW amylose; amylopectin; amylose polymerisation;  
KW non-granule bound starch synthase; non-GBSSI; altered starch; food;  
KW paper; plastic; adhesive; ss.  
XX  
OS Zea mays.  
XX  
PN WO200006755-A2.  
XX  
PD 10-FEB-2000.  
XX  
PF 26-JUL-1999; 99WO-US016296.  
XX  
PR 28-JUL-1998; 98US-0094436P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Broglie KE, Lightner JE;  
XX  
DR WPI; 2000-195311/17.  
XX  
PT Producing transgenic cereal crops with altered starch structure useful  
PT for preparing foodstuff, paper, plastic or adhesives, comprises  
PT transforming crops with chimeric sense or antisense gene construct  
PT encoding starch synthase.  
XX  
PS Claim 5; Page 52-53; 56pp; English.  
XX  
CC The present sequence is the corn soluble starch synthase (SSI) DNA  
CC sequence comprising the SSI coding region of amino acids 1-494 inserted  
CC into plasmid pSS64-C5. The chimeric gene containing the zein promoter  
CC followed by the SSI gene fragment is used as a sense construct for  
CC preparation of transgenic corn expressing altered starch structure. The  
CC starch fine structure derived from a grain of the cereal crop can be  
CC altered in the transformed cereal crop by changes in amylose to  
CC amylopectin ratio, amylopectin fine structure, increased abundance of  
CC very short amylopectin chains and in the degree of polymerisation of  
CC amylose. These modifications can be created by controlling the expression  
CC of non-GBSSI (non-granule bound starch synthase) in transgenic plants.  
CC Altered starches are useful in foods, paper, plastics or adhesives  
XX  
SQ Sequence 1415 BP; 317 A; 335 C; 397 G; 366 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 4.92e-14 Length: 1415  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0

US-10-628-525A-37 (1-39) x AAZ50642 (1-1415)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaAarg\*\*\*AlaTtpPro 20  
DB 2 ATGGCGACGCCCTCGGCGGCGCGCGCTCTCTCTCGGCGGCGCGCTCGGCGG 61  
QY 21 AlaAlaValGlyAspArgAlaAargProAargArgLeuGlnArgValLeuAargArg 39  
DB 62 GCGCGCGTGGCGACCGCGCGCGCGCTCCAGCGCGTGTGTGGCGCGCGG 118

## RESULT 3

AAT95785

## AAZ50643

XX AAZ50643 standard; cDNA; 2008 BP.  
XX  
AC AAZ50643;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Corn soluble starch synthase gene fragment inserted in pSS65-C11.  
XX  
KW Soluble starch synthase; starch fine structure; corn; transgenic plant;  
KW amylose; amylopectin; amylose polymerisation;  
KW non-granule bound starch synthase; non-GBSSI; altered starch; food;  
KW paper; plastic; adhesive; ss.  
XX  
OS Zea mays.  
XX  
PN WO200006755-A2.  
XX  
PD 10-FEB-2000.  
XX  
PF 26-JUL-1999; 99WO-US016296.  
XX  
PR 28-JUL-1998; 98US-0094436P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Broglie KE, Lightner JE;  
XX  
DR WPI; 2000-195311/17.  
XX  
PT Producing transgenic cereal crops with altered starch structure useful  
PT for preparing foodstuff, paper, plastic or adhesives, comprises  
PT transforming crops with chimeric sense or antisense gene construct  
PT encoding starch synthase.  
XX  
PS Claim 5; Page 53; 56pp; English.  
XX  
CC The present sequence is the corn soluble starch synthase (SSI) DNA  
CC sequence comprising the entire SSI coding region and a 3' UTR fragment  
CC inserted into plasmid pSS65-C11. The chimeric gene containing the zein  
CC promoter followed by the 3'UTR is used as a sense construct for  
CC preparation of transgenic corn expressing altered starch structure. The  
CC starch fine structure derived from a grain of the cereal crop can be  
CC altered in the transformed cereal crop by changes in amylose to  
CC amylopectin ratio, amylopectin fine structure, increased abundance of  
CC very short amylopectin chains and in the degree of polymerisation of  
CC amylose. These modifications can be created by controlling the expression  
CC of non-GBSSI (non-granule bound starch synthase) in transgenic plants.  
CC Altered starches are useful in foods, paper, plastics or adhesives  
XX  
SQ Sequence 2008 BP; 486 A; 463 C; 543 G; 516 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 7.32e-14 Length: 2008  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0

US-10-628-525A-37 (1-39) x AAZ50643 (1-2008)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaAarg\*\*\*AlaTtpPro 20  
DB 2 ATGGCGACGCCCTCGGCGGCGCGCGCTCTCTCTCGGCGGCGCGCTCGGCGG 61  
QY 21 AlaAlaValGlyAspArgAlaAargProAargArgLeuGlnArgValLeuAargArg 39  
DB 62 GCGCGCGTGGCGACCGCGCGCGCGCTCCAGCGCGTGTGTGGCGCGCGG 118

## RESULT 4

AAT95785

ID AAT95785 standard; cDNA to mRNA; 2383 BP.







```
XX US824790-A.
PN
PD
XX
XX
PD
XX
PF 15-DEC-1995; 95US-00572951.
XX
XX 21-JUN-1994; 94US-00263921.
PR
PR 29-NOV-1994; 94US-00346602.
XX
XX (ZENE ) ZENECA LTD.
PA
XX Guan H, Keeling PL, Knight ME;
PI
XX
XX WPI; 1998-582626/49.
DR
XX
XX Isolated nucleic acid molecule, used to produce transgenic plants -
PT comprises nucleotide sequence encoding polypeptide having soluble starch
PT synthase activity, where polypeptide is encoded by maize gene.
XX
XX Claim 1; Col 25-28; 29pp; English.
XX
XX The present sequence represents an isolated nucleic acid molecule which
CC has been isolated and comprises a nucleotide sequence encoding a
CC polypeptide having soluble starch synthase (SSS) activity, where the
CC polypeptide is encoded by a maize gene. The isolated nucleic acid
CC molecule can be used to produce transgenic plants with altered starch
CC production. The transgenic plants produced using the nucleic acid
CC molecule have an enhanced ability to produce structurally-altered starch
XX
SQ Sequence 2990 BP; 758 A; 655 C; 801 G; 776 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8e-11 Length: 2990
Score: 188.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 88.0% Indels: 1
DB: 2 Gaps: 0

US-10-628-525A-37 (1-39) x AAV66932 (1-2990)
QY 1 MetaLThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
Db 602 ATGGCAGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGGCGC-CCCTGGCGG 660
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 661 GCCGCGGTGCGCGACCGCGCGCGCGCGCGCGAGGCTCCAGCGGTGTGTGCGCGCGG 717

RESULT 9
ACL26080
ID ACL26080 standard; cDNA; 1531 BP.
XX
AC ACL26080;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:36.
XX
KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;
KW agriculture.
XX
OS Oryza sativa.
XX
XX WO2003008540-A2.
PN
XX 30-JAN-2003.
PD
XX
XX 21-JUN-2002; 2002WO-US019668.
PF
XX
XX 22-JUN-2001; 2001US-0300112P.
PR
PR 24-AUG-2001; 2001US-0314662P.
```

```
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX
XX WPI; 2003-248011/24.
DR
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 36; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 1531 BP; 181 A; 523 C; 543 G; 279 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.: 15.4 Length: 1531
Score: 74.00 Matches: 15
Percent Similarity: 65.5% Conservative: 4
Best Local Similarity: 51.7% Mismatches: 10
Query Match: 38.7% Indels: 0
DB: 11 Gaps: 0

US-10-628-525A-37 (1-39) x ACL26080 (1-1531)
QY 3 ThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAlaAla 22
Db 386 ACCGCGACGCGGTGAACGTGCGCATGTCTATCGTGGCGCATGCTCTGGGGTTCGGCG 445
QY 23 ValGlyAspArgAlaArgProArgArg 31
Db 446 TCGGGTTCCAGCAACCGCGCGCGCGC 472

RESULT 10
ADS60020/c
ID ADS60020 standard; cDNA; 1569 BP.
XX
AC ADS60020;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #12007.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
XX US2003233675-A1.
PN
XX
```

PD 18-DEC-2003.  
 XX  
 PF 20-FEB-2003; 2003US-00369493.  
 XX  
 PR 21-FEB-2002; 2002US-0360039P.  
 XX  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLATY/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX WPI; 2004-061375/06.  
 DR  
 XX  
 XX New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX  
 XX Claim 1; SEQ ID NO 35694; 122pp; English.  
 PS  
 XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition. Improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polynucleotide used in  
 CC the scope of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 1569 BP; 290 A; 525 C; 474 G; 280 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 37.3 Length: 1569  
 Score: 71.00 Matches: 16  
 Percent Similarity: 56.8% Conservative: 5  
 Best Local Similarity: 43.2% Mismatches: 14  
 Query Match: 37.2% Indels: 2  
 DB: 13 Gaps: 1  
 US-10-628-525A-37 (1-39) x ADS60020 (1-1569)  
 QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*AlaThrProAla 21  
 Db 134 AGCAGCCCTTCGGCGCCAGCGCTCGGCATTCGGCGTCTTCACCGGGATGCGCGCA 75  
 QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38  
 Db 74 GCC-----GACAGGCNAATCACCGCCGCACTGGTCGAGGTGATCAGGAGA 30  
 RESULT 11  
 ACN91862/c  
 ID ACN91862 standard; DNA; 1013 BP.  
 XX  
 AC ACN91862;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Breast cancer related marker, seq id 13012.  
 XX  
 KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003099974-A1.  
 XX  
 PD 29-MAY-2003.  
 XX  
 PF 18-JUL-2002; 2002US-00198846.  
 XX  
 PR 18-JUL-2001; 2001US-0306220P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Lillie J, Xu Y, Wang Y, Steinmann K;  
 XX WPI; 2003-787014/74.  
 DR  
 XX Novel isolated polypeptide associated with breast cancer, useful for  
 PT detecting presence of polypeptide in sample, as a marker for breast  
 PT cancer.  
 XX  
 PS Disclosure; SEQ ID NO 13012; 36pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide (I) associated with a  
 CC breast cancer which is encoded by a nucleic acid molecule comprising a  
 CC nucleotide sequence (S1). Further disclosed is an antibody that binds to  
 CC the polypeptide of the invention. The activity of the polypeptide of the  
 CC invention may be described as cytostatic. The antibody is useful for  
 CC detecting the presence of (I) in a sample. Nucleic acid molecules of the  
 CC invention are useful in the detection of breast tumours. (I) is useful as  
 CC a marker for breast cancer and in breast cancer therapy. Sequences given  
 CC in records ACN78851-ACN99934 represent nucleic acid markers associated  
 CC with breast cancer. Note: The sequence listing does not form part of the  
 CC specification but may be obtained in electronic format from the USPTO web  
 CC site at seqdata.uspto.gov/sequence.html?DocID=20030099974  
 XX  
 SQ Sequence 1013 BP; 278 A; 285 C; 213 G; 208 T; 0 U; 29 Other;  
 Alignment Scores:  
 Pred. No.: 34.8 Length: 1013  
 Score: 69.50 Matches: 19  
 Percent Similarity: 58.5% Conservative: 5  
 Best Local Similarity: 46.3% Mismatches: 14  
 Query Match: 36.4% Indels: 3  
 DB: 11 Gaps: 1  
 US-10-628-525A-37 (1-39) x ACN91862 (1-1013)  
 QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg----- 17  
 Db 943 GTGGCGCGCGCGCGCGTGTGGGGGGGGCGCGCTTTTGGGGGGCGCGGCTTGGTGGCGG 884  
 QY 18 AlaThrProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37  
 Db 883 TCTTGCCCGGGGCGCTGTGCTCTGCGCGCGCGCCCGAGGGTGTGTAGGTTTGGGGTGGCGG 824  
 QY 38 Arg 38  
 Db 823 CGC 821  
 RESULT 12  
 ABQ90655  
 ID ABQ90655 standard; DNA; 249 BP.  
 XX  
 AC ABQ90655;  
 XX  
 DT 01-OCT-2002 (first entry)  
 XX





PD 07-MAR-2002.  
XX  
PF 01-SEP-2001; 2001WO-EP010074.  
XX  
XX 01-SEP-2000; 2000DE-01043826.  
PR 05-SEP-2000; 2000DE-01044543.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX WPI; 2002-371829/40.  
DR  
XX  
XX Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
PS Claim 12; 56pp + Sequence Listing; 56pp; German.  
XX  
CC This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridised to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridisation to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridised to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABQ13410-  
CC ABQ54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX  
SQ Sequence 778 BP; 210 A; 366 C; 114 G; 88 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 52.5 Length: 778  
Score: 67.00 Matches: 19  
Percent Similarity: 55.3% Conservative: 2  
Best Local Similarity: 50.0% Mismatches: 17  
Query Match: 35.1% Indels: 0  
DB: 6 Gaps: 0  
  
US-10-628-525A-37 (1-39) x ABQ28523 (1-778)  
  
QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpProLa 21  
DB 469 GCGACACCGCGCGCGCTACAAACACTCGCGCGCTACCGCGCGCGCGCA 528  
  
QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39  
DB 529 CGCGCAGCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 582  
  
RESULT 17  
AD082611  
ID AD082611 standard; cDNA; 1971 BP.  
XX  
AC AD082611;  
XX  
XX 21-APR-2005 (first entry)  
XX  
XX Plant full length insert polynucleotide seqid 1331.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW Galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
XX protein content; gene; ss.  
OS Unidentified.  
XX  
XX US2004034888-A1.  
PN  
XX 19-FEB-2004.  
PD  
XX  
XX 28-APR-2003; 2003US-00425114.  
PF  
XX  
XX 06-MAY-1999; 99US-00304517.  
PR  
XX 05-NOV-2001; 2001US-00985678.  
XX  
XX (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX WPI; 2004-180133/17.  
XX  
XX New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 1331; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 1971 BP; 370 A; 683 C; 591 G; 327 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 151 Length: 1971  
Score: 67.00 Matches: 22  
Percent Similarity: 51.1% Conservative: 1  
Best Local Similarity: 48.9% Mismatches: 10  
Query Match: 35.1% Indels: 12  
DB: 13 Gaps: 2  
  
US-10-628-525A-37 (1-39) x AD082611 (1-1971)  
  
QY 6 AlaValGlyAlaAlaCysLeu-----LeuLeuLa 15  
DB 517 GCTGCGAGCGGTGTGTGCTCTTACCAGCTCTCCCTCGCGCGCTCGAGCTCTGTGCC 576  
  
QY 16 Arg\*\*\*AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgLeuGln 33  
DB 577 CGCGCGGTCCACCCACCGCTGTTCGGGCGAGAGGTGAGTCTGCGCGCGCGCGCGCG 636







XX Kovalic DK;  
 XX WPI; 2004-757369/74.  
 XX New recombinant DNA constructs useful in the field of biochemistry and  
 XX genetics, and in particular for producing transgenic plants with improved  
 XX biological characteristics.  
 XX Claim 1; SEQ ID NO 4312; 14pp; English.  
 XX The invention relates a recombinant DNA construct comprising a  
 XX polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:  
 XX 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences  
 XX (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,  
 XX Arabidopsis, wheat and rape but the specification does not indicate which  
 XX species is derived from which organism. Also included is a method of  
 XX producing a plant having an improved property, comprising transforming a  
 XX plant with a recombinant DNA construct comprising a promoter region  
 XX functional in a plant cell operably joined to a polynucleotide encoding a  
 XX polypeptide associated with the property, and growing the transformed  
 XX plant. The property is selected from improving plant cold tolerance, for  
 XX manipulating growth rate in plant cells by modification of the cell cycle  
 XX pathway, for improving plant drought tolerance, for providing increased  
 XX resistance to plant disease, for galactomannan production, for production  
 XX of plant growth regulators, for improving plant heat tolerance, for  
 XX improving plant tolerance to herbicides, for increasing the rate of  
 XX homologous recombination in plants, for lignin production, for improving  
 XX plant tolerance to extreme osmotic conditions, for improving plant  
 XX tolerance to pathogens or pests, for yield improvement by modification of  
 XX photosynthesis, for modifying seed oil yield and/or content, for  
 XX modifying seed protein yield and/or content, for yield improvement by  
 XX modification of carbohydrate, nitrogen or phosphorus use and/or uptake  
 XX and for yield improvement by providing improved plant growth and  
 XX development under at least one stress condition. The polynucleotide may  
 XX also encode a plant transcription factor. The methods and compositions of  
 XX the present invention are useful in the field of biochemistry and  
 XX genetics, in particular for producing transgenic plants with improved  
 XX biological characteristics such as increased yield, improved nitrogen  
 XX flow, increasing plant tolerance to cold or heat, improving plant  
 XX tolerance to extreme osmotic and drought conditions, and improving plant  
 XX tolerance to plant pests or pathogens. They can also be used in physical  
 XX arrays of molecules, plant breeding markers, computer-based storage and  
 XX analysis systems. The present sequence is one of the 5544 plant cDNA  
 XX sequences of the invention. Note: The sequence data for this patent did  
 XX not form part of the printed specification, but was obtained in  
 XX electronic format directly from USPTO at  
 XX seqdata.uspto.gov/sequence.html?DocID=20040216190.  
 XX  
 XX Sequence 1012 BP; 143 A; 340 C; 330 G; 199 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 81.5 Length: 1012  
 Score: 66.50 Matches: 19  
 Percent Similarity: 52.6% Conservatives: 1  
 Best Local Similarity: 50.0% Mismatches: 17  
 Query Match: 34.8% Indels: 1  
 DB: 13 Gaps: 1  
 US-10-628-525A-37 (1-39) x ADT18986 (1-1012)  
 QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpProAla 21  
 DB 557 GCCGCGCCCTCGAGCGCTCTCTGGGGCTGCGCGCGCGCGCTCGACTCGAATCCAC 498  
 QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
 DB 497 GCAGCAGGCGCCG 447  
 RESULT 22  
 ID AEB67003/C  
 XX AEB67003 standard; DNA; 1284 BP.

AC AEB67003;  
 XX 22-SEP-2005 (first entry)  
 XX Rice genome derived DNA sequence, SEQ ID 2148.  
 DE transcription; gene regulation; transgenic plant; RNA interference;  
 XX transformation; antibody; ds.  
 XX Oryza sp.  
 XX JP2005185101-A.  
 XX 14-JUL-2005.  
 XX 11-DEC-2002; 2002JP-00383870.  
 XX 30-MAY-2002; 2002JP-00203269.  
 XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
 XX (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.  
 XX (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.  
 XX (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.  
 XX Kikuchi H, Hayashizaki Y, Otomo Y, Matsubara K, Murakami K;  
 XX Kishimoto N, Sato K, Nagata T, Kawakami N, Yazaki J, Ishikawa M;  
 XX Doi K, Kawai J;  
 XX WPI; 2005-566181/58.  
 XX Novel DNA encoding transcription factor, derived from rice plant, useful  
 XX for obtaining transcriptional-regulatory regions in plant and for  
 XX producing modified plant.  
 XX Claim 1; SEQ ID NO 2148; 2928pp; Japanese.  
 XX The invention relates to a novel DNA sequence encoding a transcription  
 XX factor derived from a plant. The invention further comprises antisense  
 XX RNA sequences, ribozyme activity RNA, RNAi sequences, a vector,  
 XX transformed plant cells, antibodies and proteins, all related to the  
 XX novel plant DNA sequences of the invention. The novel DNA is preferably  
 XX derived from a rice-genome database. The invention further provides a  
 XX method for determining the transcription regulatory regions of the rice  
 XX genome. The novel DNA is useful for controlling the expression of a gene  
 XX in a plant and for producing a modified plant with desired and different  
 XX characteristics. The plant DNA and method enables the acquisition of many  
 XX transcriptional-regulatory regions. This polynucleotide represents a DNA  
 XX sequence taken from a rice genome clone library for use in the invention.  
 XX Note: This sequence is not shown in the specification. It has been  
 XX retrieved from a sequence listing in electronic format from the Japanese  
 XX Patent Office. The invention claims DNA sequences of SEQ ID Nos 1 to  
 XX 28469 and encoded protein sequences of SEQ ID Nos 28470 to 56791.  
 XX However, the sequence listing only provided the DNA sequences of SEQ ID  
 XX Nos 1 to 3032.  
 XX  
 XX Sequence 1284 BP; 240 A; 375 C; 435 G; 234 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 107 Length: 1284  
 Score: 66.50 Matches: 17  
 Percent Similarity: 50.0% Conservatives: 1  
 Best Local Similarity: 47.2% Mismatches: 13  
 Query Match: 34.8% Indels: 5  
 DB: 14 Gaps: 1  
 US-10-628-525A-37 (1-39) x AEB67003 (1-1284)  
 QY 3 ThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpProAla 22  
 DB 231 ACCCGCAGCAGCTCTCCGGCTGCTGC-----GCCACTTGGCCAGCGCG 187  
 QY 23 ValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38

Db 186 ACACCATCGCGCTGCTCCAGCCGAGGCCACCGAGCCTGAGAGG 139

RESULT 23  
AAD54236  
ID AAD54236 standard; DNA; 6297 BP.  
XX  
XX AAD54236;  
AC  
XX  
DT 17-JUN-2003 (first entry)  
XX  
DE Streptomyces amphibiae sp. nov. lactimidomycin ORF6 DNA.  
XX  
KW Polyketide biosynthesis; dorrigocin; DORR; lactimidomycin; LACT; gene;  
ds.  
XX  
OS Streptomyces amphibiae sp. nov.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 1. .6297  
FT /tag= a  
FT /product= "LACT ORF6 protein"  
XX  
PN WO200288176-A2.  
XX  
XX  
PD 07-NOV-2002.  
XX  
PF 26-APR-2002; 2002WO-CA000591.  
XX  
PR 26-APR-2001; 2001US-0286346P.  
XX  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
XX  
PI Farnet CM, Zazopoulos E, Staffa A, Yang X;  
XX  
XX WPI; 2003-201222/19.  
DR P-PSDB; AAE35500.  
XX  
XX Novel isolated or purified polypeptide involved in biosynthesis of  
PT polyketide dorrigocin or polyketide lactimidomycin, useful for preparing  
PT dorrigocin or lactimidomycin.  
XX  
PS Claim 6; Page 301-304; 312pp; English.  
XX  
CC The invention relates to novel proteins involved in the biosynthesis of  
CC polyketide dorrigocin (DORR) or lactimidomycin (LACT) biosynthesis by  
CC microorganisms. Sequences of the invention allow direct manipulation of  
CC dorrigocin, lactimidomycin and related chemical structures via chemical  
CC engineering of the enzymes involved in the biosynthesis of dorrigocin and  
CC lactimidomycin. They are useful for introducing chemical handles into  
CC normally inert positions that permit subsequent chemical modifications  
CC and facilitate the development of polyketides. The genes and proteins of  
CC the invention can also be used to generate a focused library of analogues  
CC around a polyketide lead candidate to fine-tune the compound for optimal  
CC properties. They are useful for generating antibodies specific for the  
CC polyketide biosynthesis. The present sequence is S. amphibiae sp. nov.  
CC lactimidomycin ORF6 DNA  
XX  
SQ Sequence 6297 BP; 854 A; 2246 C; 2293 G; 904 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 650 Length: 6297  
Score: 66.50 Matches: 19  
Percent Similarity: 58.3% Conservative: 2  
Best Local Similarity: 52.8% Mismatches: 10  
Query Match: 34.8% Indels: 5  
DB: 10 Gaps: 2

US-10-628-525A-37 (1-39) x AAD54236 (1-6297)

Qy 4 ProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaVal 23  
|||||  
Db 2704 CCGACGCTCCCGCTGCTCCAGCCGAGGCCACCGAGCCTGAGAGG--- 2760  
|||||

Qy 24 GlyAspArgAla-----ArgProArgArgLeuGlnArgValleu 36  
|||||  
Db 2761 ---GACCGTGGCCCGACACCGCCCGTGTGCGGCTGCGGACGCTGCTG 2805  
|||||

RESULT 24  
AAD54230  
ID AAD54230 standard; DNA; 50543 BP.  
XX  
XX AAD54230;  
AC  
XX  
DT 17-JUN-2003 (first entry)  
XX  
DE Streptomyces amphibiae sp. nov. lactimidomycin DNA.  
XX  
KW Polyketide biosynthesis; dorrigocin; DORR; lactimidomycin; LACT; gene;  
ds.  
XX  
OS Streptomyces amphibiae sp. nov.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 1. .1698  
FT /tag= a  
FT /product= "LACT ORF1 protein"  
FT /note= "No start codon"  
FT /partial  
FT 1908. .2162  
FT /tag= b  
FT /product= "LACT ORF2 protein"  
FT 2166. .4136  
FT /tag= c  
FT /product= "LACT ORF3 protein"  
FT /note= "No start codon"  
FT /partial  
FT 4152. .14462  
FT /tag= d  
FT /product= "LACT ORF4 protein"  
FT 14549. .39631  
FT /tag= e  
FT /product= "LACT ORF5 protein"  
FT /note= "No start codon"  
FT /partial  
FT 39628. .45924  
FT /tag= f  
FT /product= "LACT ORF6 protein"  
FT 45926. .48232  
FT /tag= g  
FT /product= "LACT ORF7 protein"  
FT 48441. .49697  
FT /tag= h  
FT /product= "LACT ORF8 protein"  
FT complement(49800. .40543)  
FT /tag= i  
FT /product= "LACT ORF9 protein"  
XX  
PN WO200288176-A2.  
XX  
PD 07-NOV-2002.  
XX  
PF 26-APR-2002; 2002WO-CA000591.  
XX  
PR 26-APR-2001; 2001US-0286346P.  
XX  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
XX  
PI Farnet CM, Zazopoulos E, Staffa A, Yang X;  
XX  
XX WPI; 2003-201222/19.  
DR P-PSDB; AAE35496; AAE35501, AAE35502, AAE35503, AAE34595, AAE34597,  
DR AAE34598, AAE34599, AAE34500.  
XX  
XX Novel isolated or purified polypeptide involved in biosynthesis of  
PT polyketide dorrigocin or polyketide lactimidomycin, useful for preparing  
PT dorrigocin or lactimidomycin.  
PT



FT XX /partial  
 PN US6410827-B1.  
 XX  
 PD 25-JUN-2002.  
 XX  
 PF 01-DEC-1999; 99US-00452238.  
 XX  
 PR 02-DEC-1998; 98US-0110592P.  
 XX  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PI Cahoon RE, Shen JB, Williams ME;  
 XX  
 DR WPI: 2002-588898/63.  
 DR P-PSDB; AAE42748.  
 XX  
 FT New nucleic acid molecule encoding geranylgeranyl pyrophosphate synthase,  
 PT useful for producing transgenic plants having altered synthase activity  
 PT and exhibiting altered amounts of carotenoids.  
 XX  
 PS Example 1; Col 35-38; 48pp; English.  
 XX  
 CC The invention relates to an isolated polynucleotide comprising a  
 CC nucleotide sequence encoding a polypeptide having geranylgeranyl  
 CC pyrophosphate synthase (GGPPS) activity. The invention is useful for  
 CC transforming a cell and producing a transgenic plant. Nucleic acid  
 CC fragments of the invention are useful to create transgenic plants in  
 CC which GGPPS polypeptides are present at higher or lower levels than  
 CC normal or in cell types or developmental stages in which they are not  
 CC normally found. Increasing the amount of GGPPS in the plant cell results  
 CC in increased amounts of carotenoids yielding brighter colours in the  
 CC flower and the fruit and higher levels of beta-carotene as well as other  
 CC terpenoids derived from GGPP. GGPPS polypeptides are useful as targets  
 CC for herbicide discovery. The nucleic acid fragments are also useful as  
 CC probes for genetically and physically mapping the genes that they are a  
 CC portion and as markers for traits linked to those genes. The information  
 CC is useful in plant breeding to develop lines with desired phenotypes. The  
 CC nucleic acid fragments are also useful as restriction fragment length  
 CC polymorphism (RFLP) markers, for physical mapping and in direct  
 CC fluorescence in situ hybridisation (FISH) mapping. The present sequence  
 CC is corn GGPP synthase cDNA  
 XX  
 SQ Sequence 365 BP; 136 A; 62 C; 72 G; 95 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 34 Length: 365  
 Score: 65.50 Matches: 16  
 Percent Similarity: 57.5% Conservative: 7  
 Best Local Similarity: 40.0% Mismatches: 12  
 Query Match: 34.3% Indels: 5  
 DB: 6 Gaps: 2  
 US-10-628-525A-37 (1-39) x AAD42748 (1-365)  
 QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpProAla 21  
 DB 132 GCATCACCACCAATCTTCAGTTCTGCTGT-----GGCCGATATAGTTGGCCAGT 82  
 QY 22 AlaValGlyAspArgAlaAlaArgProArgArgLeuGlnArg-----ValLeuArgArgArg 39  
 DB 81 GCAACAGGGGTGCTGCCTTCTCTCTGTCGACGACGAGCTGCTCTGTGGTCAGAGA 22  
 RESULT 27  
 ACA05145/c  
 ID ACA05145 standard; cDNA; 365 BP.  
 XX  
 AC ACA05145;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Corn geranylgeranyl pyrophosphate (GGPP) synthase cDNA #5.  
 XX

KW Gene; ss; plant; geranylgeranyl pyrophosphate synthase; GGPP synthase;  
 KW geranylgeranyl pyrophosphate; GGPP; corn; rice; soybean; wheat;  
 KW geranylgeranyl-diphosphate synthase; farnesyl transferase;  
 KW geranylgeranyl synthetase; terpenoid; phytoene; phytoene synthase;  
 KW carotenoid; phytohormone; gibberellin; seed germination; stem elongation;  
 KW flowering; bolting; leaf senescence; fruit senescence; herbicide;  
 KW beta-carotene.  
 XX  
 OS Zea mays.  
 XX  
 PN US2002177204-A1.  
 XX  
 PD 28-NOV-2002.  
 XX  
 XX 28-MAR-2002; 2002US-00108915.  
 PF 02-DEC-1998; 98US-0110592P.  
 XX  
 PR 01-DEC-1999; 99US-00452238.  
 XX  
 PA (CAHO/) CAHOON R E.  
 PA (SHEN/) SHEN J B.  
 PA (WILL/) WILLIAMS M E.  
 XX  
 PI Cahoon RE, Shen JB, Williams ME;  
 XX  
 DR WPI: 2003-328487/31.  
 DR P-PSDB; ABU67325.  
 XX  
 FT Novel nucleic acid molecule encoding geranylgeranyl pyrophosphate  
 PT synthase useful for producing transgenic plants having altered synthase  
 PT activity and exhibiting altered amounts of carotenoids.  
 XX  
 PS Claim 2; Page 20; 52pp; English.  
 XX  
 CC The invention discloses an isolated geranylgeranyl pyrophosphate (GGPP)  
 CC synthase polypeptide comprising a sequence from corn, rice, soybean,  
 CC wheat, or other related protein. GGPP synthase, also known as  
 CC geranylgeranyl-diphosphate synthase, farnesyl transferase and  
 CC geranylgeranyl synthetase, is a key enzyme in plant terpenoid  
 CC biosynthesis. One fate of GGPP is conversion to phytoene by phytoene  
 CC synthase, the first committed step in carotenoid biosynthesis. GGPP also  
 CC serves as a precursor in the formation of defence-related substances and  
 CC a precursor of the phytohormone gibberellin which regulates a variety of  
 CC physiological processes that include initiation of seed germination,  
 CC stimulation of stem elongation, stimulation of flowering/bolting and  
 CC regulation of leaf/fruit senescence. Also disclosed is a method for  
 CC selecting an isolated polynucleotide that affects the level of expression  
 CC of a GGPP synthase polypeptide in a plant cell. The polypeptide is useful  
 CC for evaluating at least one compound for its ability to inhibit the  
 CC activity of GGPP synthase polypeptide and as targets for herbicide  
 CC discovery. Nucleic acid fragments of the polypeptide are useful for  
 CC creating transgenic plants with an increased amounts of carotenoids  
 CC yielding brighter colours in the flower and the fruit and higher levels  
 CC of beta-carotene as well as other terpenoids derived from GGPP, as probes  
 CC for mapping the genes and as markers for traits linked to those genes.  
 CC Such information is useful in plant breeding to develop lines with  
 CC desired phenotypes. The sequences presented in ACA05141-ACA05162 are the  
 CC polynucleotides encoding the plant GGPP synthase and GGPP synthase-  
 CC related proteins  
 XX  
 SQ Sequence 365 BP; 136 A; 62 C; 72 G; 95 T; 0 U; 0 Other;  
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 Pred. No.: 34 Length: 365  
 Score: 65.50 Matches: 16  
 Percent Similarity: 57.5% Conservative: 7  
 Best Local Similarity: 40.0% Mismatches: 12  
 Query Match: 34.3% Indels: 5  
 DB: 9 Gaps: 2  
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Db      132 GCATCACCAAAATCTTCAGTTCTGCTGT-----GGGCGATATAGTTGGCCAAGT 82
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AC      AEB11213;
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XX
DT      25-AUG-2005 (first entry)
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DE      Maize GGPP synthase coding sequence, SEQ ID 9.
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XX      Plant; transgenic plant; plant breeding;
KW      geranylgeranyl pyrophosphate synthase; gene; ss.
XX
XX      Zea mays.
XX
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XX      02-JUN-2005.
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XX      10-JAN-2005; 2005US-00032643.
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XX      02-DEC-1998; 98US-0110592P.
XX      01-DEC-1999; 99US-00452238.
XX
XX      (CAHO/) CAHOON R E.
XX      (SHEN/) SHEN J B.
XX      (WILL/) WILLIAMS M E.
XX
XX      Cahoon RE, Shen JB, Williams ME;
XX
XX      WPI; 2005-504028/51.
XX      P-PSDB; AEB11214.
XX
XX      Novel polynucleotide encoding polypeptide having geranylgeranyl
XX      pyrophosphate synthase activity, useful for producing transgenic plant
XX      and useful as probes for genetically and physically mapping genes
XX      encoding above enzyme.
XX
XX      Disclosure; SEQ ID NO 9; 51pp; English.
XX
XX      The present invention relates to novel plant geranylgeranyl pyrophosphate
XX      (GGPP) synthases and their coding sequences. GGPP synthase is also known
XX      as geranylgeranyl-diphosphate synthase, farnesyl transferase and
XX      geranylgeranyl synthetase, and is a key enzyme in plant terpenoid
XX      biosynthesis. The GGPP synthase coding sequences are useful for
XX      transforming a cell, producing a transgenic plant, as probes for
XX      genetically and physically mapping the genes encoding GGPP synthase, and
XX      as markers for traits linked to genes encoding GGPP synthase, which is
XX      useful in plant breeding in order to develop lines with desired
XX      phenotypes, and also useful as restriction fragment length polymorphism
XX      markers. The present sequence is one such GGPP synthase coding sequence.
XX
XX      Sequence 365 BP; 136 A; 62 C; 72 G; 95 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      34      Length:      365
Score:          65.50   Matches:      16
Percent Similarity: 57.5% Conservative: 7
Best Local Similarity: 40.0% Mismatches: 12

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Query Match:      34.3%      Indels:      5
DB:              14         Gaps:      2

US-10-628-525A-37 (1-39) x AEB11213 (1-365)
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Db      132 GCATCACCAAAATCTTCAGTTCTGCTGT-----GGGCGATATAGTTGGCCAAGT 82
Qy      22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArg-----ValLeuArgArgArg 39
Db      81 GCAACAGGGGTGCTGCTCTCTCTCGTGAAGCAAGCGAGCTGCTCTGTTGGCTCAGAGA 22

RESULT 29
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XX      AC      AEB48334;
XX
XX      DT      22-SEP-2005 (first entry)
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XX      DE      Corn GGPP synthase FIS cDNA clone, SEQ ID NO: 9.
XX
XX      KW      Transgenic plant; feedstuff; geranylgeranyl pyrophosphate synthase;
XX      KW      geranylgeranyl-diphosphate synthase; farnesyl transferase;
XX      KW      geranylgeranyl synthase; gene; ss.
XX
XX      OS      Zea mays.
XX
XX      FH      Key
XX      FT      Location/Qualifiers
XX      FT      3..116
XX      FT      /*tag= a
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XX      FT      /note= "No start codon"
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XX      PN      US2005160489-A1.
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XX      PD      21-JUL-2005.
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XX      PR      02-DEC-1998; 98US-0110592P.
XX      01-DEC-1999; 99US-00452238.
XX
XX      (CAHO/) CAHOON R E.
XX      (SHEN/) SHEN J B.
XX      (WILL/) WILLIAMS M E.
XX
XX      Cahoon RE, Shen JB, Williams ME;
XX
XX      WPI; 2005-512287/52.
XX      P-PSDB; AEB48335.
XX
XX      New polynucleotide encoding geranylgeranyl pyrophosphate synthase, useful
XX      in plant terpenoid biosynthesis and for producing plants with increased
XX      levels of defense-related substance and phytohormone gibberellin.
XX
XX      Disclosure; SEQ ID NO 9; 51pp; English.
XX
XX      The invention relates to geranylgeranyl pyrophosphate (GGPP) synthase and
XX      its corresponding nucleic acid sequence. GGPP synthase also known as
XX      geranylgeranyl-diphosphate synthase, farnesyl transferase and
XX      geranylgeranyl synthase is a key enzyme in plant terpenoid biosynthesis.
XX      The invention also relates to methods for producing transgenic plant. The
XX      polynucleotide, polypeptide and methods of the invention are useful in
XX      plant terpenoid biosynthesis and for producing transgenic plants with
XX      increased levels of defense-related substance and important phytohormone
XX      gibberellin and specifically, for manipulating corn gene resulting in
XX      increased xanthophyll content, which has value as coloring agent in
XX      poultry feed. The present sequence is the corn GGPP synthase FIS cDNA
XX      clone.

```



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 15:18:57 ; Search time 628.922 Seconds  
(without alignments)  
2901.306 Million cell updates/sec

Title: US-10-628-525A-37

Perfect score: 191

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs06h  
-USER=US10628525 @CGN 1.1 11098 @runat\_31032006\_095118\_16742 -NCPU=6 -ICPU=3  
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-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
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2: gb\_est2:  
3: gb\_est3:  
4: gb\_hic:  
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7: gb\_est6:  
8: gb\_est7:  
9: gb\_gss1:  
10: gb\_gss2:  
11: gb\_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	191	100.0	707	8	DR810603
5	191	100.0	719	8	DR808291
6	143.5	75.1	424	2	BG556880
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AW287063	LG1_265_A	404	35.6	68	24
CD236601	SSI_35_H0	421	35.6	68	25
CD461565	SAL_32_F1	440	35.6	68	26
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CD230413	SSI_43_F1	489	35.6	68	28
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 605)
AUTHORS
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nuber,A., Robbins,D. and Lakey,N.
CONSORTIUM
Consortium for Maize Genomics
JOURNAL
Unpublished (2002)
COMMENT
Other_GSSs: CG3BC36TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: IR
Class: methylation filtered.
Location/Qualifiers
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Query Match: 100.0% Indels: 0
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US-10-628-525A-37 (1-39) x CG356137 (1-605)
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RESULT 2
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clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 606)
```



## AUTHORS

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
 Consortium for Maize Genomics  
 Unpublished (2002)  
 Contact: Cathy Whitelaw  
 TIGR

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Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@cigr.org

Seq primer: TR

Class: methylation filtered.

Location/Qualifiers

## FEATURES

source

1. .606

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMWBMA0459807"

/clone\_lib="ZM\_0.7\_1.5\_KB"

/notes="Vector: pBCKS-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.98e-13 Length: 606  
 Score: 191.00 Matches: 38  
 Percent Similarity: 97.4% Conservative: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 100.0% Indels: 0  
 DB: 9 Gaps: 0

US-10-628-525A-37 (1-39) x CC663124 (1-606)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTTPPro 20  
 Db 467 ATGGCGAGCCCTCGGCGGTGGGGCGCGGTGCTCTCTCGGGCGCGCTGGCCG 526  
 QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
 Db 527 GCCGCGGTGGCGACCGCGCGCGCGCGCGCTCCAGCGCTGCTGCGCGCGCG 583

## RESULT 3

CG242761/c  
 LOCUS  
 DEFINITION CG242761 ZM 0.7\_1.5\_KB Zea mays genomic clone ZMWBMA0743P24,  
 genomic survey sequence.

ACCESSION CG242761.1 GI:34142647

VERSION GSS.

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 673)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
 Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: CG242761

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@cigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

1. .673

## FEATURES

source

1. .673

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMWBMA0459807"

/clone\_lib="ZM\_0.7\_1.5\_KB"

/notes="Vector: pBCKS-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMWBMA0743P24"

/clone\_lib="ZM\_0.7\_1.5\_KB"

/notes="Vector: pBCKS-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.21e-13 Length: 673  
 Score: 191.00 Matches: 38  
 Percent Similarity: 97.4% Conservative: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 100.0% Indels: 0  
 DB: 10 Gaps: 0

US-10-628-525A-37 (1-39) x CG242761 (1-673)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTTPPro 20  
 Db 624 ATGGCGAGCCCTCGGCGGTGGGGCGCGGTGCTCTCTCGGGCGCGCTGGCCG 565

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
 Db 564 GCCGCGGTGGCGACCGCGCGCGCGCGCTCCAGCGCTGCTGCGCGCGCG 508

## RESULT 4

DR810603  
 LOCUS  
 DEFINITION ZM BFB0038G07.r ZM\_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005  
 ACCESSION DR810603  
 VERSION DR810603.1 GI:71429553

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 707)

Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C.,  
 Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project

Unpublished (2005)

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0038 row: G column: 07.

Location/Qualifiers

1. .707

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev\_stage="varies by tissue"

/lab\_host="DH10B T1 phage resistant"

/clone\_lib="ZM\_BFB"

/note="Vector: PCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector,

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination

rather than restriction enzymes. poly(A)+ mRNA was

prepared by Invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Alignment Scores:  
Pred. No.: 2,33e-13 Length: 707  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x DR810603 (1-707)

QY 1 MetAlaThPrSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 181 ATGGCGACGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCTGGCGG 240  
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
Db 241 GCCGCGTGGCGACCGCGCGCGCGCGCTCCAGCGGTGCTGCGCGCGG 297

RESULT 5

DR808291 719 bp mRNA linear EST 28-JUL-2005  
LOCUS ZM\_BFB\_Zea mays cDNA 5', mRNA sequence.  
DEFINITION DR808291  
ACCESSION DR808291  
VERSION DR808291.1 GI:71427241  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 719)  
Kim H., Collura, K., Waisotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wang, R., Soderlund, C., Walbot, V. and Yu, Y.  
Maize Full-length cDNA Project  
Unpublished (2005)  
Contact: Yeisoo Yu  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: yeisoo@genome.arizona.edu  
Plate: 0034 row: P column: 07.

FEATURES

Location/Qualifiers  
1..719  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultiivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM\_BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

ORIGIN

Alignment Scores:  
Pred. No.: 2,37e-13 Length: 719  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x DR808291 (1-719)

QY 1 MetAlaThPrSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 99 ATGGCGACGCCCTCGCGCGTGGCGCGCGTGCCTCTCTCGCGCGCGCTGGCGG 158  
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39  
Db 159 GCCGCGTGGCGACCGCGCGCGCGCTCCAGCGGTGCTGCGCGCGG 215

RESULT 6

BG556880  
LOCUS EML\_39\_G08\_b1\_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA  
DEFINITION BG556880  
ACCESSION BG556880  
VERSION BG556880.1 GI:13585878  
KEYWORDS EST.  
SOURCE Sorghum bicolor (sorghum)  
ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 424)  
Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and Pratt, L.H.  
An EST database from Sorghum: developing embryos  
Unpublished (2000)  
Contact: Cordonnier-Pratt MM

REFERENCE

AUTHORS Laboratory for Genomics and Bioinformatics  
TITLE The University of Georgia, Department of Plant Biology  
JOURNAL Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
COMMENT Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV  
High quality sequence stop: 410  
PolyA=No.

FEATURES  
source  
1. .424  
Location/Qualifiers  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/db\_xref="taxon:4558"  
/clone\_lib="Embryo 1 (EM1)"  
/notes="Organ: Embryos germinated for 24 hr; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

## ORIGIN

Alignment Scores:  
Pred. No.: 9.44e-08 Length: 424  
Score: 143.50 Matches: 32  
Percent Similarity: 77.3% Conservativeness: 2  
Best Local Similarity: 72.7% Mismatches: 5  
Query Match: 75.1% Indels: 5  
DB: 2 Gaps: 1

US-10-628-525A-37 (1-39) x BG556880 (1-424)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*Ala----- 18  
|||||  
Db 138 ATGGCGACGCCCTCGGCGGTGGCGGCTGCTGCTAGCGGAGCGCGCGGG 197

QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgLeuGlnArgVal 35  
|||||  
Db 198 CTTGGGCTTGGCGCGGCGGCGGATCGGCGCGCGCGCGCTCCAGCGCGTG 257

QY 36 LeuArgArgArg 39  
:::  
Db 258 GTGCGAGGCGG 269

RESULT 7  
CA282588  
LOCUS  
DEFINITION  
5', mRNA sequence.  
CA282588  
VERSION  
CA282588.1 GI:36014712  
EST.  
SOURCE  
Saccharum officinarum  
ORGANISM  
Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum  
complex.

REFERENCE  
1 (bases 1 to 465)  
Vettore,A.L., da Silva,P.R., Kemper,E.L. and Arruda,P.  
The libraries that made SUCSEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
Contact: Arruda P  
Centro de Biologia Molecular e Engenhariaia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bccccenter.fcav.unesp.br  
Plate: 001 row: G column: 11  
Seq primer: T7 Promoter Primer.  
Location/Qualifiers  
1. .465  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"

FEATURES  
source

/clone="SCCCNR1001G11"  
/lab\_host="DH10B"  
/clone\_lib="NR1"  
/notes="Organ: Pool of sugarcane tissues; Vector: pSport1;  
Site\_1: SalI; Site\_2: NotI; An unidirectional cDNA library  
generated from [pool of sugarcane tissues]. cDNA was  
prepared from polyA+ mRNA using SuperScript Plasmid  
System Kit (Invitrogen). The double-strand cDNAs were  
fractionated in a sepharose CL-2B 40cm-columns and  
fragments sizing between 0.8 and 1.5 Kb were  
directionally cloned into the vector. Details of each  
source of RNA and library construction can be obtained at  
http://sucest.lad.ic.unicamp.br/public"

## ORIGIN

Alignment Scores:  
Pred. No.: 4.28e-07 Length: 465  
Score: 138.50 Matches: 31  
Percent Similarity: 82.1% Conservativeness: 1  
Best Local Similarity: 79.5% Mismatches: 6  
Query Match: 72.5% Indels: 1  
DB: 6 Gaps: 1

US-10-628-525A-37 (1-39) x CA282588 (1-465)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg\*\*\*AlaTrpPro 20  
|||||  
Db 126 ATGGCGACGCCCTCGGCGGTGGCGGCTGCTGCTCGCCCTCGCGGCGCGGCGCG 185

QY 21 AlaAlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArg 39  
|||||  
Db 186 GGCCGC---GGCGATCGGCGCGCGCTGCTCAGCGCGTGTGTCGCGCGCGC 239

RESULT 8  
CF850352  
LOCUS  
DEFINITION

562 bp mRNA linear EST 30-OCT-2003  
pSMA013XO09f USDA-IFAPs:Expression of Phytophthora sojae genes  
during infection and propagation\_sMA Phytophthora sojae cDNA clone  
sMA013009 5, mRNA sequence.

ACCESSION  
VERSION  
CF850352.1 GI:38066006  
EST.  
Phytophthora sojae  
SOURCE  
Phytophthora sojae  
ORGANISM  
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;  
Phytophthora.

REFERENCE  
1 (bases 1 to 562)  
Tyler,B.  
Tyler,B. Not Published  
Unpublished (2003)  
Contact: Tyler B  
Tyler lab

VBI  
1880 Pratt Dr., Blacksburg, VA 24061, USA  
Tel: 540-231-7318  
Email: bmtylev@vt.edu  
PCR Primers  
FORWARD: BK reverse primer  
BACKWARD: BK reverse primer  
Plate: 013 row: O column: 09  
Seq primer: BK reverse primer  
High quality sequence stop: 562.  
Location/Qualifiers  
1. .562  
/organism="Phytophthora sojae"  
/mol\_type="mRNA"  
/db\_xref="taxon:67593"  
/clone="sMA013009"  
/tissue\_type="mycelium"  
/cell\_line="P6497"  
/dev\_stage="mycelium"  
/lab\_host="synthetic medium"  
/clone\_lib="USDA-IFAPs:Expression of Phytophthora sojae

FEATURES  
source

[illegible]

```

QY 26 ArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 233 CCGGCGAGGTCTCGCCCGCGCGGAGCTGCTCAGGCGCGG 192

RESULT 11
CV767377/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CV767377
FGAS061767 Triticum aestivum FGAS: Library 2 Gate 3 Triticum
aestivum cDNA, mRNA sequence.
CV767377
CV767377.1 GI:55611670
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 (bases 1 to 870)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, P., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress in Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_estes@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [97,617].
Plate: WEP050 row: H column: 22.

FEATURES
source
1. .870
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 2 Gate 3"
/notes="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial
parts (crown and leaf) of wheat cultivar Norstar from
control and long exposure times to low temperature. 4 mRNA
populations were combined before constructing the library;
7 days non-acclimated plants and 1, 23, and 53 days
cold-acclimated at 4C. Non-acclimated and cold-acclimated
plants were grown in vermiculite This is the only library
that was done according to the Invitrogen manual, and
therefore, a percentage of clones will not have the 3
prime end because of NotI digestion within the cDNA."

ORIGIN
Alignment Scores:
Pred. No.: 70.3 Length: 870
Score: 74.00 Matches: 16
Percent Similarity: 55.9% Conservative: 3
Best Local Similarity: 47.1% Mismatches: 15
Query Match: 38.7% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x CV767377 (1-870)

QY 6 AlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAlaValGlyAsp 25
Db 293 GCTGCTCGACTCCGCGGCGAGCTGCTCGGCTGCGCGCGGCTTGGCGAGCAACA 234

QY 26 ArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 233 CCGGCGAGGTCTCGCCCGCGCGGAGCTGCTCAGGCGCGG 192

```

```

RESULT 12
CA971120
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

CA971120 861 bp mRNA linear EST 06-JAN-2003  
 AGENCOURT 10199815 NIH MGC 126 Homo sapiens cDNA clone  
 IMAGE:6556939 5', mRNA\_sequence.

CA971120.1 GI:27503471  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

1 (bases 1 to 861)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Tissue Procurement: NCI  
 Email: cgabbs-remail.nih.gov  
 CDNA Library Preparation: Michael Brownstein Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCM2724 row: C column: 19  
 High quality sequence stop: 355.

```

FEATURES
source

```

Location/Qualifiers  
 1. .861  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:6556939"  
 /tissue\_type="mixed (pool of 40 RNAs)"  
 /lab\_host="DH10B (T1-phage-resistant)"  
 /clone\_lib="NIH MGC 126"  
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);  
 Site 2: SfiI (ggccgctcgcc); Double-stranded cDNA was  
 prepared from a pool of 40 cell line polyA+ RNAs (bladder  
 - 2% blood - 33.4% brain - 5.6% breast - 12.5% colon -  
 4% connective tissue - 1.4% eye - 1% intestine - 2.6%,  
 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -  
 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,  
 salivary gland - 1.3%, and skin - 2.3%). 5' and 3'  
 adaptors were used in cloning as follows:  
 5'-AGCAGTGTATACGAGTGGCATATGCGCGGG-3' and  
 5'-ATCTAGAGCGGCGGCGGCGGACATG-TT(30)NN-3'. Full-length  
 enriched library was constructed using the Clontech  
 Creator SMART kit and size-selected to contain the 0.5-1  
 kb size fraction (other fractions present in NIH MGC 127  
 and NIH MGC 128). Library created in the laboratory of T.  
 Ustin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC  
 Library."

```

ORIGIN

```

```

Alignment Scores:
Pred. No.: 80.1 Length: 861
Score: 73.50 Matches: 22
Percent Similarity: 43.6% Conservative: 2
Best Local Similarity: 40.0% Mismatches: 12
Query Match: 38.5% Indels: 19
DB: 6 Gaps: 2

```

US-10-628-525A-37 (1-39) x CA971120 (1-861)

```

QY 4 ProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAlaVal 23
Db 673 CCCCTTGCCTAGGCGGCTTTGTGCTCTCTCTCCACCCGGGCGAGAAACCCCGCTGGTC 732

QY 24 GlyAsp-----ArgAlaArgProArgLeu----- 32

```









```

/db_xref="taxon:9606"
/clones="IMAGE:5295457"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtccag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."
```

ORIGIN

Alignment Scores:

Pred. No.:	303	Length:	908
Score:	69.00	Matches:	13
Percent Similarity:	51.6%	Conservative:	3
Best Local Similarity:	41.9%	Mismatches:	15
Query Match:	36.1%	Indels:	0
DB:	3	Gaps:	0

US-10-628-525A-37 (1-39) x B1559341 (1-908)

QY 3 ThrProSerAlaValGlyAlaAaCysLeuLeuLeuAlaAarg\*\*\*AlaTrpProAlaAaAa 22

Db 748 ACACCGAATATCTAGGTAGTGTGTGCATCTGTAGTCCAGCTACTTGGGAAGCCGAG 689

QY 23 valGlyAspArgAlaArgProArgArgLeuGln 33

Db 688 GTGGGAGGATCACTTGTAGCCCGAGGAGGTGAGG 656

RESULT 20

CF990354/c

LOCUS

DEFINITION

2113orsicee\_3774.y1 Oryza sativa cv. LYP9 tillering whole plant

cdna library Oryza sativa (indica cultivar-group) cdna 5', mRNA

sequence.

ACCESSION

CF990354

VERSION

CF990354.1 GI:58592046

KEYWORDS

EST.

SOURCE

Oryza sativa (indica cultivar-group)

ORGANISM

Oryza sativa (indica cultivar-group)

REFERENCE

1 (bases 1 to 488)

Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W., Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J., Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q., Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P., Wu, S. and Liu, J.

AUTHORS

The Genomes of Oryza sativa: A History of Duplications

JOURNAL

PUBMED

15685292

COMMENT

Contact: Yan Zhou

Bioinformatics Department

Hangzhou Genomics Institute

No.51 Zhijiang Road, Hangzhou 310008, China

Tel: 86-571-56805886

Pax: 86-571-56805884

Email: zhouyan@genomics.org.cn

Seq primer: M13 Forward

High quality sequence stop: 488

POLYA=No.

FEATURES

source

1. .488

Location/Qualifiers

/organism="Oryza sativa (indica cultivar-group)"

/mol\_type="mRNA"

```

/cultivar="LYP9"
/db_xref="taxon:39946"
/tissue_type="whole plant"
/dev_stage="tillering"
/clone_lib="Oryza sativa cv. LYP9 tillering whole plant
cdna library"
```

ORIGIN

Alignment Scores:

Pred. No.:	182	Length:	488
Score:	68.50	Matches:	16
Percent Similarity:	52.9%	Conservative:	2
Best Local Similarity:	47.1%	Mismatches:	11
Query Match:	35.9%	Indels:	5
DB:	7	Gaps:	1

US-10-628-525A-37 (1-39) x CF990354 (1-488)

QY 5 SerAlaValGlyAlaAaCysLeuLeuLeuAlaAarg\*\*\*AlaTrpProAlaAaValGly 24

Db 208 ACAGCTTCTCCGGCTGCTGCTC-----GCCACTTGGCCAGCGCCGACCA 164

QY 25 AspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38

Db 163 TCGCCGGCTGCTCCACCGAGTCCACCGAGCCCTGAGAAGG 122

RESULT 21

AI936496/c

LOCUS

DEFINITION

wd28f04.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cdna clone

IMAGE:2329471 3', similar to SW:HK25\_HUMAN P52952 HOMEBOX PROTEIN

NKX-2.5 ; mRNA sequence.

ACCESSION

AI936496

VERSION

AI936496.1 GI:5675366

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 674)

NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TUMOR

Gene Index

Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

This clone is available royalty-free through LML ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1708 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 452.

FEATURES

source

1. .674

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2329471"

/lab\_host="DH10B"

/clone\_lib="Soares\_NFL\_T\_GBC\_S1"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site 1: Not I; Site 2: Eco RI;

Equal amounts of plasmid DNA from three normalized

libraries (fetal lung NBHL19W, testis NHT, and B-cell

NCI CGAP GCBI) were mixed, and ss circles were made in

vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of

I.M.A.G.E. clones 297480-302087 682632-687239,

726408-728711, and 729096-731399. Subtraction by Bento

Soares and M. Fatima Bonaldo."

ORIGIN



```

Db      803 GGGCGGCGCTCACGT---CGGGGCACCGCGAACCCTCCGACGC 844
|||||  |||:||||| |||  |||:||||| |||:||||| |||:|||||
RESULT 24
AW287063
LOCUS   LGI_265_A07_b2_A002 Light Grown 1 (LGI) Sorghum bicolor cDNA, mRNA
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE  Sorghum bicolor (sorghum)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 404)
AW287063.2 GI:6858996
EST.
VERSION
KEYWORDS
SOURCE  Sorghum bicolor (sorghum)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 404)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.
An EST database from Sorghum: light-grown seedlings
Unpublished (2000)
On Jan 6, 2000 this sequence version replaced gi:6676907.
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 348
POLYA=No.

FEATURES
    source
        1..404
            Location/Qualifiers
                /organism="Sorghum bicolor"
                /mol_type="mRNA"
                /db_xref="taxon:4558"
                /clone_lib="Light Grown 1 (LGI)"
                /notes="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2:
EcoRI; The library was made from poly-A RNA in the cloning
vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."

ORIGIN
Alignment Scores:
Pred. No.:      172      Length:      404
Score:          68.00    Matches:     18
Percent Similarity: 52.6%  Conservaive:  2
Best Local Similarity: 47.4% Mismatches:   14
Query Match:     35.6%  Indels:      4
DB:              1      Gaps:       1

US-10-628-525A-37 (1-39) x AW287063 (1-404)

QY      2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPProAla 21
|||||  |||:||||| |||  |||:||||| |||:||||| |||:|||||
Db      147 GCGCGCGCAACGTGCGCGCGCGCGCGCC-----GCTCTCGGTGGTGGCGGTAC 194
|||||  |||:||||| |||  |||:||||| |||:||||| |||:|||||
QY      22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
|||||  |||:||||| |||  |||:||||| |||:||||| |||:|||||
Db      195 AGACGGGGCGCGAGAGCCGTCGTCGTCGCCAGCGCGCGCGCGAGG 248
|||||  |||:||||| |||  |||:||||| |||:||||| |||:|||||

RESULT 25
CD236601
LOCUS   SSI_35_H03_g1_A012 Salt-stressed seedlings Sorghum bicolor cDNA
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE  CD236601.1 GI:30980066
EST.

```

```

Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 421)
Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,
Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Summer,E.J.,
Eastman,A. and Pratt,L.H.
An EST database from Sorghum: salt-stressed seedlings
Unpublished (2003)
Other_ESTs: SSI_35_H03_b1_A012
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTCTAAAGCTGCG).
    Location/Qualifiers
        1..421
            /organism="Sorghum bicolor"
            /mol_type="mRNA"
            /cultivar="IS3620C"
            /db_xref="taxon:4558"
            /clone="SSI_35_H03_A012"
            /lab_host="DH10B-TI phage-resistant E. coli"
            /clone_lib="Salt-stressed seedlings"
            /notes="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
library was prepared from polyA+ RNA from 9-day-old
seedlings grown in hydroponic culture. Seedlings were
transferred to a 150 mM NaCl solution and harvested at 3,
6, 12 and 24 hr following transfer. Roots and leaves were
pooled from all time points and RNA isolated.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGTGTG, 3-prime DraIII site is
CACCATGTG)."

ORIGIN
Alignment Scores:
Pred. No.:      180      Length:      421
Score:          68.00    Matches:     18
Percent Similarity: 52.6%  Conservaive:  2
Best Local Similarity: 47.4% Mismatches:   14
Query Match:     35.6%  Indels:      4
DB:              6      Gaps:       1

US-10-628-525A-37 (1-39) x CD236601 (1-421)

QY      2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPProAla 21
|||||  |||:||||| |||  |||:||||| |||:||||| |||:|||||
Db      162 GCGCGCGCAACGTGCGCGCGCGCGCC-----GCTCTCGGTGGTGGCGGTAC 209
|||||  |||:||||| |||  |||:||||| |||:||||| |||:|||||
QY      22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
|||||  |||:||||| |||  |||:||||| |||:||||| |||:|||||
Db      210 AGACGGGGCGCGAGAGCCGTCGTCGTCGCCAGCGCGCGCGAGG 263
|||||  |||:||||| |||  |||:||||| |||:||||| |||:|||||

RESULT 26
CD461565
LOCUS   SAI_32_F10_g2_A002 Salicylic acid-treated seedlings Sorghum bicolor
DEFINITION
ACCESSION
CD461565
SAI_32_F10_g2_A002 Salicylic acid-treated seedlings Sorghum bicolor
cDNA clone SAI_32_F10_A002 5', mRNA sequence.
CD461565

```

```

VERSION          CD461565.1  GI:31376662
KEYWORDS         EST.
SOURCE           Sorghum bicolor (sorghum)
ORGANISM         Sorghum bicolor
REFERENCE        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                  clade; Panicoideae; Andropogoneae; Sorghum.
                  1 (bases 1 to 440)
                  Cordonnier-Pratt M.-M., Wentzel, V., Suzuki, Y., Sugano, S.,
                  Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R.,
                  Chua Tan, N., Gonzalez, M., Lane, S., Miller, V., Nanda, P.,
                  Olaseinde, O., Eastman, A. and Pratt, L.H.
TITLE            An EST database from Sorghum: salicylic acid-treated seedlings
JOURNAL          Unpublished (2003)
COMMENT          Other ESTs: SAL 32 F10.bi A002
                  Contact: Cordonnier-Pratt MM
                  Laboratory for Genomics and Bioinformatics
                  The University of Georgia, Department of Plant Biology
                  Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                  Tel: 706 542 1860
                  Fax: 706 583 0210
                  Email: mmpratt@uga.edu
                  Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
                  the Human Genome Center, University of Tokyo Institute of Medical
                  Science; plant material and RNA prepared at Texas A & M University;
                  sequencing done in the Laboratory for Genomics and Bioinformatics,
                  University of Georgia. Sequence ends have been trimmed to exclude
                  vector and regions below Phred quality 16. Three-prime sequences
                  are presented as their reverse complement and have been trimmed to
                  exclude polyA.
                  Seq primer: Sug5 (CTTCTGCTTAAAAAGTGGC).
FEATURES         Location/Qualifiers
source           1..440
                 /organism="Sorghum bicolor"
                 /mol_type="mRNA"
                 /cultivar="BTx623"
                 /db_xref="taxon:4558"
                 /clone="SAL 32 F10 A002"
                 /lab_host="PH10B-TI phage-resistant E. coli"
                 /clone_lib="Salicylic acid-treated seedlings"
                 /note="Vector: pME18S-FL3; Site_1: XhoI; Site_2: XhoI; The
                 library was prepared from polyA+ RNA from seedlings grown
                 in hydroponic culture. At 8 days of age, medium was
                 supplemented with 1 mM salicylic acid (SA). Roots and
                 shoots were harvested after 27 and 72 hr and material from
                 both time points was combined prior to RNA isolation.
                 Double-stranded cDNA was cloned unidirectionally into
                 different DraIII sites of the pME18S-FL3 vector (5-prime
                 DraIII site is CACTGTGTG, 3-prime DraIII site is
                 CACCATGTG). XhoI excises the cDNA insert."
ORIGIN
Alignment Scores:
Pred. No.:      188          Length:      440
Score:          68.00       Matches:      18
Percent Similarity: 52.6%   Conservative: 2
Best Local Similarity: 47.4% Mismatches: 14
Query Match:    35.6%      Indels:      4
DB:             6          Gaps:       1

US-10-628-525A-37 (1-39) x CD461565 (1-440)
QY 2 AlaThrProSerAlaValGlyAlaCysLeuLeuLeuAlaArg**AlaTrpProAla 21
Db 151 GCCGGCCCAACGTGCGCCGGCGGCC-----GCTCTCGGTGGTGGCGGTAC 198
QY 22 AlaValGlyAspArgProArgProArgLeuGlnArgValLeuArgArgArg 39
Db 199 AGACGGGGCCGACGAAGCGCTCCCGCTGCTGCTCCACGGCGCGCGGAGG 252
RESULT 27
CA612682/c
LOCUS
QY 22 AlaValGlyAspArgProArgProArgLeuGlnArgValLeuArgArgArg 39
Db 199 AGACGGGGCCGACGAAGCGCTCCCGCTGCTGCTCCACGGCGCGCGGAGG 252

```

```

DEFINITION      wr1.pk0138.c10 wr1 Triticum aestivum cDNA clone wr1.pk0138.c10 5'
                end, mRNA sequence.
ACCESSION       CA612682
VERSION         CA612682.1  GI:25190979
KEYWORDS        EST.
SOURCE          Triticum aestivum (bread wheat)
ORGANISM        Triticum aestivum
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Poaceae; Triticeae; Triticum.
                1 (bases 1 to 455)
                Tingley, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
                Miao, G., Caraher, N. and Hanafey, M.K.
TITLE           DuPont Wheat cDNA Sequence
JOURNAL         Unpublished (2002)
COMMENT         Contact: Scott V. Tingley
                Crop Genetics
                E. I. DuPont de Nemours and Company
                1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
                Tel: 302-631-2602
                Fax: 302-631-2607
                Email: Scott.V.Tingley@USA.dupont.com
                Seq primer: M13.
FEATURES         Location/Qualifiers
source           1..455
                 /organism="Triticum aestivum"
                 /mol_type="mRNA"
                 /db_xref="taxon:4565"
                 /clone="wr1.pk0138.c10"
                 /tissue_type="root"
                 /clone_lib="wr1"
                 /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                 XhoI; Wheat (Triticum aestivum L.) root; 7 day old
                 seedling, light grown"
ORIGIN
Alignment Scores:
Pred. No.:      195          Length:      455
Score:          68.00       Matches:      17
Percent Similarity: 62.1%   Conservative: 1
Best Local Similarity: 58.6% Mismatches: 11
Query Match:    35.6%      Indels:      0
DB:             6          Gaps:       0

US-10-628-525A-37 (1-39) x CA612682 (1-455)
QY 10 AlaCysLeuLeuLeuAlaArg**AlaTrpProAlaAlaValGlyAspArgAlaArgPro 29
Db 118 GCGGCGTGGCTGCTAGCGACATGCGCACTCCGCGCGACAGGCTCTCAGGCACGGCCG 59
QY 30 ArgArgLeuGlnArgValLeuArgArg 38
Db 58 CGGCGTCTCCCGCGCGCAGCAGACGA 32
RESULT 28
CD230413
LOCUS
DEFINITION      SS1_43_F10.g1_A012 Salt-stressed seedlings Sorghum bicolor cDNA
                clone SS1_43_F10_A012 5', mRNA sequence.
ACCESSION       CD230413
VERSION         CD230413.1  GI:30973847
KEYWORDS        EST.
SOURCE          Sorghum bicolor (sorghum)
ORGANISM        Sorghum bicolor
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                clade; Panicoideae; Andropogoneae; Sorghum.
                1 (bases 1 to 489)
                Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S.,
                Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Summer, E.J.,
                Eastman, A. and Pratt, L.H.
TITLE           An EST database from Sorghum: salt-stressed seedlings
JOURNAL         Unpublished (2003)

```





GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 31, 2006, 22:47:42 ; Search time 52.1578 Seconds  
(without alignments)  
1329.139 Million cell updates/sec

Title: US-10-628-525A-37

Perfect score: 191

Sequence: 1 MATPSAVGACLLARXAMPVAGDPRRLQRLVRRR 39

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DBV=xlp  
-Q=/abes/ABSWEB.spool/US10628525/runat\_31032006\_095123\_16858/app.query.fasta\_1  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=150 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=30  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abs02p -USER=US10628525 @CGN 1 1 855 @runat\_31032006\_095123\_16858  
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:\*\*  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	100.0	153	3	US-08-941-445A-18
2	191	100.0	1415	3	US-09-345-214-11
3	191	100.0	1415	3	US-09-743-980-11
4	191	100.0	2008	3	US-09-345-214-12
5	191	100.0	2008	3	US-09-743-980-12
6	191	100.0	2383	3	US-09-192-909-1
7	191	100.0	2383	3	US-09-931-297-1
8	191	100.0	2491	3	US-09-345-214-5
9	191	100.0	2491	3	US-09-743-980-5
10	191	100.0	2491	3	US-09-743-980-5

Sequence 1, Appli	2	US-08-572-951-1	2990	88.0	168	10
Sequence 7, Appli	3	US-10-200-012-7	1437	34.6	66	11
Sequence 9, Appli	3	US-10-108-915-9	365	34.3	65.5	12
Sequence 8, Appli	2	US-08-891-254-8	1035	34.0	65	13
Sequence 8, Appli	2	US-08-819-539-8	1035	34.0	65	14
Sequence 8, Appli	2	US-09-030-270A-8	1035	34.0	65	15
Sequence 8, Appli	3	US-08-984-207-8	1035	34.0	65	16
Sequence 8, Appli	3	US-09-013-587-8	1035	34.0	65	17
Sequence 28, Appli	3	US-09-086-118-28	1035	34.0	65	18
Sequence 16, Appli	3	US-09-431-614-16	1035	34.0	65	19
Sequence 36, Appli	3	US-09-412-100-36	1035	34.0	65	20
Sequence 8, Appli	6	PCT-US96-08819-8	1035	34.0	65	21
Sequence 4680, Ap	3	US-09-902-540-4680	2502	33.8	64.5	22
Sequence 1230, Ap	3	US-09-902-540-1230	24754	33.8	64.5	23
Sequence 140, App	3	US-08-311-731A-140	36063	33.5	64	24
Sequence 10, Appli	3	US-09-544-398B-10	8705	33.0	63	25
Sequence 3246, Ap	3	US-09-543-771B-10	8705	33.0	63	26
Sequence 6772, Ap	3	US-09-252-991A-3246	909	32.7	62.5	27
Sequence 3322, Ap	3	US-09-902-540-6772	1197	32.7	62.5	28
Sequence 1051, Ap	3	US-09-252-991A-3322	1995	32.7	62.5	29
Sequence 11504, A	3	US-09-902-540-1051	15271	32.7	62.5	30
Sequence 11736, A	3	US-09-252-991A-11504	894	32.5	62	31
Sequence 6806, Ap	3	US-09-252-991A-11736	894	32.5	62	32
Sequence 1, Appli	2	US-08-091-569-1	1035	32.5	62	33
Sequence 1, Appli	2	US-08-203-676-1	3695	32.5	62	34
Sequence 1, Appli	2	US-08-822-238-1	3695	32.5	62	35
Sequence 562, App	3	US-09-902-540-562	4800	32.5	62	36
Sequence 669, App	3	US-09-949-002-669	38619	32.5	62	37
Sequence 833, App	3	US-09-949-002-833	38619	32.5	62	38
Sequence 11, Appl	3	US-09-843-377-11	54000	32.5	62	39
Sequence 13983, A	3	US-09-949-016-13983	57320	32.5	62	40
Sequence 4286, Ap	3	US-09-252-991A-4286	573	32.5	61.5	41
Sequence 10, Appl	3	US-09-356-952-10	6601	31.9	61	42
Sequence 15497, A	3	US-09-949-016-15497	6601	31.9	61	43
Sequence 1, Appli	3	US-09-804-778A-1	927	31.7	60.5	44
Sequence 1122, Ap	3	US-09-902-540-1122	17173	31.7	60.5	45
Sequence 13180, A	3	US-09-949-016-13180	112874	31.7	60.5	46
Sequence 1, Appli	3	US-09-214-808-1	536165	31.7	60.5	47
Sequence 159, App	3	US-09-893-737-159	624	31.4	60	48
Sequence 13, Appl	3	US-09-508-824-13	817	31.4	60	49
Sequence 440, App	3	US-09-620-312D-440	833	31.4	60	50
Sequence 371, App	3	US-09-902-540-371	1644	31.4	60	51
Sequence 10, Appl	3	US-09-614-748A-10	1879	31.4	60	52
Sequence 9, Appli	2	US-07-980-526-1	1886	31.4	60	53
Sequence 8, Appli	3	US-09-614-748A-9	1975	31.4	60	54
Sequence 5836, Ap	3	US-09-614-748A-8	2019	31.4	60	55
Sequence 1, Appli	3	US-09-252-991A-5836	2113	31.4	60	56
Sequence 7, Appli	3	US-09-193-792-1	2284	31.4	60	57
Sequence 5812, Ap	3	US-09-252-991A-5812	2391	31.4	60	58
Sequence 1, Appli	3	US-09-071-101-1	2744	31.4	60	59
Sequence 1, Appli	3	US-09-369-618-1	2744	31.4	60	60
Sequence 1, Appli	3	US-09-369-617-1	2744	31.4	60	61
Sequence 12903, A	3	US-09-252-991A-12903	2748	31.4	60	62
Sequence 12588, A	3	US-09-252-991A-12903	342	31.2	59.5	63
Sequence 5, Appli	2	US-08-494-907-5	702	31.2	59.5	64
Sequence 5, Appli	2	PCT-US96-10986-5	792	31.2	59.5	65
Sequence 13227, A	6	US-08-494-907-1	1374	31.2	59.5	66
Sequence 1, Appli	6	PCT-US96-10986-1	3680	31.2	59.5	67
Sequence 1, Appli	6	US-08-313-181-1	4086	31.2	59.5	68
Sequence 2, Appli	2	US-08-494-907-2	5076	31.2	59.5	69
Sequence 2, Appli	6	PCT-US96-10986-2	5076	31.2	59.5	70
Sequence 4, Appli	6	US-08-494-907-4	6170	31.2	59.5	71
Sequence 3, Appli	6	PCT-US96-10986-4	6170	31.2	59.5	72
Sequence 3, Appli	6	US-08-494-907-3	6387	31.2	59.5	73
Sequence 3, Appli	6	PCT-US96-10986-3	6387	31.2	59.5	74
Sequence 4, Appli	3	US-08-994-035C-4	7198	31.2	59.5	75
Sequence 4, Appli	3	US-09-395-861-4	7198	31.2	59.5	76
Sequence 14254, A	3	US-09-949-016-14254	26140	31.2	59.5	77
Sequence 14255, A	3	US-09-949-016-14255	26140	31.2	59.5	78









DB: 3 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-931-297-1 (1-2383)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTTPPro 20  
Db 29 ATGGCGACGCCCTCGGCGCGGCGCGCTCTCTCTCGGCGCGCGCTGGCCG 88

Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
Db 89 GCGCGCGTCGCGACCGCGCGCGCGCGCTCTCAGCGCGCTCGCGCGCGCG 145

RESULT 8

US-09-345-214-5

Sequence 5, Application US/09345214

Patent No. 6392120

GENERAL INFORMATION:

APPLICANT: Broglie, Jonathan E.

TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE

FILE REFERENCE: BB-1147

CURRENT APPLICATION NUMBER: US/09/345,214

CURRENT FILING DATE: 1999-06-30

EARLIER APPLICATION NUMBER: 060/094,436

EARLIER FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Microsoft Office 97

SEQ ID NO 5

LENGTH: 2491

TYPE: DNA

ORGANISM: Zea mays

US-09-345-214-5

Alignment Scores:

Pred. No.: 3-55e-14 Length: 2491

Score: 191.00 Matches: 38

Percent Similarity: 97.4% Conservative: 0

Best Local Similarity: 97.4% Mismatches: 1

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-345-214-5 (1-2491)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTTPPro 20  
Db 145 ATGGCGACGCCCTCGGCGCGGCGCGCTCTCTCTCGGCGCGCGCTGGCCG 204

Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
Db 205 GCGCGCGTCGCGACCGCGCGCGCGCTCTCAGCGCGCTCGCGCGCGCG 261

RESULT 9

US-09-743-980-5

Sequence 5, Application US/09743980

Patent No. 6570008

GENERAL INFORMATION:

APPLICANT: E. I. du Pont de Nemours and Company

TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE

FILE REFERENCE: BB-1147-A

CURRENT APPLICATION NUMBER: US/09/743,980

CURRENT FILING DATE: 2001-05-14

PRIOR APPLICATION NUMBER: 060/094,436

PRIOR FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Microsoft Office 97

SEQ ID NO 5

LENGTH: 2491

TYPE: DNA

ORGANISM: Zea mays

US-09-743-980-5

Alignment Scores:

Pred. No.: 3-55e-14 Length: 2491

Score: 191.00 Matches: 38

Percent Similarity: 97.4% Conservative: 0

Best Local Similarity: 97.4% Mismatches: 1

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-743-980-5 (1-2491)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTTPPro 20  
Db 145 ATGGCGACGCCCTCGGCGCGGCGCGCTCTCTCTCGGCGCGCGCTGGCCG 204

Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
Db 205 GCGCGCGTCGCGACCGCGCGCGCGCTCTCAGCGCGCTCGCGCGCGCG 261

RESULT 10

US-08-572-951-1

Sequence 1, Application US/08572951

Patent No. 5824790

GENERAL INFORMATION:

APPLICANT: KESLING, PETER L.

APPLICANT: KNIGHT, MARY E.

APPLICANT: GUAN, HANPING

TITLE OF INVENTION: MODIFICATION OF STARCH

TITLE OF INVENTION: SYNTHESIS IN PLANTS

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DABBY & CUSHMAN

ADDRESSEE: Intellectual Property Group of

ADDRESSEE: Pillsbury Madison & Sutro LLP

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/572,951

FILING DATE: 15-DEC-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/263,921

FILING DATE: 21-JUN-1994

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Paul N. Kokulis

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 222957/1.02.15C

TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2990 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-572-951-1

Alignment Scores:

Pred. No.: 2.89e-11 Length: 2990

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Score: 168.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 88.0% Indels: 1
DB: 2 Gaps: 0

US-10-628-525A-37 (1-39) x US-08-572-951-1 (1-2990)

QY 1 MetaAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
Db 602 ARGGGAGCCCTCGGCGCGTGGCGCGCGGTGCTCTCTCGCGGGGC-GCCTGGCGG 660
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 661 GCCGCGTGGCGAGCGCGCGCGCGCGGAGGCTCCAGCGGTGCTGCGCGCGG 717

RESULT 11
US-10-200-012-7
; Sequence 7, Application US/10200012
; Patent No. 6955905
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: PR/SET- Domain Containing Nucleic Acids,
; FILE OF INVENTION: Polypeptides, Antibodies and Methods of Use
; FILE REFERENCE: P-LJ 5301
; CURRENT APPLICATION NUMBER: US/10/200,012
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 09/910,478
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)...(1161)
US-10-200-012-7

Alignment Scores:
Pred. No.: 42.1 Length: 1437
Score: 66.00 Matches: 19
Percent Similarity: 55.3% Conservative: 2
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 34.6% Indels: 0
DB: 3 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-200-012-7 (1-1437)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAla 21
Db 1023 CGGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 1082
QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 1083 CGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1136

RESULT 12
US-10-108-915-9/c
; Sequence 9, Application US/10108915
; Patent No. 6855868
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Shen, Jennie
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases
; FILE REFERENCE: BB1286 US NA
; CURRENT APPLICATION NUMBER: US/10/108,915
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/452,238
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/110,592
```

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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Zea mays
US-10-108-915-9

Alignment Scores:
Pred. No.: 10.7 Length: 365
Score: 65.50 Matches: 16
Percent Similarity: 57.5% Conservative: 7
Best Local Similarity: 40.0% Mismatches: 12
Query Match: 34.3% Indels: 5
DB: 3 Gaps: 2

US-10-628-525A-37 (1-39) x US-10-108-915-9 (1-365)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAla 21
Db 132 GCATCACCACAAATCTTCAGTTCTGCCTGT-----GGCGGATATAGTTGGCCAA 82
QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArg-----ValLeuArgArg 39
Db 81 GCACACAGGGGTGCTGCCTTCTCTGTCGACCAAGCGAGCTGCTCTGTGCTGACAGA 22

RESULT 13
US-08-891-254-8
; Sequence 8, Application US/08891254
; Patent No. 5776889
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Beer, Steven V.
; TITLE OF INVENTION: Hypersensitive Response
; TITLE OF INVENTION: Induced Resistance In Plants
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,254
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,775
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 14603/10050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1035 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-891-254-8

Alignment Scores:
```

```
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: 2 Gaps: 1

US-10-628-525A-37 (1-39) x US-08-891-254-8 (1-1035)

QY 15 AlaArg***AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgLe 32
Db 464 GCCAGGGCGCCTGGCGGAAGCGCTGCAGGAGATCGAGCAGATCCTCGCCCGAGCTCGGCG 523

QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 14
US-08-819-539-8
; Sequence 8, Application US/08819539
; Patent No. 5859324
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Beer, Steven V.
; TITLE OF INVENTION: Hypersensitive Response
; TITLE OF INVENTION: Induced Resistance In Plants
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,539
; FILING DATE: 17-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/475,775
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 14603/10050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 1035 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-819-539-8

Alignment Scores:
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: 2 Gaps: 1

US-10-628-525A-37 (1-39) x US-08-819-539-8 (1-1035)

QY 15 AlaArg***AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgLe 32
Db 464 GCCAGGGCGCCTGGCGGAAGCGCTGCAGGAGATCGAGCAGATCCTCGCCCGAGCTCGGCG 523

QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 15
US-09-030-270A-8
; Sequence 8, Application US/09030270A
; Patent No. 5977060
; GENERAL INFORMATION:
; APPLICANT: Zitter, Thomas A.
; APPLICANT: Wei, Zhong-Min
; TITLE OF INVENTION: INSECT CONTROL WITH A
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,270A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,226
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1521
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 1035 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-030-270A-8

Alignment Scores:
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: 2 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-030-270A-8 (1-1035)

QY 15 AlaArg***AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgLe 32
Db 464 GCCAGGGCGCCTGGCGGAAGCGCTGCAGGAGATCGAGCAGATCCTCGCCCGAGCTCGGCG 523

QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 16
US-08-984-207-8
; Sequence 8, Application US/08984207
```

Patent No. 6235974  
GENERAL INFORMATION:  
APPLICANT: Qiu, Dewen  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED  
IN PLANTS BY SEED TREATMENT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: P.O. Box 1051, Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984,207  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/033,230  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1201  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1035 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-984-207-8  
Alignment Scores:  
Pred. No.: 38.9 Length: 1035  
Score: 65.00 Matches: 17  
Percent Similarity: 67.9% Conservative: 2  
Best Local Similarity: 60.7% Mismatches: 6  
Query Match: 34.0% Indels: 3  
DB: 3 Gaps: 1

US-10-628-525A-37 (1-39) x US-08-984-207-8 (1-1035)

QY 15 AlaArg\*\*AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32  
Db 464 GCAGGGCGGCTGCGCGAAGCGCTGCAGGAGATCGAGCATCTCGCCAGCTCGGG 523  
QY 32 uGlnArgValLeuArgArgArg 39  
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 17

US-09-013-587-8  
Sequence 8, Application US/09013587  
Patent No. 6277814  
GENERAL INFORMATION:  
APPLICANT: Qiu, Dewen  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/013,587  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,048  
FILING DATE: 27-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1501  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1035 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-09-013-587-8  
Alignment Scores:  
Pred. No.: 38.9 Length: 1035  
Score: 65.00 Matches: 17  
Percent Similarity: 67.9% Conservative: 2  
Best Local Similarity: 60.7% Mismatches: 6  
Query Match: 34.0% Indels: 3  
DB: 3 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-013-587-8 (1-1035)

QY 15 AlaArg\*\*AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32  
Db 464 GCAGGGCGGCTGCGCGAAGCGCTGCAGGAGATCGAGCATCTCGCCAGCTCGGG 523  
QY 32 uGlnArgValLeuArgArgArg 39  
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 18

US-09-086-118-28  
Sequence 28, Application US/09086118  
Patent No. 6583107  
GENERAL INFORMATION:

APPLICANT: Laby, Ronald J.  
APPLICANT: Beer, Steven V.  
APPLICANT: Wei, Zhong-Min  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
FRAGMENTS ELICITING A HYPERSENSITIVE RESPONSE AND USES  
TITLE OF INVENTION: FRAGMENTS ELICITING A HYPERSENSITIVE RESPONSE AND USES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,118
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,109
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-086-118-28

Alignment Scores:
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-086-118-28 (1-1035)
QY 15 AlaArg**AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32
Db 464 GCCAGGGCGGCTGGCGGAGCGCTGCAGGAGATCGAGCAGATCTCTGCCCGAGCTCGGCG 523
QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 19
US-09-431-614-16
; Sequence 16, Application US/09431614
; Patent No. 6624139
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Schading, Richard L.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
; TITLE OF INVENTION: RESISTANCE
; FILE REFERENCE: 21829/41 (BEC-003)
; CURRENT APPLICATION NUMBER: US/09/431,614
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/107,243
; EARLIER FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Pseudomonas solanacearum
; US-09-431-614-16

Alignment Scores:
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-086-118-28 (1-1035)
QY 15 AlaArg**AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32
Db 464 GCCAGGGCGGCTGGCGGAGCGCTGCAGGAGATCGAGCAGATCTCTGCCCGAGCTCGGCG 523
QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 19
US-09-431-614-16
; Sequence 16, Application US/09431614
; Patent No. 6624139
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Schading, Richard L.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
; TITLE OF INVENTION: RESISTANCE
; FILE REFERENCE: 21829/41 (BEC-003)
; CURRENT APPLICATION NUMBER: US/09/431,614
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/107,243
; EARLIER FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Pseudomonas solanacearum
; US-09-431-614-16

Alignment Scores:
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-086-118-28 (1-1035)
QY 15 AlaArg**AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32
Db 464 GCCAGGGCGGCTGGCGGAGCGCTGCAGGAGATCGAGCAGATCTCTGCCCGAGCTCGGCG 523
QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 21
PCT-US96-08819-8
; Sequence 8, Application PC/TUS9608819
; GENERAL INFORMATION:
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED
; TITLE OF INVENTION: RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08819

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US-10-628-525A-37 (1-39) x US-09-431-614-16 (1-1035)
QY 15 AlaArg**AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32
Db 464 GCCAGGGCGGCTGGCGGAGCGCTGCAGGAGATCGAGCAGATCTCTGCCCGAGCTCGGCG 523
QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 20
US-09-412-100-36
; Sequence 36, Application US/09412100
; Patent No. 6858707
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Fan, Hao
; APPLICANT: Niggenmeyer, Jennifer L.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FRAGMENTS WHICH ARE
; TITLE OF INVENTION: ACTIVE BUT DO NOT ELICIT A HYPERSENSITIVE RESPONSE
; FILE REFERENCE: 21829/31 (BEC-002)
; CURRENT APPLICATION NUMBER: US/09/412,100
; CURRENT FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/103,050
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Pseudomonas solanacearum
; US-09-412-100-36

Alignment Scores:
Pred. No.: 38.9 Length: 1035
Score: 65.00 Matches: 17
Percent Similarity: 67.9% Conservative: 2
Best Local Similarity: 60.7% Mismatches: 6
Query Match: 34.0% Indels: 3
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-412-100-36 (1-1035)
QY 15 AlaArg**AlaTrpPro-AlaAlaValGlyAspArgAla-----ArgProArgArgle 32
Db 464 GCCAGGGCGGCTGGCGGAGCGCTGCAGGAGATCGAGCAGATCTCTGCCCGAGCTCGGCG 523
QY 32 uGlnArgValLeuArgArgArg 39
Db 524 GCGGCGGTGCTGCGCGCGCGG 545

RESULT 21
PCT-US96-08819-8
; Sequence 8, Application PC/TUS9608819
; GENERAL INFORMATION:
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED
; TITLE OF INVENTION: RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08819

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; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36063 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
; US-08-311-731A-140

Alignment Scores:
Pred. No.: 2,6e+03 Length: 36063
Score: 64.00 Matches: 12
Percent Similarity: 63.2% Conservative: 0
Best Local Similarity: 63.2% Mismatches: 7
Query Match: 33.5% Indels: 0
DB: Gaps: 0

US-10-628-525A-37 (1-39) x US-08-311-731A-140 (1-36063)

QY 7 valGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPProAlaAlaValGlyAsp 25
Db 13474 GTCGGTCAAGATGTTGGCTTCTGCTACGCCGAGCATGCGCTCGGTGTGTGTGAC 13418

RESULT 25
US-09-544-398B-10
; Sequence 10, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US 09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 8705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-10

Alignment Scores:
Pred. No.: 719 Length: 8705
Score: 63.00 Matches: 14
Percent Similarity: 58.1% Conservative: 4
Best Local Similarity: 45.2% Mismatches: 11
Query Match: 33.0% Indels: 1
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-544-398B-10 (1-8705)

QY 8 GlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPProAlaAlaValGlyAspArgAla 27
Db 13474 GTCGGTCAAGATGTTGGCTTCTGCTACGCCGAGCATGCGCTCGGTGTGTGAC 13418

RESULT 26
US-09-543-771B-10
; Sequence 10, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US 09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 8705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-10

Alignment Scores:
Pred. No.: 719 Length: 8705
Score: 63.00 Matches: 14
Percent Similarity: 58.1% Conservative: 4
Best Local Similarity: 45.2% Mismatches: 11
Query Match: 33.0% Indels: 1
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-543-771B-10 (1-8705)

QY 8 GlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPProAlaAlaValGlyAspArgAla 27
Db 7584 GGTGATGTGTGTGCTGTAGCCCCAGCTACTTTGGAGGCTGAGGTGGAGATCACTT 7643

RESULT 27
US-09-252-991A-3246
; Sequence 3246, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US 09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3246
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3246
```

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Db 7584 GGTGATGTGTGTGCTGTAGCCCCAGCTACTTTGGAGGCTGAGGTGGAGATCACTT 7643

QY 28 ArgProArg-----ArgLeuGlnArgValLeu 36
Db 7644 GAGCCCGAGGAGTGGAGGCTGCAGCGAGTCATG 7676

RESULT 26
US-09-543-771B-10
; Sequence 10, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US 09/543,771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 8705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-10

Alignment Scores:
Pred. No.: 719 Length: 8705
Score: 63.00 Matches: 14
Percent Similarity: 58.1% Conservative: 4
Best Local Similarity: 45.2% Mismatches: 11
Query Match: 33.0% Indels: 1
DB: Gaps: 1

US-10-628-525A-37 (1-39) x US-09-543-771B-10 (1-8705)

QY 8 GlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPProAlaAlaValGlyAspArgAla 27
Db 7584 GGTGATGTGTGTGCTGTAGCCCCAGCTACTTTGGAGGCTGAGGTGGAGATCACTT 7643

RESULT 27
US-09-252-991A-3246
; Sequence 3246, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US 09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3246
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3246
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Alignment Scores:
Pred. No.: 68.3 Length: 909
Score: 62.50 Matches: 15
Percent Similarity: 59.4% Conservative: 4
Best Local Similarity: 46.9% Mismatches: 12
Query Match: 32.7% Indels: 1
DB: 3 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-252-991A-3246 (1-909)
QY 4 ProSerAlaVal---GlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAlaAla 22
Db 207 CGGCGCCGAGTACCGGAGCGCTCTCCGACTGGTGGCGGATGCCCTTGGCGCTGGCTCC 266
QY 23 ValGlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 267 GCAGACCGTCTGGTGGACCTCGCGCCGCGCACCG 302

RESULT 28
US-09-902-540-6772/c
; Sequence 6772, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6772
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6772

Alignment Scores:
Pred. No.: 92.6 Length: 1197
Score: 62.50 Matches: 17
Percent Similarity: 58.6% Conservative: 0
Best Local Similarity: 58.6% Mismatches: 11
Query Match: 32.7% Indels: 1
DB: 3 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-902-540-6772 (1-1197)
QY 11 CysLeuLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAspArgAlaArgProArg 30
Db 697 TCGCTCGGCCAGCCGCGGACGCTGGCGGACGACGAGTGGCGCGGCTCGA---AGA 641
QY 31 ArgLeuGlnArgValLeuArgArgArg 39
Db 640 CGAGGTGCTCGTACACCTCGTCGGAGA 614

RESULT 29
US-09-252-991A-3322/c
; Sequence 3322, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3322
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3322

Alignment Scores:
Pred. No.: 163 Length: 1995
Score: 62.50 Matches: 15
Percent Similarity: 59.4% Conservative: 4
Best Local Similarity: 46.9% Mismatches: 12
Query Match: 32.7% Indels: 1
DB: 3 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-252-991A-3322 (1-1995)
QY 4 ProSerAlaVal---GlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAlaAla 22
Db 1891 CGGCGCCGAGTACCGGAGCGCTCTCCGACTGGTGGCGGATGCCCTTGGCGCTGGCTCC 1832
QY 23 ValGlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 1831 GCAGACCGTCTGGTGGACCTCGCGCCGCGCACCG 1796

RESULT 30
US-09-902-540-1051
; Sequence 1051, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1051
; LENGTH: 15271
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1051

Alignment Scores:
Pred. No.: 1.54e+03 Length: 15271
Score: 62.50 Matches: 17
Percent Similarity: 58.6% Conservative: 0
Best Local Similarity: 58.6% Mismatches: 11
Query Match: 32.7% Indels: 1
DB: 3 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-902-540-1051 (1-15271)
QY 11 CysLeuLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAspArgAlaArgProArg 30
Db 2949 TCGCTCGGCCAGCCGCGGACGCTGGCGGACGACGAGTGGCGCGGCTCGA---AGA 3005
QY 31 ArgLeuGlnArgValLeuArgArgArg 39
Db 3006 CGAGGTGCTCGTACACCTCGTCGGAGA 3032

Search completed: March 31, 2006, 23:22:30
Job time : 69.1578 secs
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445
; FILING DATE: 30-SEP-1997
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Not Relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..153
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-628-525-18
Alignment Scores:
Pred. No.: 2.5e-19 Length: 153
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
US-10-628-525A-37 (1-39) x US-10-628-525-18 (1-153)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPPro 20
Db 1 ATGGCGACGCGCCCTCGGCGCGCGCGCGCGCTCTCTCTCGCGCGCGCGCGCGCGCG 60
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 61 GCCGCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 117
RESULT 3
US-09-931-297-1
; Sequence 1, Application US/09931297
; Publication No. US20020088023A1
; GENERAL INFORMATION:
; APPLICANT: Jens Kossmann
; Claus Froberg
; TITLE OF INVENTION: Nucleic acid molecules encoding soluble
; starch synthases from maize
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/931,297
; FILING DATE: 16-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/192,909
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 196 19 918.2
; FILING DATE: 17-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley, Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: GFB-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-96-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2383 base pairs
; TYPE: nucleotide
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; TISSUE TYPE: endosperm
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..1950
; OTHER INFORMATION: /function= "starch synthesis"
; /product= "soluble starch synthase"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-931-297-1
Alignment Scores:
Pred. No.: 4.03e-18 Length: 2383
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-628-525A-37 (1-39) x US-09-931-297-1 (1-2383)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPPro 20
Db 29 ATGGCGACGCGCCCTCGGCGCGCGCGCGCGCTCTCTCTCGCGCGCGCGCGCGCG 88
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 89 GCCGCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 145
RESULT 4
US-10-109-048-1142
; Sequence 1142, Application US/10109048
; Publication No. US20040107461A1
; GENERAL INFORMATION:
; APPLICANT: COMMURI, PADMA
; APPLICANT: KEELING, PETER L.
; APPLICANT: RAMIREZ, NONA
; APPLICANT: MCKEAN, ANGELA
; APPLICANT: GAO ZHONG
; APPLICANT: GUAN, HANPING
; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS
; FILE REFERENCE: 2461-76
; CURRENT APPLICATION NUMBER: US/10/109,048
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/279,720
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 1154
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1142
; LENGTH: 2991
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
```



```
Db 349 ATGCCAGCCCTCCCAATCGATCCGATGCTTCATGATGGCAGGGCGTAGGCGGCG 230
Qy 18 -----AlaTTP----- 19
Db 289 GAGTCTTCTGCTGTCGCAACGCGAGGACGCGGGCGTGTGGATGCGCGGACGCGGCGG 230
Qy 20 -----ProAlaAlaValGlyAspArgAlaArgPro 29
Db 229 ATCCCTGCCCCCGCGCGTGGCGCGCGCGCGCGCGCG 191

RESULT 8
US-10-425-115-6595
; Sequence 6595, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 6595
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_106006C.1
US-10-425-115-6595

Alignment Scores:
Pred. No.: 0.229 Length: 307
Score: 72.00 Matches: 14
Percent Similarity: 78.9% Conservative: 1
Best Local Similarity: 73.7% Mismatches: 4
Query Match: 37.7% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-425-115-6595 (1-307)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTP 19
Db 211 TTGGTTACGCCCTCGTTCGAGGCTGCTCGGTCTCTCTCGCGGCTACGCTGG 267

RESULT 9
US-10-369-493-35694/c
; Sequence 35694, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35694
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35694

Alignment Scores:
Pred. No.: 1.68 Length: 1569
Score: 69.50 Matches: 19
Percent Similarity: 58.5% Conservative: 5
Best Local Similarity: 46.3% Mismatches: 14
Query Match: 36.4% Indels: 3
DB: 5 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-369-493-35694 (1-1569)

Qy 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPProAla 21
Db 134 AGCAGCCCTCGCGCGCCAGCGCTCGGCATTTCGGGTCTTCACCGGATGCGCGCA 75

RESULT 10
US-10-198-846-13012/c
; Sequence 13012, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; FILE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13012
; LENGTH: 1013
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997,
; LOCATION: 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007,
; LOCATION: 1008, 1009, 1010, 1011, 1012, 1013
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13012

Alignment Scores:
Pred. No.: 1.8 Length: 1013
Score: 69.50 Matches: 19
Percent Similarity: 58.5% Conservative: 5
Best Local Similarity: 46.3% Mismatches: 14
Query Match: 36.4% Indels: 3
DB: 5 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-198-846-13012 (1-1013)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg----- 17
Db 943 GTGGCGGGCGCGCGCGTGTGGGGGGCGCGCGCTTTTGGGGGGCGCGGTGGTGGCGGG 884

Qy 18 AlaTTPProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 883 TCTTGGCGGGCGCGCTGTGCTCTGCGCGCGCGCGCGGTCTTGAGGTTTGGGGTGGCGG 824

Qy 38 Arg 38
Db 823 CGC 821

RESULT 11
US-10-767-701-12477
; Sequence 12477, Application US/10767701
; Publication No. US20040172684A1
```

```
Score: 71.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 14
Query Match: 37.2% Indels: 2
DB: 6 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-369-493-35694 (1-1569)

Qy 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTTPProAla 21
Db 134 AGCAGCCCTCGCGCGCCAGCGCTCGGCATTTCGGGTCTTCACCGGATGCGCGCA 75

Qy 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38
Db 74 GCC-----GACAGGCAATCACCGCGCCACTGTGTCGACGTGATCAGGAGA 30

RESULT 10
US-10-198-846-13012/c
; Sequence 13012, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; FILE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13012
; LENGTH: 1013
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997,
; LOCATION: 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007,
; LOCATION: 1008, 1009, 1010, 1011, 1012, 1013
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13012

Alignment Scores:
Pred. No.: 1.8 Length: 1013
Score: 69.50 Matches: 19
Percent Similarity: 58.5% Conservative: 5
Best Local Similarity: 46.3% Mismatches: 14
Query Match: 36.4% Indels: 3
DB: 5 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-198-846-13012 (1-1013)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg----- 17
Db 943 GTGGCGGGCGCGCGCGTGTGGGGGGCGCGCGCTTTTGGGGGGCGCGGTGGTGGCGGG 884

Qy 18 AlaTTPProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 883 TCTTGGCGGGCGCGCTGTGCTCTGCGCGCGCGCGCGGTCTTGAGGTTTGGGGTGGCGG 824

Qy 38 Arg 38
Db 823 CGC 821

RESULT 11
US-10-767-701-12477
; Sequence 12477, Application US/10767701
; Publication No. US20040172684A1
```





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; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; NUMBER OF SEQ ID NOS: 2003-03-03
; SEQ ID NO 15113
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 15113
US-10-363-345A-15113

Alignment Scores:
Pred. No.: 3.24 Length: 778
Score: 67.00 Matches: 19
Percent Similarity: 55.3% Conservative: 2
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 35.1% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-363-345A-15113 (1-778)
QY 2 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 21
Db 310 GCGACACCGACCGCCACACCGCGCTACAAACACACTCGCCCGCGCTACCGCCCGCGCA 251
QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39
Db 250 CGCGCAGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 197

RESULT 15
US-10-363-345A-15114
; Sequence 15114, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; NUMBER OF SEQ ID NOS: 2003-03-03
; SEQ ID NO 15114
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 15114
US-10-363-345A-15114

Alignment Scores:
Pred. No.: 3.24 Length: 778
Score: 67.00 Matches: 19
Percent Similarity: 55.3% Conservative: 2
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 35.1% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-363-345A-15114 (1-778)
QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db 469 GCGACACCGACCGCCACACCGCGCTACAAACACACTCGCCCGCGCTACCGCCCGCGCA 528

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QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39
Db 529 CGCGCAGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 582

RESULT 16
US-10-363-483A-15113/c
; Sequence 15113, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 15113
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 15113
US-10-363-483A-15113

Alignment Scores:
Pred. No.: 3.24 Length: 778
Score: 67.00 Matches: 19
Percent Similarity: 55.3% Conservative: 2
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 35.1% Indels: 0
DB: 9 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-363-483A-15113 (1-778)
QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db 310 GCGACACCGACCGCCACACCGCGCTACAAACACACTCGCCCGCGCTACCGCCCGCGCA 251
QY 22 AlaValGlyAspArgAlaArgProArgLeuGlnArgValLeuArgArgArg 39
Db 250 CGCGCAGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 197

RESULT 17
US-10-363-483A-15114
; Sequence 15114, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 15114
; LENGTH: 778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 15114
US-10-363-483A-15114

Alignment Scores:
Pred. No.: 3.24 Length: 778
Score: 67.00 Matches: 19
Percent Similarity: 55.3% Conservative: 2

```



```
; ORGANISM: Oryza sativa
US-10-259-165-55

Alignment Scores:
Pred. No.: 4.76 Length: 960
Score: 66.50 Matches: 17
Percent Similarity: 50.0% Conservative: 1
Best Local Similarity: 47.2% Mismatches: 13
Query Match: 34.8% Indels: 5
DB: 6 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-259-165-55 (1-960)

Qy 3 ThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAla 22
Db 124 ACCCGGACAGCTTCTCGGCTGCTGC-----GCCACTTGGCCAGCGCG 80

Qy 23 ValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38
Db 79 ACACCATCGCGGCTCGTCCAGCCGAGGCCAGCCCTGAGAAGG 32

RESULT 21
US-10-259-165-289/c
; Sequence 289, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, FumiYaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR FILING DATE: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 289
; LENGTH: 1011
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-289

Alignment Scores:
Pred. No.: 5.02 Length: 1011
Score: 66.50 Matches: 17
Percent Similarity: 50.0% Conservative: 1
Best Local Similarity: 47.2% Mismatches: 13
Query Match: 34.8% Indels: 5
DB: 6 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-259-165-289 (1-1011)

Qy 3 ThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAla 22
Db 124 ACCCGGACAGCTTCTCGGCTGCTGC-----GCCACTTGGCCAGCGCG 80

Qy 23 ValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38
Db 79 ACACCATCGCGGCTCGTCCAGCCGAGGCCAGCCCTGAGAAGG 32
```

## RESULT 22

```
US-10-739-930-4312/c
; Sequence 4312, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 4312
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAB-23APR03-CLUSTER19701_2
US-10-739-930-4312

Alignment Scores:
Pred. No.: 5.02 Length: 1012
Score: 66.50 Matches: 19
Percent Similarity: 52.6% Conservative: 1
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 34.8% Indels: 1
DB: 8 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-739-930-4312 (1-1012)

Qy 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAla 21
Db 557 GCGCGCCTCGAGCGCTCTTGGGGTGCCCGCGACGGCTCGCACTCGAACC 498

Qy 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
Db 497 GACGACGAGCGCGC---CGCGCGCGCGGGGACGACGACGCGGGAAGA 447
```

## RESULT 23

```
US-10-132-134-37
; Sequence 37, Application US/10132134
; Publication No. US20030171562A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Yang, Xianshu
; APPLICANT: Staffa, Alfredo
; APPLICANT: Zazopoulos, Emmanuel
; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES
; FILE REFERENCE: 3012-2US
; CURRENT APPLICATION NUMBER: US/10/132,134
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 6297
; TYPE: DNA
; ORGANISM: Streptomyces amphibiosporus
US-10-132-134-37

Alignment Scores:
Pred. No.: 32 Length: 6297
Score: 66.50 Matches: 19
Percent Similarity: 58.3% Conservative: 2
Best Local Similarity: 52.8% Mismatches: 10
Query Match: 34.8% Indels: 5
DB: 6 Gaps: 2

US-10-628-525A-37 (1-39) x US-10-132-134-37 (1-6297)

Qy 4 ProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAlaVal 23
Db 2704 CCGACGCTCCCGGTCGCCCTGTCTGGAGCTGGTCCGCGGCTGGACCCACGCC 2760
```



```
; TYPE: DNA
; ORGANISM: Zea mays
US-11-032-643-9

Alignment Scores:
Pred. No.: 2.52 Length: 365
Score: 65.50 Matches: 16
Percent Similarity: 57.5% Conservative: 7
Best Local Similarity: 40.0% Mismatches: 12
Query Match: 34.3% Indels: 5
DB: 10 Gaps: 2

US-10-628-525A-37 (1-39) x US-11-032-643-9 (1-365)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db 132 GCATCACCACAAATCTTCAGTTCTGCTGT-----GGGCGATATAGTTGCCAAGT 82

QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArg-----ValLeuArgArgArg 39
Db 81 GCAACAGGGGTGCTGCTTCTCTCTGTCGAAGCAAGCGAGCTGCTCTGTGTCGTACAGA 22

RESULT 28
US-11-032-490-9/c
; Sequence 9, Application US/11032490
; Publication No. US20050160489A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Shen, Jennie
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: Geranyl Pyrophosphate Synthases
; FILE REFERENCE: BB1286 US NA
; CURRENT APPLICATION NUMBER: US/11/032,490
; PRIOR FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/110,592
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Zea mays
US-11-032-490-9

Alignment Scores:
Pred. No.: 2.52 Length: 365
Score: 65.50 Matches: 16
Percent Similarity: 57.5% Conservative: 7
Best Local Similarity: 40.0% Mismatches: 12
Query Match: 34.3% Indels: 5
DB: 10 Gaps: 2

US-10-628-525A-37 (1-39) x US-11-032-490-9 (1-365)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
Db 132 GCATCACCACAAATCTTCAGTTCTGCTGT-----GGGCGATATAGTTGCCAAGT 82

QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArg-----ValLeuArgArgArg 39
Db 81 GCAACAGGGGTGCTGCTTCTCTCTGTCGAAGCAAGCGAGCTGCTCTGTGTCGTACAGA 22

RESULT 29
US-10-425-114-16430
; Sequence 16430, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingsong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
```

```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 16430
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-037-D11_FLI
US-10-425-114-16430

Alignment Scores:
Pred. No.: 5.68 Length: 815
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 7 Gaps: 3

US-10-628-525A-37 (1-39) x US-10-425-114-16430 (1-815)

QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTrp 19
Db 202 GCGACCCCTGCGCGCGCGGTTTCGAGACGAACGTGT-----CCAGGAGCGTGG 249

QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 250 CCGGCGCGAGCGGTGGAGGTGTGTCGCGCACTTCGCGCGCTCCAGGAGACGCTCAAGG 309

QY 35 ValLeuArgArgArg 39
Db 310 CGGAGCGCGACGACGG 324

RESULT 30
US-10-425-115-134772
; Sequence 134772, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 134772
; LENGTH: 1232
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_54396C.1
US-10-425-115-134772

Alignment Scores:
Pred. No.: 8.63 Length: 1232
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-10-425-115-134772 (1-1232)

QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTrp 19
Db 458 GCGACCCCTGCGCGCGGTTTCGAGACGAACGTGT-----CCAGGAGCGTGG 505
```

Qy	20	ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg	34
Db	506	CGGCGCGACGCTGGAGGTGTGCGGCACTTCGGCGGCTCCAAGGAGACGCTCAAGG	565
Qy	35	ValLeuArgArgArg	39
Db	566	CGGAGCGGACGACGG	580

Search completed: April 2, 2006, 02:06:06  
Job time : 202.256 secs

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2006, 01:09:48 ; Search time 121.78 Seconds  
(without alignments)  
1278.753 Million cell updates/sec

Title: US-10-628-525a-37

Perfect score: 191

Sequence: 1 MATPSAVGACLLARXWPAVGDRAFRRLQRLVLR 39

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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-Q=/abs/ABSSWEB spool/US10628525/runat\_31032006\_095139\_17270/app\_query.fasta.1  
-DB=Published Applications NA.New -OPMT=fastap -SUPPIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=150 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=0 -MODES=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abs05h  
-USER=US10628525 @CGN 1.1 2249 @runat\_31032006\_095139\_17270 -NCPU=6 -ICPU=3  
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.New:

1: /SID55/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
2: /SID55/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /SID55/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /SID55/ptodata/2/pubpna/PTC\_NEW\_PUB.seq.\*  
5: /SID55/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /SID55/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
7: /SID55/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
8: /SID55/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
9: /SID55/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
10: /SID55/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
11: /SID55/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
12: /SID55/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
13: /SID55/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
14: /SID55/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
15: /SID55/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	100.0	2970	11	US-11-096-568A-26590
2	67	35.1	495	6	US-09-925-065A-774283
C					Sequence 26590, A

67	35.1	495	6	US-09-925-065A-837264	Sequence 837264, A
67	35.1	1958	11	US-11-096-568A-265982	Sequence 265982, A
66	34.6	1437	14	US-11-121-438-7	Sequence 7, Appl1
6	33.5	3954	8	US-10-750-185-42605	Sequence 42605, A
64	33.5	3954	8	US-10-750-185-42605	Sequence 42605, A
62	32.5	1201	8	US-10-995-561-31039	Sequence 31039, A
62	32.5	1258	11	US-11-096-568A-11773	Sequence 11773, A
62	32.5	103660	8	US-10-995-561-13253	Sequence 13253, A
61.5	32.2	2073	11	US-11-096-568A-11714	Sequence 11714, A
61	31.9	201	8	US-10-995-561-31046	Sequence 31046, A
60	31.4	1191	8	US-10-750-185-34977	Sequence 34977, A
60	31.4	1191	8	US-10-750-185-34977	Sequence 34977, A
60	31.4	1268	14	US-11-037-243-23	Sequence 23, Appl1
59.5	31.2	1930	11	US-11-077-619-87	Sequence 87, Appl1
59	30.9	508	6	US-09-925-065A-371296	Sequence 371296, A
59	30.9	523	10	US-10-301-480-441295	Sequence 441295, A
59	30.9	523	10	US-10-301-480-1054704	Sequence 1054704, A
59	30.9	673	9	US-10-301-480-39100	Sequence 39100, A
59	30.9	673	10	US-10-301-480-652509	Sequence 652509, A
59	30.9	800	6	US-09-925-065A-39710	Sequence 39710, A
59	30.9	800	9	US-10-301-480-140948	Sequence 140948, A
59	30.9	800	10	US-10-301-480-754357	Sequence 754357, A
59	30.9	962	11	US-11-096-568A-15852	Sequence 15852, A
59	30.9	1841	11	US-11-096-568A-20625	Sequence 20625, A
58.5	30.6	981	11	US-11-096-568A-9238	Sequence 9238, App
58.5	30.6	5189	14	US-11-000-688-884	Sequence 884, App
58	30.4	529	10	US-10-301-480-362244	Sequence 362244, A
58	30.4	529	10	US-10-301-480-975653	Sequence 975653, A
58	30.4	539	6	US-09-925-065A-285243	Sequence 285243, A
58	30.4	591	6	US-09-925-065A-563303	Sequence 563303, A
58	30.4	615	6	US-09-925-065A-800272	Sequence 800272, A
58	30.4	671	6	US-09-925-065A-694569	Sequence 694569, A
58	30.4	712	6	US-09-925-065A-694570	Sequence 694570, A
58	30.4	712	14	US-11-108-172-354	Sequence 354, App
58	30.4	903	10	US-10-301-480-576910	Sequence 576910, A
58	30.4	903	10	US-10-301-480-1190319	Sequence 1190319, A
58	30.4	1064	9	US-10-301-480-28301	Sequence 28301, A
58	30.4	1064	10	US-10-301-480-641710	Sequence 641710, A
58	30.4	2898	14	US-11-000-463-141	Sequence 141, App
58	30.4	2898	14	US-11-000-463-613	Sequence 613, App
58	30.4	3851	14	US-11-090-739-119	Sequence 119, App
58	30.4	4104	14	US-11-154-227-94	Sequence 154, App
58	30.4	4650	14	US-11-154-227-102	Sequence 102, App
58	30.4	138627	9	US-10-330-773-159	Sequence 159, App
58	30.4	151169	14	US-11-121-086-38	Sequence 38, Appl
57.5	30.1	2894	14	US-11-128-061-742	Sequence 742, App
57.5	30.1	2894	14	US-11-128-049-742	Sequence 742, App
57.5	30.1	4358	8	US-10-750-185-60148	Sequence 60148, A
57.5	30.1	4358	8	US-10-750-623-60148	Sequence 60148, A
57.5	30.1	4358	6	US-09-925-065A-700432	Sequence 700432, A
57	29.8	404	6	US-09-925-065A-700432	Sequence 700432, A
57	29.8	404	6	US-09-925-065A-700432	Sequence 700432, A
57	29.8	919	10	US-10-301-480-560937	Sequence 560937, A
57	29.8	919	10	US-10-301-480-117436	Sequence 117436, A
57	29.8	16382	14	US-11-108-172-1112	Sequence 1112, App
57	29.8	16382	14	US-11-000-688-239	Sequence 239, App
57	29.8	90120	9	US-10-330-773-390	Sequence 390, App
56.5	29.6	539	6	US-09-925-065A-570109	Sequence 570109, A
56.5	29.6	539	6	US-09-925-065A-168746	Sequence 168746, A
56.5	29.6	959	10	US-10-301-480-543371	Sequence 543371, A
56.5	29.6	959	10	US-10-301-480-1156780	Sequence 1156780, A
56.5	29.6	1258	11	US-11-096-568A-20425	Sequence 20425, A
56.5	29.6	1720	11	US-11-096-568A-12769	Sequence 12769, A
56	29.3	512	14	US-11-000-688-599	Sequence 599, App
56	29.3	512	14	US-11-000-688-599	Sequence 599, App
56	29.3	516	6	US-09-925-065A-728639	Sequence 728639, A
56	29.3	523	6	US-09-925-065A-807927	Sequence 807927, A
56	29.3	525	6	US-09-925-065A-786401	Sequence 786401, A
56	29.3	538	6	US-09-925-065A-636233	Sequence 636233, A
56	29.3	551	14	US-11-181-587-23	Sequence 23, Appl1
56	29.3	557	6	US-09-925-065A-530374	Sequence 530374, A
56	29.3	570	6	US-09-925-065A-321873	Sequence 321873, A
56	29.3	570	6	US-09-925-065A-321874	Sequence 321874, A
56	29.3	572	10	US-10-301-480-396441	Sequence 396441, A
56	29.3	572	10	US-10-301-480-396442	Sequence 396442, A





US-09-925-065A-774283

**Alignment Scores:**

Pred. No.:	52.2	Length:	495
Score:	67.0%	Matches:	18
Percent Similarity:	51.1%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	14
Query Match:	35.1%	Indels:	8
DB:	6	Gaps:	2

US-10-628-525A-37 (1-39) x US-09-925-065A-774283 (1-495)

[illegible]

## RESULT 3

```

US-09-925-065A-837264/c
; Sequence 837264, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 837264
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-837264

```

**Alignment Scores:**

Pred. No.:	52.2	Length:	495
Score:	67.00	Matches:	18
Percent Similarity:	51.1%	Conservative:	5
Best Local Similarity:	40.0%	Mismatches:	14
Query Match:	35.1%	Indels:	8
DB:	6	Gaps:	2

US-10-628-525A-37 (1-39) x US-09-925-065A-837264 (1-495)

QY 3 ThrProSerAlaValGlyAlaAlaCys-----LeuLeuLeuAla 15  
 ::::|  
 Db 311 TCCCCACGTCCTGTGTGGCGTGCATGTCCCAAGCCTCCAAGGGCCCCACCCCTCACAGGC 252  
 ::::|  
 QY 16 Arg\*\*\*AlaTProAlaAlaVal---GlyAspArgAlaArgProArgArgLeuGlnArg 34  
 ::::|  
 Db 251 AGAGTGCTGTGGCCCCACAGCCCTCAGTGGGAGCGTGGGCGCCAGGGATCTGAGGTTTC 192  
 ::::|  
 QY 35 ValLeuArgArgArg 39  
 ::::|

Db 191 ACTGGAGAGACGT 177

## RESULT 4

```

US-11-096-568A-26982
; Sequence 26982, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fr
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26982
; LENGTH: 1958
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1958)
; OTHER INFORMATION: Ceres Seq. ID no. 13636500
US-11-096-568A-26982

```

**Alignment Scores:**

Pred. No.:	191	Length:	1958
Score:	67.00	Matches:	22
Percent Similarity:	51.1%	Conservative:	1
Best Local Similarity:	48.9%	Mismatches:	10
Query Match:	35.1%	Indels:	12
DB:	11	Gaps:	2

US-10-628-525A-37 (1-39) x US-11-096-568A-26982 (1-1958)

Qy	6	AlaValGlyAlaAlaCysLeu	-----LeuLeuAla 15
Db	472	GCTGCAGGGCGTCTGCTCTTACCACGCTCTCCCTCGGCGCTGCGCTCCGACTCTCGAGCTCCTGGCC	531
Qy	16	Arg***AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgArgLeuGln	33
Db	532	CGGGCGTCCACCCACACGCTGTCCGCGAGGAGTGGAGCTCGCCCCCGCCGCCGCCGC	591
Qy	34	ArgValLeuArgArg	38
Db	592	CGGCATCGCGTGG	606

## RESULT 5

```

US-11-121-438-7
; Sequence 7, Application US/1121438
; Publication No. US20060014173A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: PR/SET- Domain Containing Nucleic Acids,
; TITLE OF INVENTION: Polypeptides, Antibodies and Methods of Use
; FILE REFERENCE: P-LJ 5301
; CURRENT APPLICATION NUMBER: US/11/121,438
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US/10/200,012
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 09/910,478
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)...(1161)
US-11-121-438-7

```

**Alignment Scores:**

```
Pred. No.: 188 Length: 1437
Score: 66.00 Matches: 19
Percent Similarity: 55.3% Conservatives: 2
Best Local Similarity: 50.0% Mismatches: 17
Query Match: 34.6% Indels: 0
DB: 14 Gaps: 0

US-10-628-525A-37 (1-39) x US-11-121-438-7 (1-1437)

QY 2 AlaThrProSerAlaValGlyAlaAalaCysLeuLeuLeuAlaArg***AlaTrpProAla 21
||| |||:|||||
Db 1023 GCGGACCGCGCGCCAGCAGCCGCTGCAGGCACACTGCGCGCGCTGCGCGCCGCA 1082
||| |||:|||||

QY 22 AlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
||| |||:|||||
Db 1083 CCGGACGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1136
||| |||:|||||

RESULT 6
US-10-750-185-42605
; Sequence 42605, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 42605
; LENGTH: 3954
; TYPE: DNA
; ORGANISM: Bovine 19866880645803
US-10-750-185-42605

Alignment Scores:
Pred. No.: 851 Length: 3954
Score: 64.00 Matches: 18
Percent Similarity: 52.4% Conservatives: 4
Best Local Similarity: 42.9% Mismatches: 12
Query Match: 33.5% Indels: 8
DB: 8 Gaps: 2

US-10-628-525A-37 (1-39) x US-10-750-185-42605 (1-3954)

QY 6 AlaValGlyAlaAalaCysLeuLeuLeuAlaArg-----***AlaTrp 19
||| |||:|||||
Db 3725 GCGCTGGAGCGGAGCCTTTGAGGTAGCCCGAGTACTGGCGGAAAGAGCTGCTGG 3784
||| |||:|||||

QY 20 ProAlaAlaValGlyAspArgAlaArgProArgArg-----LeuGlnArgValLeuArg 37
||| |||:|||||
Db 3785 CCAGCCCGGCGGAGGAGCAGATCTGCTCTGTCGCGGCGCCCTTCGCCCGCGCGCGC 3844
||| |||:|||||

QY 38 ArgArg 39
||| |||:|||||
Db 3845 AGCGCA 3850
||| |||:|||||

RESULT 8
US-10-995-561-31039/c
; Sequence 31039, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31039
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-31039

Alignment Scores:
Pred. No.: 89.7 Length: 201
Score: 62.00 Matches: 11
Percent Similarity: 58.3% Conservatives: 3
Best Local Similarity: 45.8% Mismatches: 10
Query Match: 32.5% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-995-561-31039 (1-201)

QY 11 CysLeuLeuLeuAlaAArg***AlaTrpProAlaAlaValGlyAspArgAlaArgProArg 30
||| |||:|||||
Db 150 TGTGCACTGGTAGTCCAGTACTTGGGAGGCGGAGGTGGGAGAAATCACYTGAGCTAGG 91
||| |||:|||||
```

QY 31 ArgLeuGlnArg 34  
| | | | | : : : : :  
Db 90 AGGTTGAGCGG 79

## RESULT 9

US-11-096-568A-11773  
; Sequence 11773, Application US/11096568A  
; Publication No. US20060048240A1

; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

; TITLE OF INVENTION: Therby

; FILE REFERENCE: 2750-1592PUS2

; CURRENT APPLICATION NUMBER: US/11/096,568A

; CURRENT FILING DATE: 2005-04-01

; NUMBER OF SEQ ID NOS: 34471

; SEQ ID NO 11773

; LENGTH: 1258

; TYPE: DNA

; ORGANISM: Triticum aestivum

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(1258)

; OTHER INFORMATION: Ceres Seq. ID no. 13656983

US-11-096-568A-11773

## Alignment Scores:

Pred. No.:	505	Length:	1258
Score:	62.00	Matches:	21
Percent Similarity:	62.2%	Conservative:	2
Best Local Similarity:	56.8%	Mismatches:	8
Query Match:	32.5%	Indels:	6
DB:	11	Gaps:	2

US-10-628-525A-37 (1-39) x US-11-096-568A-11773 (1-1258)

QY 8 GlyAlaAlaCysLeuLeuAlaArg-----\*\*\*AlaTrpProAlaAla 22

Db 280 GCGCGCGCGGATCTCTCCAGCGACTTCGCGCTGGAGCGCGCGCGCTCGCGCGC 339

QY 23 ValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39

Db 340 GTCGCGCGCGCGCGCGCGCGCGCGCTT---CGAGTTCTCGTGGCGAG 387

## RESULT 10

US-10-995-561-13253/c

; Sequence 13253, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13253

; LENGTH: 103660

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(103660)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-995-561-13253

## Alignment Scores:

Pred. No.:	3,22e+04	Length:	103660
Score:	62.00	Matches:	11
Percent Similarity:	58.3%	Conservative:	3

Best Local Similarity: 45.8%  
Query Match: 32.5%  
DB: 8  
Mismatches: 10  
Indels: 0  
Gaps: 0

US-10-628-525A-37 (1-39) x US-10-995-561-13253 (1-103660)

QY 11 CysLeuLeuAlaArg\*\*\*AlaTrpProAlaAlaValGlyAspArgAlaArgProArg 30

Db 44152 TGTGCACTGGTAGTCCAGCTACTTGGAGCGCGAGTGGAGAGATCACTGAGCCAGG 44093

QY 31 ArgLeuGlnArg 34

Db 44092 AGGTTGAGCGG 44081

## RESULT 11

US-11-096-568A-11714

; Sequence 11714, Application US/11096568A

; Publication No. US20060048240A1

; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nikolai et al.

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

; TITLE OF INVENTION: Therby

; FILE REFERENCE: 2750-1592PUS2

; CURRENT APPLICATION NUMBER: US/11/096,568A

; CURRENT FILING DATE: 2005-04-01

; NUMBER OF SEQ ID NOS: 34471

; SEQ ID NO 11714

; LENGTH: 2073

; TYPE: DNA

; ORGANISM: Triticum aestivum

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(2073)

; OTHER INFORMATION: Ceres Seq. ID no. 13656435

US-11-096-568A-11714

## Alignment Scores:

Pred. No.:	929	Length:	2073
Score:	61.50	Matches:	20
Percent Similarity:	63.6%	Conservative:	1
Best Local Similarity:	60.6%	Mismatches:	5
Query Match:	32.2%	Indels:	7
DB:	11	Gaps:	1

US-10-628-525A-37 (1-39) x US-11-096-568A-11714 (1-2073)

QY 7 ValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpProAlaAlaValGlyAsp--A 26

Db 564 GTTGGCGCGCACTGGCGCTGGCGCTCAGG-----CGCGCGCGCGCGC 608

QY 26 ArgAlaArgProArgArgLeuGlnArgValLeuArg 37

Db 609 GTGCTCGGCTCGACAACTTCAACGGCTACTACGA 643

## RESULT 12

US-10-995-561-31046/c

; Sequence 31046, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 31046

; LENGTH: 201

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-995-561-31046

```

Alignment Scores:
Pred. No.: 118 Length: 201
Score: 61.00 Matches: 11
Percent Similarity: 58.3% Conservative: 3
Best Local Similarity: 45.8% Mismatches: 10
Query Match: 31.9% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-995-561-31046 (1-201)

QY 11 CysLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAspArgAlaArgProArg 30
    ||| |||:::
    ||| |||:::
    ||| |||:::
Db 157 TGTGCACTGGTAGTCCAGCTACTTGGGAGCGGAGGTGGGAGATCACTTGGAGCCKAG 98
    ||| |||:::
    ||| |||:::
    ||| |||:::
QY 31 ArgLeuGlnArg 34
    ||| |||:::
    ||| |||:::
    ||| |||:::
Db 97 AGTTGAGCGG 86
    ||| |||:::
    ||| |||:::
    ||| |||:::

RESULT 13
US-10-750-185-34977
; Sequence 34977, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34977
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Bovine 19866881212167
US-10-750-185-34977

Alignment Scores:
Pred. No.: 836 Length: 1191
Score: 60.00 Matches: 13
Percent Similarity: 51.9% Conservative: 1
Best Local Similarity: 48.1% Mismatches: 13
Query Match: 31.4% Indels: 0
DB: 8 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-750-185-34977 (1-1191)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAla 21
    ||| |||:::
    ||| |||:::
    ||| |||:::
Db 540 GCCGCTCGGTCTGCCGCGCGCGCGCGCGCTCCCGCCCTGCTCGATGGCCTCCA 599
    ||| |||:::
    ||| |||:::
    ||| |||:::
QY 22 AlaValGlyAspArgAlaArg 28
    ||| |||:::
    ||| |||:::
    ||| |||:::
Db 600 GCAGCTGGCAGCAGCAGCAG 620
    ||| |||:::
    ||| |||:::
    ||| |||:::

RESULT 14
US-10-750-623-34977
; Sequence 34977, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34977
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Bovine 19866881212167
US-10-750-623-34977

Alignment Scores:
Pred. No.: 1.53e+03 Length: 2268
Score: 60.00 Matches: 11
Percent Similarity: 59.1% Conservative: 2
Best Local Similarity: 50.0% Mismatches: 9
Query Match: 31.4% Indels: 0
DB: 14 Gaps: 0

US-10-628-525A-37 (1-39) x US-11-037-243-23 (1-2268)

QY 8 GlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAspArgAla 27
    ||| |||:::
    ||| |||:::
    ||| |||:::

```

```

Db 1201 GGTGCTGATGTCTCTCCACGTACAGAACGGGTTGGCTCCAGCGCTAGGCGGATCATGC 1142
Qy 28 ArgPro 29
Db 1141 CGGCCG 1136

RESULT 16
US-11-077-619-87/c
; Sequence 87, Application US/11077619
; Publication No. US20060040279A1
; GENERAL INFORMATION:
; APPLICANT: Feesche, Joerg
; APPLICANT: Maurer, Karl-Heinz
; APPLICANT: Breves, Roland
; APPLICANT: Schweder, Thomas
; APPLICANT: Hecker, Michael
; APPLICANT: Juergen, Britta
; APPLICANT: Voigt, Birgit
; TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
; FILE REFERENCE: HENK-0122 / H5692
; CURRENT APPLICATION NUMBER: US/11/077,619
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/009979
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: DE 10242433.0
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1930)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1730)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (201)..(203)
; OTHER INFORMATION: First codon translated as Met
US-11-077-619-87

Alignment Scores:
Pred. No.: 1.51e-03 Length: 1930
Score: 59.50 Matches: 14
Percent Similarity: 60.0% Conservative: 4
Best Local Similarity: 46.7% Mismatches: 11
Query Match: 31.2% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-37 (1-39) x US-11-077-619-87 (1-1930)
Qy 7 ValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAla----ValGlyAsp 25
Db 507 CTTTCGGCGTCTGCGCTTACTTGCAGAGTCCAGACCAAGAGTGAATTCGTGAC 448
Qy 26 ArgAlaArgProArgArgLeuGlnArgVal 35
Db 447 CGAGCGGACCCCGCGGATGTACGCCCTG 418

RESULT 17
US-09-925-065A-371296
; Sequence 371296, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1930)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1730)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (201)..(203)
; OTHER INFORMATION: First codon translated as Met
US-11-077-619-87

Alignment Scores:
Pred. No.: 1.51e-03 Length: 1930
Score: 59.50 Matches: 14
Percent Similarity: 60.0% Conservative: 4
Best Local Similarity: 46.7% Mismatches: 11
Query Match: 31.2% Indels: 1
DB: 1 Gaps: 1

US-10-628-525A-37 (1-39) x US-11-077-619-87 (1-1930)
Qy 7 ValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAla----ValGlyAsp 25
Db 507 CTTTCGGCGTCTGCGCTTACTTGCAGAGTCCAGACCAAGAGTGAATTCGTGAC 448
Qy 26 ArgAlaArgProArgArgLeuGlnArgVal 35
Db 447 CGAGCGGACCCCGCGGATGTACGCCCTG 418

RESULT 18
US-10-301-480-441295
; Sequence 441295, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 441295
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-441295

Alignment Scores:
Pred. No.: 509 Length: 523
Score: 59.00 Matches: 11
Percent Similarity: 58.3% Conservative: 3
Best Local Similarity: 45.8% Mismatches: 10
Query Match: 30.9% Indels: 0
DB: 1 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-301-480-441295 (1-523)
Qy 6 AlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAsp 25
Db 3 GCAC TAGCAATTAATGTTTAAATTTGTTCAAAATTTATTTGGCCAGAACGAGTAGGTGAC 62

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; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 371296
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-371296

Alignment Scores:
Pred. No.: 495 Length: 508
Score: 59.00 Matches: 11
Percent Similarity: 58.3% Conservative: 3
Best Local Similarity: 45.8% Mismatches: 10
Query Match: 30.9% Indels: 0
DB: 6 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-925-065A-371296 (1-508)
Qy 6 AlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAsp 25
Db 3 GCAC TAGCAATTAATGTTTAAATTTGTTCAAAATTTATTTGGCCAGAACGAGTAGGTGAC 62
Qy 26 ArgAlaArgPro 29
Db 63 ATGCCCCACCT 74

RESULT 18
US-10-301-480-441295
; Sequence 441295, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 441295
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-441295

Alignment Scores:
Pred. No.: 509 Length: 523
Score: 59.00 Matches: 11
Percent Similarity: 58.3% Conservative: 3
Best Local Similarity: 45.8% Mismatches: 10
Query Match: 30.9% Indels: 0
DB: 1 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-301-480-441295 (1-523)
Qy 6 AlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAlaValGlyAsp 25
Db 3 GCAC TAGCAATTAATGTTTAAATTTGTTCAAAATTTATTTGGCCAGAACGAGTAGGTGAC 62

```



```
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39710
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-39710

Alignment Scores:
Pred. No.: 759          Length: 800
Score: 59.00           Matches: 11
Percent Similarity: 53.8% Conservatives: 3
Best Local Similarity: 42.3% Mismatches: 12
Query Match: 30.9%      Indels: 0
DB: 6                  Gaps: 0

US-10-628-525A-37 (1-39) x US-09-925-065A-39710 (1-800)

QY 8 GlyAlaAaCysLeuLeuAlaArg**AlaTrpProAlaAlaValGlyAspArgAla 27
Db 583 GGTGTTGTATGTATGCCACTTGTGCCAGCTACCTGGGAGGCTGAAGTGGGAGGACTGCTT 524
QY 28 ArgProArgArgLeuGln 33
Db 523 AGCCCGAGAGGTTGAGG 506

RESULT 23
US-10-301-480-140948/c
; Sequence 140948, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US 60/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140948
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-140948

Alignment Scores:
Pred. No.: 759          Length: 800
Score: 59.00           Matches: 11
Percent Similarity: 53.8% Conservatives: 3
Best Local Similarity: 42.3% Mismatches: 12
Query Match: 30.9%      Indels: 0
DB: 9                  Gaps: 0

US-10-628-525A-37 (1-39) x US-10-301-480-140948 (1-800)

QY 8 GlyAlaAaCysLeuLeuAlaArg**AlaTrpProAlaAlaValGlyAspArgAla 27
Db 583 GGTGTTGTATGTATGCCACTTGTGCCAGCTACCTGGGAGGCTGAAGTGGGAGGACTGCTT 524
QY 28 ArgProArgArgLeuGln 33
Db 523 AGCCCGAGAGGTTGAGG 506

RESULT 24
US-10-301-480-754357/c
; Sequence 754357, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US 60/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140948
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-140948

Alignment Scores:
Pred. No.: 759          Length: 800
Score: 59.00           Matches: 11
Percent Similarity: 53.8% Conservatives: 3
Best Local Similarity: 42.3% Mismatches: 12
Query Match: 30.9%      Indels: 0
DB: 9                  Gaps: 0

US-10-628-525A-37 (1-39) x US-10-301-480-140948 (1-800)

QY 8 GlyAlaAaCysLeuLeuAlaArg**AlaTrpProAlaAlaValGlyAspArgAla 27
Db 583 GGTGTTGTATGTATGCCACTTGTGCCAGCTACCTGGGAGGCTGAAGTGGGAGGACTGCTT 524
QY 28 ArgProArgArgLeuGln 33
Db 523 AGCCCGAGAGGTTGAGG 506

RESULT 25
US-11-096-568A-15852
; Sequence 15852, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15852
; LENGTH: 962
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(962)
; OTHER INFORMATION: Ceres Seq. ID no. 12349152
US-11-096-568A-15852

Alignment Scores:
Pred. No.: 903          Length: 962
Score: 59.00           Matches: 19
Percent Similarity: 60.0% Conservatives: 2
Best Local Similarity: 54.3% Mismatches: 12
Query Match: 30.9%      Indels: 2
DB: 11                 Gaps: 1

US-10-628-525A-37 (1-39) x US-11-096-568A-15852 (1-962)

QY 5 SerAlaValGlyAlaAaCysLeuLeuAlaArg**AlaTrpProAlaAlaValGly 24
Db 306 GCTGAGTGGGCACTGTCAGCACTTCTTCGCCCGGGCCAGCC-----GCAGAGTACCG 359
```

```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 754357
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-754357

Alignment Scores:
Pred. No.: 759          Length: 800
Score: 59.00           Matches: 11
Percent Similarity: 53.8% Conservatives: 3
Best Local Similarity: 42.3% Mismatches: 12
Query Match: 30.9%      Indels: 0
DB: 10                 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-301-480-754357 (1-800)

QY 8 GlyAlaAaCysLeuLeuAlaArg**AlaTrpProAlaAlaValGlyAspArgAla 27
Db 583 GGTGTTGTATGTATGCCACTTGTGCCAGCTACCTGGGAGGCTGAAGTGGGAGGACTGCTT 524
QY 28 ArgProArgArgLeuGln 33
Db 523 AGCCCGAGAGGTTGAGG 506

RESULT 25
US-11-096-568A-15852
; Sequence 15852, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15852
; LENGTH: 962
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(962)
; OTHER INFORMATION: Ceres Seq. ID no. 12349152
US-11-096-568A-15852

Alignment Scores:
Pred. No.: 903          Length: 962
Score: 59.00           Matches: 19
Percent Similarity: 60.0% Conservatives: 2
Best Local Similarity: 54.3% Mismatches: 12
Query Match: 30.9%      Indels: 2
DB: 11                 Gaps: 1

US-10-628-525A-37 (1-39) x US-11-096-568A-15852 (1-962)

QY 5 SerAlaValGlyAlaAaCysLeuLeuAlaArg**AlaTrpProAlaAlaValGly 24
Db 306 GCTGAGTGGGCACTGTCAGCACTTCTTCGCCCGGGCCAGCC-----GCAGAGTACCG 359
```





Search completed: April 2, 2006, 02:03:49  
Job time : 131.78 secs

```
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 362244
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-362244

Alignment Scores:
Pred. No.:      679      Length:      529
Score:          58.00    Matches:      15
Percent Similarity: 51.5% Conservative: 2
Best Local Similarity: 45.5% Mismatches: 16
Query Match:      30.4% Indels:      0
DB:              10      Gaps:      0

US-10-628-525A-37 (1-39) x US-10-301-480-362244 (1-529)

QY      4 ProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAlaVal 23
      |||||:::|||||:::|||||:::|||||
Db      301 CCTCTGCGGTAGCGCGCGGTGCGGTATAGCCCTCCGCGGTGTGCAGCGCGGTGCTG 360

QY      24 GlyAspArgAlaArgProArgArgLeuGlnArgValLeu 36
      |||||:::|||||:::|||||
Db      361 GTTGTTCAGCGCGCGCGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 399

RESULT 30
US-10-301-480-975653
; Sequence 975653, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 975653
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-975653

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Score:          58.00    Matches:      15
Percent Similarity: 51.5% Conservative: 2
Best Local Similarity: 45.5% Mismatches: 16
Query Match:      30.4% Indels:      0
DB:              10      Gaps:      0

US-10-628-525A-37 (1-39) x US-10-301-480-975653 (1-529)

QY      4 ProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAlaAlaVal 23
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Db      301 CCTCTGCGGTAGCGCGCGGTGCGGTATAGCCCTCCGCGGTGTGCAGCGCGGTGCTG 360

QY      24 GlyAspArgAlaArgProArgArgLeuGlnArgValLeu 36
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Db      361 GTTGTTCAGCGCGCGCGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 399
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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 20:18:18 ; Search time 1066.11 Seconds  
(without alignments)  
2022.653 Million cell updates/sec

Title: US-10-628-525A-37

Perfect score: 191

Sequence: 1 MATPSAVGACLLARXANPAVGDRAFRRLQRLVLR 39

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Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	191	100.0	153	53	US-10-628-525A-18
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7	191	100.0	2008	74	US-60-094-436-12

Sequence 58, Appl  
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Sequence 11, Appl  
Sequence 12, Appl

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10	191	100.0	2971	42	US-10-109-048-1142	Sequence 1142, Ap	83	67	35.1	1971	51	US-10-425-114-1331	Sequence 1331, Ap
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75	67	35.1	778	50	US-10-363-483A-15113	Sequence 15113, A	C 148	65.5	34.3	852	31	US-09-708-427-70237	Sequence 70237, Ap
76	67	35.1	778	50	US-10-363-483A-15114	Sequence 15114, A	C 149	65.5	34.3	855	29	US-09-654-617-259710	Sequence 259710, A
77	67	35.1	1461	31	US-09-760-495-263	Sequence 263, App	C 150	65.5	34.3	855	29	US-09-654-617-259710	Sequence 259710, A
78	67	35.1	1461	42	US-10-143-775-263	Sequence 263, App	C 150	65.5	34.3	855	29	US-09-654-617-259710	Sequence 259710, A
79	67	35.1	1775	72	US-11-218-305-17942	Sequence 17942, A							
80	67	35.1	1958	69	US-11-096-568A-26982	Sequence 26982, A							

```
RESULT 1
US-09-402-254-58
; Sequence 58, Application US/09402254
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; FILE REFERENCE: 2461-52
; CURRENT APPLICATION NUMBER: US/09/402,254
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: PCT/US98/06660
; EARLIER FILING DATE: 1998-04-03
; EARLIER APPLICATION NUMBER: 60/042,939
; EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(153)
US-09-402-254-58
Alignment Scores:
Pred. No.: 5.06e-17 Length: 153
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 24

US-10-628-525A-37 (1-39) x US-09-402-254-58 (1-153)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
DB 1 ATGGCGACGCCCTCGGCGCGTGGCGCGCGTCTCTCTCTCGCGCGCGCGCTGGCGG 60
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
DB 61 GCCGCGCTCGCGACCGCGCGCGCGCGCGCGCTCCAGCGCGTCTCGCGCGCGCG 117

RESULT 2
US-09-625-406-18
; Sequence 18, Application US/09625406
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,406
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/941,445
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..153
US-09-625-406-18
Alignment Scores:
Pred. No.: 5.06e-17 Length: 153
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 28

US-10-628-525A-37 (1-39) x US-09-625-406-18 (1-153)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
DB 1 ATGGCGACGCCCTCGGCGCGTGGCGCGCGTCTCTCTCTCGCGCGCGCGCTGGCGG 60
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
DB 61 GCCGCGCTCGCGACCGCGCGCGCGCGCGCGCTCCAGCGCGTCTCGCGCGCGCG 117

RESULT 3
US-10-336-753-58
; Sequence 58, Application US/10336753
; GENERAL INFORMATION:
; APPLICANT: Guan, Hanping
; APPLICANT: Keeling, Peter L.
; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN
; FILE REFERENCE: 2461-52
; CURRENT APPLICATION NUMBER: US/10/336,753
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US/09/402,254
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/06660
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/042,939
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(153)
US-10-336-753-58
Alignment Scores:
Pred. No.: 5.06e-17 Length: 153
Score: 191.00 Matches: 38
Percent Similarity: 97.4% Conservative: 0
Best Local Similarity: 97.4% Mismatches: 1
Query Match: 100.0% Indels: 0
```



Alignment Scores:  
 Pred. No.: 9.78e-16 Length: 1415  
 Score: 191.00 Matches: 38  
 Percent Similarity: 97.4% Conservatives: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 100.0% Indels: 0  
 DB: 74 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-094-436-11 (1-1415)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
 Db 2 ATGGGAGCCCTCGGCGCGTGGGCGCGTGCCTCTCTCGGCGGGCGCGCTGGCCG 61  
 Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
 Db 62 GCCGCGTGGCGACCGCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGG 118

RESULT 7

US-60-094-436-12  
 ; Sequence 12, Application US/60094436  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lightner, Jonathan E.  
 ; APPLICANT: Broglie, Karen E.  
 ; APPLICANT: E. I. du Pont de Nemours and Company  
 ; TITLE OF INVENTION: Modification of Starch Biosynthetic Enzyme Gene  
 ; FILE REFERENCE: BB-1147-P1  
 ; CURRENT APPLICATION NUMBER: US/60/094,436  
 ; CURRENT FILING DATE: 1998-07-28  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Microsoft Word Version 7.0A  
 ; SEQ ID NO 12  
 ; LENGTH: 2008  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-60-094-436-12

Alignment Scores:  
 Pred. No.: 1.56e-15 Length: 2008  
 Score: 191.00 Matches: 38  
 Percent Similarity: 97.4% Conservatives: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 100.0% Indels: 0  
 DB: 74 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-094-436-12 (1-2008)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
 Db 2 ATGGGAGCCCTCGGCGCGTGGGCGCGTGCCTCTCTCGGCGGGCGCGCTGGCCG 61  
 Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
 Db 62 GCCGCGTGGCGACCGCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGG 118

RESULT 8

US-60-094-436-9  
 ; Sequence 9, Application US/60094436  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lightner, Jonathan E.  
 ; APPLICANT: Broglie, Karen E.  
 ; APPLICANT: E. I. du Pont de Nemours and Company  
 ; TITLE OF INVENTION: Modification of Starch Biosynthetic Enzyme Gene  
 ; FILE REFERENCE: BB-1147-P1  
 ; CURRENT APPLICATION NUMBER: US/60/094,436  
 ; CURRENT FILING DATE: 1998-07-28  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Microsoft Word Version 7.0A  
 ; SEQ ID NO 9  
 ; LENGTH: 2491

; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-60-094-436-9

Alignment Scores:  
 Pred. No.: 2.08e-15 Length: 2491  
 Score: 191.00 Matches: 38  
 Percent Similarity: 97.4% Conservatives: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 100.0% Indels: 0  
 DB: 74 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-094-436-9 (1-2491)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
 Db 145 ATGGGAGCCCTCGGCGCGTGGGCGCGTGCCTCTCTCGGCGGGCGCGCTGGCCG 204  
 Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
 Db 205 GCCGCGTGGCGACCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGG 261

RESULT 9

US-11-096-568A-26590  
 ; Sequence 26590, Application US/11096568A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nikolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096,568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO 26590  
 ; LENGTH: 2970  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays subsp. mays  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)-(2970)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 13579604  
 US-11-096-568A-26590

Alignment Scores:  
 Pred. No.: 2.62e-15 Length: 2970  
 Score: 191.00 Matches: 38  
 Percent Similarity: 97.4% Conservatives: 0  
 Best Local Similarity: 97.4% Mismatches: 1  
 Query Match: 100.0% Indels: 0  
 DB: 69 Gaps: 0

US-10-628-525A-37 (1-39) x US-11-096-568A-26590 (1-2970)

Qy 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
 Db 602 ATGGGAGCCCTCGGCGCGTGGGCGCGTGCCTCTCTCGGCGGGCGCGCTGGCCG 661  
 Qy 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
 Db 662 GCCGCGTGGCGACCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGG 718

RESULT 10

US-10-109-048-1142  
 ; Sequence 1142, Application US/10109048  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COMMURI, PADMA  
 ; APPLICANT: KEELING, PETER L.  
 ; APPLICANT: RAMIREZ, NONA  
 ; APPLICANT: MCKEAN, ANGELA  
 ; APPLICANT: GAO, ZHONG  
 ; APPLICANT: GUAN, HANPING  
 ; TITLE OF INVENTION: GLUCAN CHAIN LENGTH DOMAINS  
 ; FILE REFERENCE: 2461-76

1 CURRENT APPLICATION NUMBER: US/10/109,048  
2 CURRENT FILING DATE: 2003-03-04  
3 PRIOR APPLICATION NUMBER: 60/279,720  
4 PRIOR FILING DATE: 2001-03-30  
5 NUMBER OF SEQ ID NOS: 1154  
6 SOFTWARE: Patentin Ver. 2.1  
7 SEQ ID NO 1142  
8 LENGTH: 2991  
9 TYPE: DNA  
10 ORGANISM: Zea mays  
11 FEATURE:  
12 NAME/KEY: modified\_base  
13 LOCATION: (2709)  
14 OTHER INFORMATION: a, t, c, g, other or unknown  
15 US-10-109-048-1142

Alignment Scores:  
Pred. No.: 2,65e-15 Length: 2991  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 42 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-109-048-1142 (1-2991)

QY 1 MetaAlaThPrSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 602 ATGGCGACCCCTCGGCGCGTGGCGCGCGCTCTCTCGCGCGCGCCCTGGCGG 661  
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
Db 662 GCCGCGCTCGGCGACCGCGCGCGCGCGCTCCAGCGGTCTGCGCGCGCGG 718

## RESULT 11

US-10-425-115-54073/c  
1 Sequence 54073, Application US/10425115  
2 GENERAL INFORMATION:  
3 APPLICANT: La Rosa, Thomas J.  
4 APPLICANT: Kovalic, David K.  
5 APPLICANT: Zhou, Yihua  
6 APPLICANT: Cao, Yongwei  
7 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
8 FILE REFERENCE: 38-21(53222)B  
9 CURRENT APPLICATION NUMBER: US/10/425,115  
10 CURRENT FILING DATE: 2003-04-28  
11 NUMBER OF SEQ ID NOS: 369326  
12 SEQ ID NO 54073  
13 LENGTH: 3123  
14 TYPE: DNA  
15 ORGANISM: Zea mays  
16 FEATURE:  
17 NAME/KEY: unsure  
18 LOCATION: (1)..(3123)  
19 OTHER INFORMATION: unsure at all n locations  
20 FEATURE:  
21 OTHER INFORMATION: Clone ID: MRT4577\_149315C.1  
22 US-10-425-115-54073

Alignment Scores:  
Pred. No.: 2,81e-15 Length: 3123  
Score: 191.00 Matches: 38  
Percent Similarity: 97.4% Conservative: 0  
Best Local Similarity: 97.4% Mismatches: 1  
Query Match: 100.0% Indels: 0  
DB: 51 Gaps: 0

US-10-628-525A-37 (1-39) x US-10-425-115-54073 (1-3123)

QY 1 MetaAlaThPrSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 2390 ATGGCGACCCCTCGGCGCGTGGCGCGCGCTCTCTCTCGCGCGCGCCCTGGCGG 2331

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
Db 2330 GCCGCGCTCGGCGACCGCGCGCGCGCGCTCCAGCGGTCTGCGCGCGCGG 2274

## RESULT 12

US-09-077-564-1  
1 Sequence 1, Application US/09077564  
2 GENERAL INFORMATION:  
3 APPLICANT: Knight, Mary E.  
4 APPLICANT: Keeling, Peter L.  
5 TITLE OF INVENTION: Modification of Starch Synthesis in  
6 TITLE OF INVENTION: Plants  
7 NUMBER OF SEQUENCES: 32  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: ZENECA Ag Products  
10 STREET: 1800 Concord Pike  
11 CITY: Wilmington  
12 STATE: DE  
13 COUNTRY: USA  
14 ZIP: 19850  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: Floppy disk  
17 COMPUTER: IBM PC compatible  
18 OPERATING SYSTEM: PC-DOS/MS-DOS  
19 SOFTWARE: PatentIn Release #1.0, Version #1.25  
20 CURRENT APPLICATION DATA: US/09/077,564  
21 APPLICATION NUMBER: 04-DEC-1998  
22 FILING DATE: 14-DEC-1998  
23 CLASSIFICATION: 800  
24 PRIOR APPLICATION DATA:  
25 APPLICATION NUMBER: PCT/GB96/02990  
26 FILING DATE: 04-DEC-1996  
27 PRIOR APPLICATION DATA:  
28 APPLICATION NUMBER: GB 9524938.9  
29 FILING DATE: 06-DEC-1995  
30 ATTORNEY/AGENT INFORMATION:  
31 NAME: Hohenschutz, Liza D.  
32 REGISTRATION NUMBER: 33,712  
33 REFERENCE/DOCKET NUMBER: SEE 45052/UST  
34 TELECOMMUNICATION INFORMATION:  
35 TELEPHONE: (302) 886-1699  
36 INFORMATION FOR SEQ ID NO: 1:  
37 SEQUENCE CHARACTERISTICS:  
38 LENGTH: 2992 base pairs  
39 TYPE: nucleic acid  
40 STRANDEDNESS: single  
41 TOPOLOGY: unknown  
42 MOLECULE TYPE: cDNA  
43 IMMEDIATE SOURCE:  
44 CLONE: NUMBER 1  
45 US-09-077-564-1

Alignment Scores:  
Pred. No.: 3,68e-15 Length: 2992  
Score: 190.00 Matches: 39  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 99.5% Indels: 0  
DB: 20 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-077-564-1 (1-2992)

QY 1 MetaAlaThPrSerAlaValGlyAlaAlaCysLeuLeuAlaArg\*\*\*AlaTrpPro 20  
Db 602 ATGGCGACCCCTCGGCGCGTGGCGCGCGCTCTCTCTCGCGCGCGCCCTGGCGG 661  
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39  
Db 662 GCCGCGCTCGGCGACCGCGCGCGCGCGCTCCAGCGGTCTGCGCGCGCGG 718

## RESULT 13

US-09-619-643-9073





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RESULT 17
US-09-619-643-17333
; Sequence 17333, Application US/09619643
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; APPLICANT: Lalugudi, Raghunath V.
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51230)B
; CURRENT APPLICATION NUMBER: US/09/619,643
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 17333
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3151-012-Q1-K1-E9
US-09-619-643-17333

Alignment Scores:
Pred. No.: 3,01e-14 Length: 462
Score: 176.00 Matches: 35
Percent Similarity: 89.7% Conservative: 0
Best Local Similarity: 89.7% Mismatches: 4
Query Match: 92.1% Indels: 0
DB: 28 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-619-643-17333 (1-462)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
DB 69 ATGGCGACGCCCTCGGCGCGCGCGAGTGCCTCTCTCGCGCGCGCGCGCGCG 128
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
DB 129 GCCGCGTCTGGCGACCGCGCGCGCGCGCGCTCCAGCGGTGTGTCGCGCGCG 185

RESULT 18
US-60-145-148-845
; Sequence 845, Application US/60145148
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Deng, Molian
; APPLICANT: Fisher, Dane K.
; APPLICANT: Miller, Philip W.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51230)A
; CURRENT APPLICATION NUMBER: US/60/145,148
; CURRENT FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 3994
; SEQ ID NO 845
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-012-Q1-K1-E9
US-60-145-148-845

Alignment Scores:
Pred. No.: 3,01e-14 Length: 462
Score: 176.00 Matches: 35
Percent Similarity: 89.7% Conservative: 0
Best Local Similarity: 89.7% Mismatches: 4
Query Match: 92.1% Indels: 0
DB: 75 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-145-148-845 (1-462)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
DB 69 ATGGCGACGCCCTCGGCGCGCGCGCGAGTGCCTCTCTCTCGCGCGCGCGCGCG 128
```

```
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
DB 129 GCCGCGTCTGGCGACCGCGCGCGCGCGCTCCAGCGGTGTGTCGCGCGCG 185

RESULT 19
US-09-654-617-269739
; Sequence 269739, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 269739
; LENGTH: 1034
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION:
US-09-654-617-269739

Alignment Scores:
Pred. No.: 8,8e-14 Length: 1034
Score: 176.00 Matches: 35
Percent Similarity: 89.7% Conservative: 0
Best Local Similarity: 89.7% Mismatches: 4
Query Match: 92.1% Indels: 0
DB: 29 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-654-617-269739 (1-1034)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
DB 69 ATGGCGACGCCCTCGGCGCGCGCGAGTGCCTCTCTCTCGCGCGCGCGCGCG 128
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
DB 129 GCCGCGTCTGGCGACCGCGCGCGCGCGCTCCAGCGGTGTGTCGCGCGCG 185

RESULT 20
US-09-684-016-269739
; Sequence 269739, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 269739
; LENGTH: 1034
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION:
US-09-684-016-269739

Alignment Scores:
Pred. No.: 8,8e-14 Length: 1034
Score: 176.00 Matches: 35
Percent Similarity: 89.7% Conservative: 0
Best Local Similarity: 89.7% Mismatches: 4
Query Match: 92.1% Indels: 0
DB: 29 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-684-016-269739 (1-1034)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTrpPro 20
DB 69 ATGGCGACGCCCTCGGCGCGCGCGAGTGCCTCTCTCTCGCGCGCGCGCGCG 128
```

```
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArgArg 39
Db 129 GCCGGCTGCGGACCGCGCGCGCGCGCGCGCTCCAGCGCGTCTCCAGCGCGG 185

RESULT 21
US-09-850-147-1953
; Sequence 1953, Application US/09850147
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(51914)B
; CURRENT APPLICATION NUMBER: US/09/850,147
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 60/202,213
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/684,016
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 18014
; SEQ ID NO 1953
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; OTHER INFORMATION: Clone ID: LIB3476-015-P1-K1-B5
US-09-850-147-1953

Alignment Scores:
Pred. No.: 9.5e-10 Length: 370
Score: 143.50 Matches: 32
Percent Similarity: 77.3% Conservative: 2
Best Local Similarity: 77.3% Mismatches: 5
Query Match: 75.1% Indels: 5
DB: 33 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-850-147-1953 (1-370)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***Ala----- 18
Db 129 ATGGCGAGCGCTCGCGCGCGCGCGCTGCTCGTCTAGCGGAGCGCGCGCGG 188
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35
Db 189 CTGGGCTTTGGCGCGCGCGCGCGCGATCGGCGCGCGCGCGCTCCAGCGGTG 248
QY 36 LeuArgArgArg 39
Db 249 GTGCGCAGGCGG 260

RESULT 22
US-60-202-213-1950
; Sequence 1950, Application US/60202213
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(51914)A
; CURRENT APPLICATION NUMBER: US/60/202,213
; CURRENT FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 17986
; SEQ ID NO 1950
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; OTHER INFORMATION: Clone ID: LIB3476-015-P1-K1-B5
US-60-202-213-1950

Alignment Scores:
Pred. No.: 9.5e-10 Length: 370
Score: 143.50 Matches: 32
Percent Similarity: 77.3% Conservative: 2
Best Local Similarity: 77.3% Mismatches: 5
Query Match: 75.1% Indels: 5
DB: 33 Gaps: 1
```

```
Percent Similarity: 77.3% Conservative: 2
Best Local Similarity: 72.7% Mismatches: 5
Query Match: 75.1% Indels: 5
DB: 76 Gaps: 1

US-10-628-525A-37 (1-39) x US-60-202-213-1950 (1-370)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***Ala----- 18
Db 129 ATGGCGAGCGCTCGCGCGCGCGCGCTGCTCGTCTAGCGGAGCGCGCGCGG 188
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35
Db 189 CTGGGCTTTGGCGCGCGCGCGCGCGATCGGCGCGCGCGCGCTCCAGCGGTG 248
QY 36 LeuArgArgArg 39
Db 249 GTGCGCAGGCGG 260

RESULT 23
US-09-654-617-454633
; Sequence 454633, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 454633
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Sorghum bicolor
US-09-654-617-454633

Alignment Scores:
Pred. No.: 9.7e-10 Length: 376
Score: 143.50 Matches: 32
Percent Similarity: 77.3% Conservative: 2
Best Local Similarity: 72.7% Mismatches: 5
Query Match: 75.1% Indels: 5
DB: 29 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-654-617-454633 (1-376)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***Ala----- 18
Db 135 ATGGCGAGCGCTCGCGCGCGCGCGCTGCTCGTCTAGCGGAGCGCGCGCGG 194
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35
Db 195 CTGGGCTTTGGCGCGCGCGCGCGCGATCGGCGCGCGCGCGCTCCAGCGGTG 254
QY 36 LeuArgArgArg 39
Db 255 GTGCGCAGGCGG 266

RESULT 24
US-09-684-016-454633
; Sequence 454633, Application US/09684016
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/684,016
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 454633
; LENGTH: 376
```

```
/ TYPE: DNA
/ ORGANISM: Sorghum bicolor
US-09-684-016-454633

Alignment Scores:
Pred. No.: 9.7e-10 Length: 376
Score: 143.50 Matches: 32
Percent Similarity: 77.3% Conservative: 2
Best Local Similarity: 72.7% Mismatches: 5
Query Match: 75.1% Indels: 5
DB: 29 Gaps: 1

US-10-628-525A-37 (1-39) x US-09-684-016-454633 (1-376)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***Ala----- 18
Db 135 ATGGGACCCCTCGGCGCGCGCGCGTCTGCTCTAGCGGAGCCCGCGCGG 194
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35
Db 195 CTTGGCTTGGCGCGCGCGCGCGATCGGCGCGCGCGCGGCTCCAGCGCGTG 254
QY 36 LeuArgArgArg 39
Db 255 GTGCGAGCGCG 266

RESULT 25
US-10-767-701-13043
/ Sequence 13043, Application US/10767701
/ GENERAL INFORMATION:
/ APPLICANT: Kovacic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53535)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ CURRENT FILING DATE: 2004-01-29
/ NUMBER OF SEQ ID NOS: 63128
/ SEQ ID NO 13043
/ LENGTH: 2670
/ TYPE: DNA
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS52_1
US-10-767-701-13043

Alignment Scores:
Pred. No.: 1.32e-08 Length: 2670
Score: 143.50 Matches: 32
Percent Similarity: 77.3% Conservative: 2
Best Local Similarity: 72.7% Mismatches: 5
Query Match: 75.1% Indels: 5
DB: 61 Gaps: 1

US-10-628-525A-37 (1-39) x US-10-767-701-13043 (1-2670)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***Ala----- 18
Db 138 ATGGGACCCCTCGGCGCGCGCGCGTCTGCTCTAGCGGAGCCCGCGCGG 197
QY 19 -----TrpProAlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgVal 35
Db 198 CTTGGCTTGGCGCGCGCGCGCGATCGGCGCGCGCGCGGCTCCAGCGCGTG 257
QY 36 LeuArgArgArg 39
Db 258 GTGCGAGCGCG 269

RESULT 26
US-60-171-627-1369
/ Sequence 1369, Application US/60171627
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Yandell, Mark
/ TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS ESSENTIAL
/ TITLE OF INVENTION: FOR SURVIVAL, NUCLEIC ACID MOLECULES ENCODING ESSENTIAL
/ FILE REFERENCE: CL000177
/ CURRENT APPLICATION NUMBER: US/60/171,627
/ CURRENT FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 2237
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1369
/ LENGTH: 7492
/ TYPE: DNA
/ ORGANISM: Drosophila
US-60-171-627-1369

Alignment Scores:
Pred. No.: 410 Length: 7492
Score: 74.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 16
Query Match: 38.7% Indels: 0
DB: 75 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-171-627-1369 (1-7492)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTTPPro 20
Db 4941 ATGGGCACCAAGCAGCTTGGGCAAAATAGTATTGACCGCATCGCGAAGCCATGCGCG 5000
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 5001 GCTGTGTCAGAGATAGGCTTAAAGCAGGAGTTTGTAGTAGAATCTTCGC 5051

RESULT 27
US-60-173-464-14199
/ Sequence 14199, Application US/60173464
/ GENERAL INFORMATION:
/ APPLICANT: Li, Peter W.D.
/ TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR, PROTEINS AND USES
/ FILE REFERENCE: THEREOF
/ FILE REFERENCE: CL000173
/ CURRENT APPLICATION NUMBER: US/60/173,464
/ CURRENT FILING DATE: 1999-12-29
/ NUMBER OF SEQ ID NOS: 30269
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14199
/ LENGTH: 7492
/ TYPE: DNA
/ ORGANISM: Drosophila
US-60-173-464-14199

Alignment Scores:
Pred. No.: 410 Length: 7492
Score: 74.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 16
Query Match: 38.7% Indels: 0
DB: 75 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-173-464-14199 (1-7492)
QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTTPPro 20
Db 4941 ATGGGCACCAAGCAGCTTGGGCAAAATAGTATTGACCGCATCGCGAAGCCATGCGCG 5000
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 5001 GCTGTGTCAGAGATAGGCTTAAAGCAGGAGTTTGTAGTAGAATCTTCGC 5051

RESULT 28
US-60-167-217-17335
/ Sequence 17335, Application US/60167217
```

```
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W. D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; FILE REFERENCE: CL000152
; CURRENT APPLICATION NUMBER: US/60/167,217
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 23195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17335
; LENGTH: 7495
; TYPE: DNA
; ORGANISM: Drosophila
US-60-167-217-17335

Alignment Scores:
Pred. No.: 410 Length: 7495
Score: 74.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 16
Query Match: 38.7% Indels: 0
DB: 75 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-167-217-17335 (1-7495)

QY 1 MetaAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTtpPro 20
Db 4941 ATGGGCACCAAGAGCAGCTGGGCAATAGTATTTCACCGCATCGCGAAGCCATGGCCG 5000

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 5001 GCTGTGTCAGAGATAGGCTAAAGCAGGGATTTTAGTAGAATTCTTCGC 5051

RESULT 29
US-60-161-932-184
; Sequence 184, Application US/60161932
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containin the Nucleic Acid Sequences
; FILE REFERENCE: CL000122
; CURRENT APPLICATION NUMBER: US/60/161,932
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 2626
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 53583
; TYPE: DNA
; ORGANISM: Drosophila
US-60-161-932-184

Alignment Scores:
Pred. No.: 5,63e+03 Length: 53583
Score: 74.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 16
Query Match: 38.7% Indels: 0
DB: 75 Gaps: 0

US-10-628-525A-37 (1-39) x US-60-161-932-184 (1-53583)

QY 1 MetaAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTtpPro 20
Db 37623 ATGGGCACCAAGAGCAGCTGGGCAATAGTATTTCACCGCATCGCGAAGCCATGGCCG 37682

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 37683 GCTGTGTCAGAGATAGGCTAAAGCAGGGATTTTAGTAGAATTCTTCGC 37733

RESULT 30
US-09-528-237A-965/c
```

```
; Sequence 965, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; TITLE OF INVENTION: Sequences and Uses Thereof
; FILE REFERENCE: CL000284
; CURRENT APPLICATION NUMBER: US/09/528,237A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 965
; LENGTH: 54050
; TYPE: DNA
; ORGANISM: Drosophila
US-09-528-237A-965

Alignment Scores:
Pred. No.: 5,69e+03 Length: 54050
Score: 74.00 Matches: 16
Percent Similarity: 56.8% Conservative: 5
Best Local Similarity: 43.2% Mismatches: 16
Query Match: 38.7% Indels: 0
DB: 25 Gaps: 0

US-10-628-525A-37 (1-39) x US-09-528-237A-965 (1-54050)

QY 1 MetaAlaThrProSerAlaValGlyAlaAlaCysLeuLeuLeuAlaArg***AlaTtpPro 20
Db 15961 ATGGGCACCAAGAGCAGCTGGGCAATAGTATTTCACCGCATCGCGAAGCCATGGCCG 15902

QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArg 37
Db 15901 GCTGTGTCAGAGATAGGCTAAAGCAGGGATTTTAGTAGAATTCTTCGC 15851
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Search completed: April 2, 2006, 03:27:31  
Job time : 1078.11 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 1, 2006, 21:21:57 ; Search time 72.9357 Seconds  
(without alignments)  
1603.719 Million cell updates/sec

Title: US-10-628-525A-37

Perfect score: 191

Sequence: 1 MATPSNVGAACILLARXPAVGDPRRLQVLRRR 39

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6698573 seqs, 1499593917 residues

Total number of hits satisfying chosen parameters: 13397146

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/abes/ABSSWEB spool/US10628525/runat\_31032006\_095132\_17106/app.query.fasta\_1  
-DB=Pending Patents NA New -QPMT=fastap -SUFFIX=p2n.rnnp -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=150 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=30 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=abss06h  
-USER=US10628525 @CGN 1 1 1552 @runat\_31032006\_095132\_17106 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WAE TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending Patents NA New:  
1: /SID55/ptodata/2/pna/PCT NEW COMB.seq.\*  
2: /SID55/ptodata/2/pna/US05 NEW COMB.seq.\*  
3: /SID55/ptodata/2/pna/US07 NEW COMB.seq.\*  
4: /SID55/ptodata/2/pna/US08 NEW COMB.seq.\*  
5: /SID55/ptodata/2/pna/US09 NEW COMB.seq.\*  
6: /SID55/ptodata/2/pna/US10 NEW COMB.seq.\*  
7: /SID55/ptodata/2/pna/US10 NEW COMB.seq.1.\*  
8: /SID55/ptodata/2/pna/US11 NEW COMB.seq.\*  
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12: /SID55/ptodata/2/pna/US60 NEW COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	100.0	153	8	US-11-330-822-62
2	186	97.4	324	10	US-11-227-183A-9073
3	176	92.1	462	10	US-11-227-183A-17333
4	67	35.1	359	8	US-11-353-150-43602
5	67	35.1	1958	7	US-10-953-349-38532

6	67	35.1	1958	8	US-11-056-355B-8207	Sequence 8207, Ap
7	67	35.1	1958	8	US-11-056-355B-15424	Sequence 15424, A
8	66.5	34.8	520	8	US-11-353-150-13452	Sequence 13452, A
9	65.5	34.3	391	8	US-11-353-150-47903	Sequence 47903, A
10	65.5	34.3	441	8	US-11-353-150-5560	Sequence 5560, Ap
11	65.5	34.3	450	8	US-11-353-150-43740	Sequence 43740, A
12	65.5	34.3	506	8	US-11-353-150-12500	Sequence 12500, A
13	65.5	34.3	517	8	US-11-330-364-15086	Sequence 15086, A
14	65.5	34.3	549	8	US-11-353-150-14496	Sequence 14496, A
15	64.5	33.8	452	8	US-11-353-150-11403	Sequence 11403, A
16	64.5	33.8	12499	10	US-11-266-748A-30547	Sequence 30547, A
17	64	33.5	502	10	US-11-266-748A-13015	Sequence 13015, A
18	63	33.0	416	10	US-11-314-008-3670	Sequence 3670, Ap
19	63	33.0	2869	12	US-60-751-455-406	Sequence 406, App
20	63	33.0	8705	7	US-10-240-851A-10	Sequence 10, Appl
21	62.5	32.7	334	8	US-11-239-610A-7822	Sequence 7822, Ap
22	62.5	32.7	357	8	US-11-239-610A-18886	Sequence 18886, A
23	62.5	32.7	379	8	US-11-353-150-63898	Sequence 63898, A
24	62.5	32.7	395	8	US-11-353-150-47816	Sequence 47816, A
25	62.5	32.7	755	7	US-10-289-526-1524	Sequence 1524, Ap
26	62.5	32.7	2300	12	US-60-762-056-17573	Sequence 17573, A
27	62.5	32.7	2300	12	US-60-762-056-17574	Sequence 17574, A
28	62.5	32.7	2300	12	US-60-762-056-41263	Sequence 41263, A
29	62	32.5	1000	10	US-11-266-748A-395580	Sequence 395580, Sequence 466626,
30	62	32.5	1000	10	US-11-266-748A-466626	Sequence 466626, Sequence 5842, A
31	62	32.5	1258	8	US-11-056-355B-65842	Sequence 65842, A
32	62	32.5	1383	12	US-60-772-786-75	Sequence 75, Appl
33	62	32.5	2303	8	US-11-360-355-81526	Sequence 81526, A
34	62	32.5	2300	12	US-60-762-056-14174	Sequence 14174, A
35	62	32.5	3110	8	US-11-360-355-2775	Sequence 2775, Ap
36	62	32.5	3521	8	US-11-360-355-78416	Sequence 78416, A
37	62	32.5	3757	8	US-11-360-355-14379	Sequence 14379, A
38	62	32.5	9288	10	US-11-266-748A-22728	Sequence 22728, A
39	61.5	32.2	431	10	US-11-227-183A-979	Sequence 979, App
40	61.5	32.2	461	7	US-10-953-349-30799	Sequence 30799, A
41	61.5	32.2	2073	8	US-11-056-355B-65853	Sequence 65853, A
42	61	31.9	844	10	US-11-266-748A-94331	Sequence 94331, A
43	61	31.9	844	10	US-11-266-748A-147142	Sequence 147142, Sequence 26513,
44	61	31.9	1021	10	US-11-266-748A-262513	Sequence 262513, Sequence 323030,
45	61	31.9	1021	10	US-11-266-748A-323030	Sequence 323030, Sequence 33785, A
46	61	31.9	1097	7	US-10-953-349-33785	Sequence 33785, A
47	61	31.9	1097	8	US-11-056-355B-3807	Sequence 3807, Ap
48	61	31.9	1097	8	US-11-056-355B-5274	Sequence 5274, Ap
49	61	31.9	1097	8	US-11-056-355B-11617	Sequence 11617, A
50	61	31.9	1097	8	US-11-056-355B-13376	Sequence 13376, A
51	61	31.9	3213	10	US-11-266-748A-57722	Sequence 57722, A
52	61	31.9	3640	12	US-60-751-430-961	Sequence 961, App
53	60.5	31.7	266	1	PCT-US05-47111-543	Sequence 543, App
54	60.5	31.7	266	12	US-60-752-355-543	Sequence 543, App
55	60.5	31.7	535	6	US-10-515-373-615	Sequence 615, App
56	60.5	31.7	1088	10	US-11-266-748A-366896	Sequence 366896, Sequence 450275,
57	60.5	31.7	1088	10	US-11-266-748A-450275	Sequence 450275, Sequence 16437, A
58	60.5	31.7	2300	12	US-60-762-056-16437	Sequence 16437, A
59	60.5	31.7	2300	12	US-60-762-056-21708	Sequence 21708, A
60	60.5	31.7	2899	10	US-11-266-748A-26672	Sequence 26672, A
61	60	31.4	279	8	US-11-360-355-46316	Sequence 46316, A
62	60	31.4	436	8	US-11-360-355-32867	Sequence 32867, A
63	60	31.4	718	10	US-11-266-748A-214421	Sequence 214421, Sequence 237041,
64	60	31.4	718	10	US-11-266-748A-237041	Sequence 237041, Sequence 3, Appl,
65	60	31.4	936	7	US-10-502-832-3	Sequence 118260, Sequence 118260,
66	60	31.4	1000	10	US-11-266-748A-118260	Sequence 118260, Sequence 160424,
67	60	31.4	1000	10	US-11-266-748A-160424	Sequence 160424, Sequence 402945,
68	60	31.4	1000	10	US-11-266-748A-402945	Sequence 402945, Sequence 473991,
69	60	31.4	1000	10	US-11-266-748A-473991	Sequence 473991, Sequence 9, Appl,
70	60	31.4	1692	7	US-10-567-728-9	Sequence 9, Appl,
71	60	31.4	1758	8	US-11-174-307B-3643	Sequence 3643, Ap
72	60	31.4	2075	8	US-11-360-355-13119	Sequence 13119, A
73	60	31.4	2083	10	US-11-266-748A-72831	Sequence 72831, A
74	60	31.4	2083	10	US-11-266-748A-107509	Sequence 107509, Sequence 125642,
75	60	31.4	2083	10	US-11-266-748A-125642	Sequence 125642, Sequence 31506, A
76	60	31.4	2300	12	US-60-762-056-31506	Sequence 31506, A
77	60	31.4	2307	10	US-11-266-748A-27954	Sequence 27954, A
78	60	31.4	2669	10	US-11-288-493-65	Sequence 65, Appl

Sequence 3417, Ap		Sequence 49, Appl		Sequence 51, Appl		Sequence 35728, A		Sequence 385464, A		Sequence 439107, A		Sequence 250781, A		Sequence 311298, A		Sequence 11432, A		Sequence 24423, A		Sequence 25116, A		Sequence 25118, A		Sequence 1872, Ap		Sequence 1792, Ap		Sequence 8, Appl		Sequence 515, Appl		Sequence 23699, A		Sequence 66, Appl		Sequence 24973, A		Sequence 35887, A		Sequence 16754, A		Sequence 17605, A		Sequence 3050, Ap		Sequence 55029, A		Sequence 75881, A		Sequence 1190, Ap		Sequence 7356, Ap		Sequence 365564, A		Sequence 448943, A		Sequence 27765, A		Sequence 415618, A		Sequence 6427, Ap		Sequence 478666, A		Sequence 9327, Ap		Sequence 58785, A		Sequence 5651, Ap		Sequence 17390, A		Sequence 37356, A		Sequence 26690, A		Sequence 299, Appl		Sequence 61869, A		Sequence 76728, A		Sequence 108183, A		Sequence 119422, A		Sequence 4335, Ap		Sequence 37132, A		Sequence 31172, A		Sequence 9239, Ap		Sequence 22579, Ap		Sequence 30783, A		Sequence 65422, A		Sequence 29790, A		Sequence 12006, A		Sequence 13, Appl		Sequence 29722, A		Sequence 20, Appl		Sequence 23290, A		Sequence 45609, A		Sequence 7629, Ap		Sequence 70300, A		Sequence 5670, Ap		Sequence 13585, A		Sequence 15332, A		Sequence 98667, A		Sequence 151478, A		Sequence 188686, A		Sequence 242507, A		Sequence 178001, A																																																																																																																																																																																																																		
60	31.4	2674	12	US-60-751-420-3417	60	31.4	2884	8	US-11-370-121-49	60	31.4	2884	8	US-11-370-121-51	60	31.4	3301	10	US-11-266-748A-355728	60	31.4	3301	10	US-11-266-748A-385464	60	31.4	3301	10	US-11-266-748A-439107	60	31.4	3301	10	US-11-266-748A-250781	60	31.4	3301	10	US-11-266-748A-311298	60	31.4	3301	10	US-11-266-748A-11432	60	31.4	3301	10	US-11-266-748A-24423	60	31.4	3301	10	US-11-266-748A-25116	60	31.4	3301	10	US-11-266-748A-25118	60	31.4	3301	10	US-11-266-748A-1872	60	31.4	3301	10	US-11-266-748A-1792	60	31.4	3301	10	US-11-266-748A-8	60	31.4	3301	10	US-11-266-748A-515	60	31.4	3301	10	US-11-266-748A-23699	60	31.4	3301	10	US-11-266-748A-66	60	31.4	3301	10	US-11-266-748A-24973	60	31.4	3301	10	US-11-266-748A-35887	60	31.4	3301	10	US-11-266-748A-16754	60	31.4	3301	10	US-11-266-748A-17605	60	31.4	3301	10	US-11-266-748A-3050	60	31.4	3301	10	US-11-266-748A-55029	60	31.4	3301	10	US-11-266-748A-75881	60	31.4	3301	10	US-11-266-748A-1190	60	31.4	3301	10	US-11-266-748A-7356	60	31.4	3301	10	US-11-266-748A-85564	60	31.4	3301	10	US-11-266-748A-448943	60	31.4	3301	10	US-11-266-748A-27765	60	31.4	3301	10	US-11-266-748A-415618	60	31.4	3301	10	US-11-266-748A-6427	60	31.4	3301	10	US-11-266-748A-478666	60	31.4	3301	10	US-11-266-748A-9327	60	31.4	3301	10	US-11-266-748A-58785	60	31.4	3301	10	US-11-266-748A-5651	60	31.4	3301	10	US-11-266-748A-17390	60	31.4	3301	10	US-11-266-748A-37356	60	31.4	3301	10	US-11-266-748A-26690	60	31.4	3301	10	US-11-266-748A-299	60	31.4	3301	10	US-11-266-748A-61869	60	31.4	3301	10	US-11-266-748A-76728	60	31.4	3301	10	US-11-266-748A-108183	60	31.4	3301	10	US-11-266-748A-119422	60	31.4	3301	10	US-11-266-748A-4335	60	31.4	3301	10	US-11-266-748A-37132	60	31.4	3301	10	US-11-266-748A-31172	60	31.4	3301	10	US-11-266-748A-9239	60	31.4	3301	10	US-11-266-748A-22579	60	31.4	3301	10	US-11-266-748A-30783	60	31.4	3301	10	US-11-266-748A-65422	60	31.4	3301	10	US-11-266-748A-29790	60	31.4	3301	10	US-11-266-748A-12006	60	31.4	3301	10	US-11-266-748A-13	60	31.4	3301	10	US-11-266-748A-29722	60	31.4	3301	10	US-11-266-748A-20	60	31.4	3301	10	US-11-266-748A-149-20	60	31.4	3301	10	US-11-266-748A-23290	60	31.4	3301	10	US-11-266-748A-45609	60	31.4	3301	10	US-11-266-748A-7629	60	31.4	3301	10	US-11-266-748A-70300	60	31.4	3301	10	US-11-266-748A-5670	60	31.4	3301	10	US-11-266-748A-13585	60	31.4	3301	10	US-11-266-748A-15332	60	31.4	3301	10	US-11-266-748A-98667	60	31.4	3301	10	US-11-266-748A-151478	60	31.4	3301	10	US-11-266-748A-188686	60	31.4	3301	10	US-11-266-748A-242507	60	31.4	3301	10	US-11-266-748A-178001
79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150																																																																																																																																																																																																																																																																																	
ALIGNMENTS		RESULT 1		US-11-330-822-62		; Sequence 62, Application US/11330822		; GENERAL INFORMATION:		; APPLICANT: KEELING, PETER L.		; TITLE OF INVENTION: PLANT LIKE STARCHES AND THE METHOD OF MAKING THEM IN		; TITLE OF INVENTION: HOSTS		; FILE REFERENCE: 15053-04		; CURRENT APPLICATION NUMBER: US/11/330,822		; PRIOR FILING DATE: 2006-01-11		; PRIOR APPLICATION NUMBER: PCT/US98/06660		; PRIOR FILING DATE: 1998-04-03		; PRIOR APPLICATION NUMBER: 60/042,939		; PRIOR FILING DATE: 1997-04-04		; NUMBER OF SEQ ID NOS: 86		; SOFTWARE: PatentIn Ver. 3.3		; SEQ ID NO 62		; LENGTH: 153		; TYPE: DNA		; ORGANISM: Zea mays		; FEATURE:		; NAME/KEY: CDS		; LOCATION: (1)..(153)		US-11-330-822-62		Alignment Scores:		Pred. No.:		1.13e-18		Length:		153		Matches:		38		Conservative:		0		Misindels:		1		Indels:		0		Gaps:		0		US-10-628-525A-37 (1-39) x US-11-330-822-62 (1-153)		QY		1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro		20		Db		1 ATGGGACGCCCTCG																																																																																																																																																																																																																																																														



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Best Local Similarity: 97.4% Mismatches: 1
Query Match: 97.4% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-37 (1-39) x US-11-227-183A-9073 (1-324)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
DB 153 ATGGCGACGCCCTCGGCGCGTGGCGCGCTGCTCTTCTCGCGCGCGCTGGCGC 212
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38
DB 213 GCCCGCGTGGCGACCGCGCGCGCGCGCTCCAGCGCGTGTCTGCGCGCGC 266

RESULT 3
US-11-227-183A-17333
; Sequence 17333, Application US/11227183A
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated with
; FILE REFERENCE: 16517.336 - 38-21(51230)C/US
; CURRENT APPLICATION NUMBER: US/11/227,183A
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: US 09/619,643
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 32236
; SEQ ID NO 17333
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3151-012-Q1-K1-E9
US-11-227-183A-17333

Alignment Scores:
Pred. No.: 7,25e-16 Length: 462
Score: 176.00 Matches: 35
Percent Similarity: 89.7% Conservative: 0
Best Local Similarity: 89.7% Mismatches: 4
Query Match: 92.1% Indels: 0
DB: 10 Gaps: 0

US-10-628-525A-37 (1-39) x US-11-227-183A-17333 (1-462)

QY 1 MetAlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpPro 20
DB 69 ATGGCGACGCCCTCGGCGCGTGGCGCGAGTGTCTCTCTCGCGCGCGCTGGCGC 128
QY 21 AlaAlaValGlyAspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 39
DB 129 GCCCGCGTGGCGACCGCGCGCGCGCGCTCCAGCGGTGTCTGCGCGCGCGC 185

RESULT 4
US-11-353-150-43602
; Sequence 43602, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 43602
; LENGTH: 359
```

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; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3066-044-Q1-K1-F5
US-11-353-150-43602

Alignment Scores:
Pred. No.: 3,62 Length: 359
Score: 67.00 Matches: 22
Percent Similarity: 51.1% Conservative: 1
Best Local Similarity: 48.9% Mismatches: 10
Query Match: 35.1% Indels: 12
DB: 8 Gaps: 2

US-10-628-525A-37 (1-39) x US-11-353-150-43602 (1-359)

QY 6 AlaValGlyAlaAlaCysLeu-----LeuLeuAla 15
DB 170 GCTGCGAGCGCTGCTGTCTTACCACGTCTCTCCCTCGCGCTGCTCTCGACTCTCTGGCC 229
QY 16 Arg***AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgArgLeuGln 33
DB 230 CGCGCGTCTCCACCCACCGCTGTCCGCGAGGAGGTGAGCTCGCCCCCGCGCGCGC 289
QY 34 ArgValLeuArgArg 38
DB 290 CGGCATGCGCGTGG 304

RESULT 5
US-10-953-349-38532
; Sequence 38532, Application US/10953349
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38532
; LENGTH: 1958
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (208)..(208)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (247)..(247)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-38532

Alignment Scores:
Pred. No.: 33,4 Length: 1958
Score: 67.00 Matches: 22
Percent Similarity: 51.1% Conservative: 1
Best Local Similarity: 48.9% Mismatches: 10
Query Match: 35.1% Indels: 12
DB: 7 Gaps: 2

US-10-628-525A-37 (1-39) x US-10-953-349-38532 (1-1958)

QY 6 AlaValGlyAlaAlaCysLeu-----LeuLeuAla 15
DB 472 GCTGCGAGCGCTGCTGTCTTACCACGTCTCTCCCTCGCGCTGCTCTCGACTCTCTGGCC 531
QY 16 Arg***AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgArgLeuGln 33
DB 532 CGCGCGTCTCCACCCACCGCTGTCCGCGAGGAGGTGAGCTCGCCCCCGCGCGCGC 591
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QY 34 ArgValLeuArgArg 38
|||
Db 592 CGGCATGCGGTCGG 606

RESULT 6
US-11-056-355B-8207
; Sequence 8207, Application US/11056355B
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 8207
; LENGTH: 1958
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1958)
; OTHER INFORMATION: Ceres Seq. ID no. 13636500
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1958)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177043
; OTHER INFORMATION: as cited in SEQ ID NO 57425
US-11-056-355B-8207

Alignment Scores:
Pred. No.: 33.4 Length: 1958
Score: 67.00 Matches: 22
Percent Similarity: 51.1% Conservative: 1
Best Local Similarity: 48.9% Mismatches: 10
Query Match: 35.1% Indels: 12
DB: 8 Gaps: 2

US-10-628-525A-37 (1-39) x US-11-056-355B-8207 (1-1958)
QY 6 AlaValGlyAlaAlaCysLeu-----LeuLeuAla 15
|||
Db 472 GCTGCAGGCGCTGCTCTACACAGTCTCCCTCGCGCTCGCTCGGACTCTCTGGCC 531
|||
QY 16 Arg***AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgArgLeuGln 33
|||
Db 532 CGCGGCGTCCACCCACGCTGTCCGCGGAGGAGTGTGAGCTCGCCCCCGCGCGCGC 591
|||
QY 34 ArgValLeuArgArg 38
|||
Db 592 CGGCATGCGGTCGG 606

RESULT 7
US-11-056-355B-15424
; Sequence 15424, Application US/11056355B
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 15424
; LENGTH: 1958
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1958)
; OTHER INFORMATION: Ceres Seq. ID no. 13636500
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1958)
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177043
; OTHER INFORMATION: as cited in SEQ ID NO 57425
US-11-056-355B-8207

Alignment Scores:
Pred. No.: 33.4 Length: 1958
Score: 67.00 Matches: 22
Percent Similarity: 51.1% Conservative: 1
Best Local Similarity: 48.9% Mismatches: 10
Query Match: 35.1% Indels: 12
DB: 8 Gaps: 2

US-10-628-525A-37 (1-39) x US-11-056-355B-8207 (1-1958)
QY 6 AlaValGlyAlaAlaCysLeu-----LeuLeuAla 15
|||
Db 472 GCTGCAGGCGCTGCTCTACACAGTCTCCCTCGCGCTCGCTCGGACTCTCTGGCC 531
|||
QY 16 Arg***AlaTrpProAlaAlaVal-----GlyAspArgAlaArgProArgArgLeuGln 33
|||
Db 532 CGCGGCGTCCACCCACGCTGTCCGCGGAGGAGTGTGAGCTCGCCCCCGCGCGCGC 591
|||
QY 34 ArgValLeuArgArg 38
|||
Db 592 CGGCATGCGGTCGG 606

RESULT 8
US-11-353-150-13452
; Sequence 13452, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; FILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 13452
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: cC-zmpo14820021b07d1
US-11-353-150-13452

Alignment Scores:
Pred. No.: 6.95 Length: 520
Score: 66.50 Matches: 20
Percent Similarity: 51.1% Conservative: 3
Best Local Similarity: 44.4% Mismatches: 11
Query Match: 34.8% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-13452 (1-520)
QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTrp 19
|||
Db 294 GCGACCCCTGCGCGCGCGGCTGTGAGACGAAAGTGT-----CCAGGAGCGTGG 341
|||
; TYPE: DNA
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QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
    |||||
Db 342 CCGCGCGGCGGTGGAGGTGGAGTGGCGGCACCTTCGGCGCGGTCCAAGGAGACGCTCAAGG 401
    |||||
QY 35 ValLeuArgArgArg 39
    |||||
Db 402 CGGAGCGGACGACGG 416

RESULT 9
US-11-353-150-47903
; Sequence 47903, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 47903
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-028-Q1-K1-P2
US-11-353-150-47903

Alignment Scores:
Pred. No.: 6.69 Length: 391
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-47903 (1-391)

QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTTrp 19
    |||||
Db 202 CGGACCCCTGCGCGCGCGGTTCGAGACGACGTGT-----CCAGGAGCGGTGG 249
    |||||
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
    |||||
Db 250 CCGGCGCGACGGTGGAGGTGGTGGCGGCACCTTCGGCGCGGTCCAAGGAGACGCTCAAGG 309
    |||||
QY 35 ValLeuArgArgArg 39
    |||||
Db 310 CGGAGCGGACGACGG 324

RESULT 10
US-11-353-150-5560
; Sequence 5560, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 5560
```

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; LENGTH: 441
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB148-010-Q1-E1-H11
US-11-353-150-5560

Alignment Scores:
Pred. No.: 7.93 Length: 441
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-5560 (1-441)

QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTTrp 19
    |||||
Db 228 GCGACCCCTGCGCGCGCGGTTCGAGACGACGTGT-----CCAGGAGCGGTGG 275
    |||||
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
    |||||
Db 276 CCGGCGCGACGGTGGAGGTGGTGGCGGCACCTTCGGCGCGGTCCAAGGAGACGCTCAAGG 335
    |||||
QY 35 ValLeuArgArgArg 39
    |||||
Db 336 CGGAGCGGACGACGG 350

RESULT 11
US-11-353-150-43740
; Sequence 43740, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 43740
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-048-Q1-K1-E5
US-11-353-150-43740

Alignment Scores:
Pred. No.: 8.04 Length: 450
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-43740 (1-450)

QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTTrp 19
    |||||
Db 209 GCGACCCCTGCGCGCGCGGTTCGAGACGACGTGT-----CCAGGAGCGGTGG 256
    |||||
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
    |||||
Db 257 CCGGCGCGACGGTGGAGGTGGTGGCGGCACCTTCGGCGCGGTCCAAGGAGACGCTCAAGG 316
    |||||
QY 35 ValLeuArgArgArg 39
```

```

;
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(517)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3279-223-Q6-K6-A10
US-11-330-364-15086

Alignment Scores:
Pred. No.: 9.65 Length: 517
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-330-364-15086 (1-517)
QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTrp 19
Db 210 GCGACCCCTGCGCGCGCGGTTCCGAGACGAACGTGT-----CCAGGAGCGTGG 257
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 258 CCGGCGCGACGGTGGAGGTGTGTCGCGGCACCTTCGCGCGCTCCAAGGAGACGCTCAAGG 317
QY 35 ValLeuArgArgArg 39
Db 318 CGGAGGCGGACGACGG 332

RESULT 14
US-11-353-150-14496
; Sequence 14496, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 14496
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: cC-zmpo148068g10d1
US-11-353-150-14496

Alignment Scores:
Pred. No.: 10.4 Length: 549
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-14496 (1-549)
QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTrp 19
Db 194 GCGACCCCTGCGCGCGCGGTTCCGAGACGAACGTGT-----CCAGGAGCGTGG 241
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 242 CCGGCGCGACGGTGGAGGTGTGTCGCGGCACCTTCGCGCGCTCCAAGGAGACGCTCAAGG 301
QY 35 ValLeuArgArgArg 39

;
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(517)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3279-223-Q6-K6-A10
US-11-330-364-15086

Alignment Scores:
Pred. No.: 9.65 Length: 517
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-330-364-15086 (1-517)
QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTrp 19
Db 210 GCGACCCCTGCGCGCGCGGTTCCGAGACGAACGTGT-----CCAGGAGCGTGG 257
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 258 CCGGCGCGACGGTGGAGGTGTGTCGCGGCACCTTCGCGCGCTCCAAGGAGACGCTCAAGG 317
QY 35 ValLeuArgArgArg 39
Db 318 CGGAGGCGGACGACGG 332

RESULT 14
US-11-353-150-14496
; Sequence 14496, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 14496
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: cC-zmpo148068g10d1
US-11-353-150-14496

Alignment Scores:
Pred. No.: 10.4 Length: 549
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-14496 (1-549)
QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTrp 19
Db 194 GCGACCCCTGCGCGCGCGGTTCCGAGACGAACGTGT-----CCAGGAGCGTGG 241
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 242 CCGGCGCGACGGTGGAGGTGTGTCGCGGCACCTTCGCGCGCTCCAAGGAGACGCTCAAGG 301
QY 35 ValLeuArgArgArg 39

;
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(517)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3279-223-Q6-K6-A10
US-11-330-364-15086

Alignment Scores:
Pred. No.: 9.38 Length: 506
Score: 65.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 34.3% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-12500 (1-506)
QY 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuLeuAlaArg***AlaTrp 19
Db 209 GCGACCCCTGCGCGCGCGGTTCCGAGACGAACGTGT-----CCAGGAGCGTGG 256
QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
Db 257 CCGGCGCGACGGTGGAGGTGTGTCGCGGCACCTTCGCGCGCTCCAAGGAGACGCTCAAGG 316
QY 35 ValLeuArgArgArg 39
Db 317 CGGAGGCGGACGACGG 331

RESULT 13
US-11-330-364-15086
; Sequence 15086, Application US/11330364
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Andersen, Scott E.
; APPLICANT: Dubois, Patrice
; APPLICANT: Mahadeo, Debbie A.
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.352 - 38-21(51721)C/US
; CURRENT APPLICATION NUMBER: US/11/330,364
; CURRENT FILING DATE: 2006-01-12
; PRIOR APPLICATION NUMBER: US 09/696,664
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/161,619
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 17472
; SEQ ID NO 15086
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Zea mays
```

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Db 302 CGGAGGCGACGCG 316
|||||
RESULT 15
US-11-353-150-11403
; Sequence 11403, Application US/11353150
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Comer, Timothy W.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 16517,365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 11403
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: cc-zmpol48071b09b1
US-11-353-150-11403

Alignment Scores:
Pred. No.: 11.3 Length: 452
Score: 64.50 Matches: 20
Percent Similarity: 48.9% Conservative: 2
Best Local Similarity: 44.4% Mismatches: 12
Query Match: 33.8% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-11403 (1-452)
Qy 2 AlaThrProSerAlaValGlyAla-----AlaCysLeuLeuAlaArg***AlaTrp 19
|||||
Db 219 GCGACCCCTGCGCGCGGCTTCGAGACGAACTGT-----CCAGGAGCGTGG 266
|||||
Qy 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
|||||
Db 267 CCGGCGCGACGCGTGGAGGTGTGTGCGGCACCTTTGCGCGCTCAAGGAGCGCTCAAGG 326
|||||
Qy 35 ValLeuArgArgArg 39
|||||
Db 327 CGGAGGCGACGACGG 341

RESULT 16
US-11-266-748A-30547/c
; Sequence 30547, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
```

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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30547
; LENGTH: 12499
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-30547

Alignment Scores:
Pred. No.: 874 Length: 12499
Score: 64.50 Matches: 21
Percent Similarity: 40.7% Conservative: 3
Best Local Similarity: 35.6% Mismatches: 10
Query Match: 33.8% Indels: 25
DB: 10 Gaps: 2

US-10-628-525A-37 (1-39) x US-11-266-748A-30547 (1-12499)
Qy 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrpProAla 21
|||||
Db 206 GCGTGGCGCGCTGCTCCAGCGCGAGCTGT-----AGCGCGGAGACAGCGCTCCA 156
|||||
Qy 22 AlaValGly----- 24
|||||
Db 155 GCTCTGGGCAAGCGAACTCTCTGCGACGCGCGCGCGCGCTTGTCTCCGG 96
|||||
Qy 25 -----AspArgAlaArgProArgArgLeuGlnArgValLeuArgArg 38
|||||
Db 95 CCGCGCGCTCGGCGCGCGCGCTGCGCGCGCGCTCGCGCGCGCTCGCGCGCGCTCGCGCGCG 39

RESULT 17
US-11-266-748A-13015/c
; Sequence 13015, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13015
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (332)..(332)
; OTHER INFORMATION: n is a, c, g, or t
```





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; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 16517.365 - 38-21(15459)D/US
; CURRENT APPLICATION NUMBER: US/11/353,150
; CURRENT FILING DATE: 2006-02-14
; PRIOR APPLICATION NUMBER: 09/565,386
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/132,860
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 83523
; SEQ ID NO 47816
; LENGTH: 395
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-034-Q1-K1-E10
US-11-353-150-47816

Alignment Scores:
Pred. No.: 18.5 Length: 395
Score: 62.50 Matches: 19
Percent Similarity: 48.9% Conservative: 3
Best Local Similarity: 42.2% Mismatches: 12
Query Match: 32.7% Indels: 11
DB: 8 Gaps: 3

US-10-628-525A-37 (1-39) x US-11-353-150-47816 (1-395)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeuAlaArg***AlaTrp 19
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 207 GCGACCCCTGCGCGCGCGGTTCCGAGACGACGTGT-----CCAGGAGCGTGG 254
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 20 ProAla-----AlaValGlyAspArgAlaArgProArgArgLeuGlnArg 34
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 255 CCGGCGCGACGGTGAGGTGGTGCCGCGCACTTCGCGCGCTCCAAAGAGACGCTCAAGG 314
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 35 ValLeuArgArgArg 39
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 315 CGGAGCGCGACGACGG 329
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 25
US-10-289-526-1524/c
; Sequence 1524, Application US/10289526
; GENERAL INFORMATION:
; APPLICANT: Askenazi, Manor
; APPLICANT: Driggers, Edward M.
; APPLICANT: Norman, Thea
; APPLICANT: Zimmer, Daniel P.
; APPLICANT: Royer, John C.
; APPLICANT: Salama, Sofie R.
; APPLICANT: Trueheart, Joshua
; APPLICANT: Madden, Kevin T.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING GENES REGULATING
; FILE OF INVENTION: METABOLITE PRODUCTION
; FILE REFERENCE: 14184-017001
; CURRENT APPLICATION NUMBER: US/10/289,526
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/332,903
; PRIOR FILING DATE: 2001-11-06
; NUMBER OF SEQ ID NOS: 1912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1524
; LENGTH: 755
; TYPE: DNA
; ORGANISM: Aspergillus terreus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) . . (755)
; OTHER INFORMATION: n = A,T,C or G
US-10-289-526-1524

Alignment Scores:
Pred. No.: 43.2 Length: 755
```

```
Score: 62.50 Matches: 18
Percent Similarity: 48.9% Conservative: 4
Best Local Similarity: 40.0% Mismatches: 16
Query Match: 32.7% Indels: 7
DB: 7 Gaps: 2

US-10-628-525A-37 (1-39) x US-10-289-526-1524 (1-755)

QY 2 AlaThrProSerAlaValGlyAlaAlaCysLeuLeu-----LeuAla 15
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 715 GCTCAGCAGCGTGGCGCGCGCACCGCGGTGTACTGCATCTTGCCCGCTTGGCGCGGTGGCC 656
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 16 Arg***AlaTrpProAlaAlaValGlyAspArgAlaArgPro---ArgArgLeuGlnArg 34
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 655 CGGCGAGTGTGGCTTGCAGACACCACGACCGCGCTGCTGGTGGCGTCCGCTGGAGGAGG 596
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 35 ValLeuArgArgArg 39
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 595 ACGATCGCGCGCGCG 581
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 26
US-60-762-056-17573
; Sequence 17573, Application US/60762056
; GENERAL INFORMATION:
; APPLICANT: Trinklein, Nathan D
; APPLICANT: Aldred, Shelley Force
; APPLICANT: Cooper, Sara J
; APPLICANT: Myers, Richard M
; TITLE OF INVENTION: FUNCTIONAL ARRAYS FOR HIGH THROUGHPUT CHARACTERIZATION OF GENE
; FILE OF INVENTION: EXPRESSION REGULATORY ELEMENTS
; FILE REFERENCE: 33102-701.102
; CURRENT APPLICATION NUMBER: US/60/762,056
; CURRENT FILING DATE: 2006-01-24
; NUMBER OF SEQ ID NOS: 45096
; SEQ ID NO 17573
; LENGTH: 2300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-762-056-17573

Alignment Scores:
Pred. No.: 186 Length: 2300
Score: 62.50 Matches: 18
Percent Similarity: 66.7% Conservative: 6
Best Local Similarity: 50.0% Mismatches: 10
Query Match: 32.7% Indels: 2
DB: 12 Gaps: 1

US-10-628-525A-37 (1-39) x US-60-762-056-17573 (1-2300)

QY 5 SerAlaValGlyAlaAlaCysLeuLeuAlaAlaArg***AlaTrpProAlaAlaValGly 24
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1662 TCGGCGCGTGGTGGCGGTGCTCCGACGCTGGCT---CGCTCTATCCGCTTTGCTAGGG 1718
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 25 AspArgAla-ArgProArgArgLeuGlnArgValLeuArgArgArg 39
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1719 GAGTGAGTCCGCGCGCGCGAACCAGCGGCTGAGGAGCGCGG 1764
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 27
US-60-762-056-17574
; Sequence 17574, Application US/60762056
; GENERAL INFORMATION:
; APPLICANT: Trinklein, Nathan D
; APPLICANT: Aldred, Shelley Force
; APPLICANT: Cooper, Sara J
; APPLICANT: Myers, Richard M
; TITLE OF INVENTION: FUNCTIONAL ARRAYS FOR HIGH THROUGHPUT CHARACTERIZATION OF GENE
; FILE OF INVENTION: EXPRESSION REGULATORY ELEMENTS
; FILE REFERENCE: 33102-701.102
; CURRENT APPLICATION NUMBER: US/60/762,056
; CURRENT FILING DATE: 2006-01-24
; NUMBER OF SEQ ID NOS: 45096
; SEQ ID NO 17574
```



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; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 466626
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-466626

Alignment Scores:
Pred. No.:      73.8      Length:      1000
Score:          62.00      Matches:      14
Percent Similarity: 54.8%      Conservative: 3
Best Local Similarity: 45.2%      Mismatches: 10
Query Match:      32.5%      Indels:      4
DB:               10      Gaps:        1

US-10-628-525A-37 (1-39) x US-11-266-748A-466626 (1-1000)

QY      4 ProSerAlaValGlyAlaAlaCysLeuLeu-----LeuAlaArg***AlaTrp 19
Db      333 CTGGAGTCTCTGGTTCTGCGCCCTTCTGCGCGCACCCCTCTCGCGAGTCCACTGG 392

QY      20 ProAlaAlaValGlyAspArgAlaArgProArg 30
Db      393 GGGGCGCAGCGGGCTCCAGAGCCAGGCTCGG 425

Search completed: April 2, 2006, 04:06:47
Job time : 79.9357 secs

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